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Wang, O., Fang, F., Fu, Y., Pan, H., Edelmann, L. and Roe, B.A.
Direct Submission
Submitted (17-DEC-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
7 (bases 1 to 2007)
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Submitted (26-JAN-2000) Department Of Chemistry
Submitted (26-JAN-2000) Department Of Chemistry
Submitted (03-FEB-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                     Wang, Q., Fang, F., Direct Submission
                                                                                                                                          OK 73019, USA
                                                                                                                                                                     Submitted (01-FEB-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Wang,Q., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A.
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The University Of Oklahoma, 620 Parrington Oval, Room 208
OK 73019, USA
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Wang, C., Fang, F., Fu, Y., Pan, H., Edelmann, L. and Roe, B.A. Homo sapiens Chromosome 22q12 PAC Clone pac699j1 In CES-DGCR Regi
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                                                                                                                                                                                                                                                                                                                                                                   18 GAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGAC
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                                                                                                                                CAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Mar 12, 2000 this sequence version replaced gi:6958024. Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below. AC008132(pac99506) 136107 145670 (0) overlaps AC008103(pac699j1) 1 32871 175358 (0) overlaps AC008103(pac699j1) 1 44355 (54202) AC007325(b48) 71505 165050 (0) overlaps AC008103(pac699j1) 1 44355 (54202) AC007325(b48) 71505 165050 (0) overlaps AC008103(pac699j1) 1 49144 (4413) AC008103(pac699j1) 56194 98557 (0) overlaps AC007326(p423) 1 42365 (60533).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The University Of Oklahoma, OK 73019, USA 11 (bases 1 to 98557)
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Submitted (05-FEB-2000) Department Of Chemistry & Submitted (05-FEB-2000) 
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4 (bases I to 106650)
Zhan, M. and Roe, B.A.
                                                                                                            OR 73019, USA
ON Sep 25, 1999 this sequence version replaced gi:5919292.
On Sep 25, 1999 this sequence version replaced gi:5919292.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.
AC008018(b379n11) 146090 180888 (0) overlaps AC007708(b563b9) 1
34927 (71723) AC007708(b563b9) 1843 106650 (0) overlaps
AC009288(p413m7) 1 101851 (39025).
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Zhan, M. and Roe, B.A.
Direct Submission
Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
Submitted (31-MAY-2000) Department Of Chemistry,
Submitted
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Submitted (13-MAY-2000) Dep
The University Of Oklahoma,
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Direct Submission
Submitted (25-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University Of Oklahoma,
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5 (bases 1 to
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HTG.
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/organism="Homo sapiens"
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                                                                   1. .106650
                                                                                     Location/Qualifiers
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om 208, Norman,
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Local Similarity 84.78;
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Hua,A., Emanuel,B. and Roe,B.A.

Direct Submission
Submitted (19-NOV-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                       OK 73019, USA
3 (bases 1 to 140876)
                                                                                                       Submitted (13-AUG-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                           2 (bases 1 to 140876)
Hua,A., Emanuel,B. and Roe,B.A.
Direct Submission
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2 (bases l
                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 140876)
Hua, A., Emanuel, B. and Roe, B.A.
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Pred. No. 1.7e-23;
0; Mismatches 69
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Local Similarity 84.5%;
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5 (bases 1 to 140876)
Hua.A., Emanuel.B. and Roe,B.A.
Direct Submission
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Direct Submission

Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 520 Parrington Oval, Room 208, Norman
                                                                                           AC007981 175358 bp DNA linear PRI 27-M
Homo sapiens chromosome 22q11 clone b291, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 140876)
            Homo sapiens
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/clone="p413m7"
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/db_xref="taxon:9606"
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Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata;

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(bases 1 to 175358)

Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.

Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.

Direct Submission

Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry,

Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry,

Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry,
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Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Koe,B.A.
Direct Submission
Submitted (15-JAN-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                          OK 73019, USA
On May 20, 2000 this sequence version replaced g1:7940350.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.
AC008132(pac99506) 4747 145670 (0) overlaps AC007981(b291) 1 142425 (32936) AC007981(b291) 59901 175358 (0) overlaps AC007325(b48) 1 115948 (49102) AC007981(b291) 132871 175358 (0) overlaps
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OK 73019, USA
5 (bases 1 to 175358)
Fu.Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.
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Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.
Direct Submission
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Submitted (08-JAN-2000) Department Of Chemistry And Biochemistry.
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OK 73019, USA
OK 73019, USA
OK 75019, USA
Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.
Direct Submission
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Submitted (20-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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1 (bases 1 to 175358)
Fu.Y., Pan, H., Shaikh, T., Kurahashi, H., Emanuel, B. and Roe, B.A.
Homo sapiens Chromosome 22q11 BAC Clone b291 In CES-DGCR Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The University Of Oklahoma, 620 Parrington Oval,
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/chromosome="22q11"
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/db_xref="taxon:9606"
                                                                                                                                                            Location
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                                                                                                                                                         Qualifiers
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                                         3 (bases 1 to 180884)
Zhan,M. and Roe,B.A.
Direct Submission
Submitted (01-NOV-1999) Depai
The University Of Oklahoma, (
OK 73019, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180884)
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Homo sapiens chromosome 22q11 clone
AC008018
                                                                                                                                                                                                   Zhan,M. and Roe,B.A.

Direct Submission
Submitted (10-JUL-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
4 (bases 1 to 180884)
Zhan, M. and Roe, B.A.
                                                                                                                                                                                                 OK 73019,
                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                      Department Of Chemistry And Biochemistry, oma, 620 Parrington Oval, Room 208, Norman
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Qy 422 GGACGCCCAGGGAATCGCCGAGGATGTCGCCAAGGGATCGCCAACGAGGACGCCGC 481
Qy 362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
OY 302 CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC 361
QY 242 CCACGCTTCGCCAACGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGG 301
QY 182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
QY 122 CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGT 181
OY 65 CGCTAATGAGGACCACCCACTGCATCGCCAACGAGGAAGCCGCCAGGGCATCGC 121
Qy 5 CTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCAT. 64
Query Match 65.1%; Score 325.4; DB 9; Length 180884; Best Local Similarity 81.0%; Pred. No. 1.1e-21; Matches 404; Conservative 0; Mismatches 91; Indels 4; Gaps 2;
FEATURES Location/Qualifiers 1180884 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="23q11" /chromosome="23q11" BASE COUNT 48190 a 42579 c 41490 g 48625 t ORIGIN
ON 73019, USA COMMENT On May 20, 2000 this sequence version replaced gi:7940354. Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single
REFERENCE 6 (bases I to 180884) AUTHORS Zhan,M. and Roe,B.A. TITLE Direct Submission JOURNAL Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
REFERENCE 5 (bases 1 to 180884) AUTHORS Zhan, M. and Roe, B.A. TITLE Direct Submission JOURNAL Submitted (20-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
TITLE Direct Submission JOURNAL Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, HSA

Search completed: October 10, 2002, 18:41:42 Job time: 1359.87 secs

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Sequence 16 from Patent WO0153349.
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                                                                        Small cell lung cancer associated antigens and uses therefor Patent: WO 0153349-A 16 26-JUL-2001; LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL SLOAM-KETTERING CANCER CENTER (US); CORNELL RESEARCH FOUNDATION, INC. (US)
                                                                                                                                                                             Chen, Y.T
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 748)
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Homo sapiens
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/organism="Homo sapiens"
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AC011718 Homo sapi
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U75930 Orgyia pseu
AL022022 Mycobacte
AL355585 Homo sapi
AP003373 Oryza sat
AL117481 Homo sapi
AL123069 Homo sapi
AL13561 Homo sapi
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tch 100.0%; Score 500; DB 6; al Similarity 100.0%; Pred. No. 1.6e-36; 500; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                  Small cell lung cancer associated antigens and uses therefor Patent: WO 0153349-A 15 26-JUL-2001; LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL
                                                                                                                                                                                                                                                                                                         Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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                                                                                                                                                                                                                                                                                         Stockert, E., Scanlan, M.J., Jager, D., Old, L.J., Gure, A.O. and
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                                                                                                                                                                                                                                                Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                         Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2448 bp mRNA linear PRI 18-FEB-2000
Homo sapiens mRNA; cDNA DKFZp434Cl96 (from clone DKFZp434Cl96);
Partial cds.
                                                                                                                                                                                                                                  Genome Project.
                                                                                                                                                                                                                                                                                                                                                                Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S Direct Submission
                                                                                                                                                                                                                  This clone (DKFZp434C196) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL133561.1 GI:6599133
/clone="DKFZp434C196"
/tissue_type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
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polyA_signal
polyA_site
BASE COUNT 64
                                                                                       DEFINITION
                                                                                                                                                        RESULT 4
AL356585/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                          CCCAGGGCATCGCCAACAAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGACGCCGCCCAGGGATCGCCGAGGATGTCGCCACAGGGCATCGCCAACGAGGACGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATCGCTAATGAGGACACCACCCAGGGCATCGCCAACGAGGAAGCCGCCCAGGGCATCG 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGACGCCGCCCAGGGAATCGCCGAGGATGTCGCCACAGGGCCAACGAGGACGCCG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCCCAGGGCATCGCCAACG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCGCCAACGGGGACGCCACCAAGGGCCATGGGCAACGAGGTCACCATCCACGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499;
Homo sapiens chromosome 13 clone RPI1-341D18, PROGRESS ***, 13 unordered pieces. AL356585
                                                                                                                            AL356585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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2418
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<1. .1744
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/db_xref="GI:6599134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
1. .1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DKFZp434C196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              727 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 g
                                                                                                                        184590 bp
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                                                                                                                        linear
                                                                                   *** SEQUENCING
                                                                                                                        HTG 20-JAN-2001
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SOURCE
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                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                     source
             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LOB752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 179028 bases at least 040
Consensus quality: 181067 bases at least 020
Consensus quality: 182019 bases at least 020
Insert size: 183390; sum-of-contigs
Insert size: 183390; sum-of-contigs
Ouality coverage: 4.32x in 020 bases; sum-of-contigs
Ouality coverage: 4.32x in 020 bases; sum-of-contigs
Coverage: 4.20x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requests: clonerequest@sanger.ac.uk
On Aug 14, 2000 this sequence version replaced gi:9213941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97290 97389; gap of 100 bp 100519; contig of 3128 bp in length 100518 100617; gap of 100 bp 100618 116404; contig of 15787 bp in length 116405 116504; gap of 100 bp 116505 124935; contig of 100 bp in length 124936 125035; gap of 100 bp 125036 127757; contig of 2722 bp in length 127758 127857; gap of 100 bp 100 bp 1006187; gap of 1
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36486 36585: gap of 100 bp
61227 61326: gap of 100 bp
61327 66064: contig of 24641 bp in length
61327 66064: contig of 24738 bp in length
86065 86164: gap of 100 bp
92535 92534: contig of 6370 bp in length
92535 97380: contig of 6370 bp in length
92535 97380: contig of 4655 bp in length
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157030 184590: contig of 27561 bp in length
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140284 143272: cont
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1. .36485
                                                                                                                                                                                                                                                         Location/Qualifiers
1. .184590
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contig of 2989 bp
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Db 122923 TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCAGG 122864
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                                                                                                                                                                                                                                                                                              Db 123103 GCATCGCTAATGAGGACACCACCCAGGGCATCGCCAACGAGGAAGCCGCCCCAGGGCATCG
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ORIGIN
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Best Local :
                            misc_feature
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361 CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACG
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OY 421 AGBACGCCCCAGGGAATCGCCGAAGATCTCCCCAAGGGCATCGCCAACGAGGACGCCG 480
Db 122743 AGGACGCCCAGGGAATCGCCGAAGGATGTCGCCACAGGGCATCGCCAACGAGGACGCCG 122684
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Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a complete sequence of the insert of KB1183D5 clone. The proximal adjacent clone is KB876E2 (Acc. #AP000551) with 379-bp overlapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone KB1183D5 on chromosome 22q11.2 published Only in DataBase (1999) In press 2 (bases 1 to 157086)
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/ PU_lemily = Aluse/y / /evidence=not.experimental 20593. 20669 / rpt_family="Aluse/q" / rpt_family="Aluse/q" / evidence=not_experimental	/evidence=not_experimental complement(2037520445) /rnt familv="aluen/c"	20326 20374 /rpt_family="(TG)n"	<pre>/rpt_tamily="AluSp/q" /evidence=not_experimental</pre>	<pre>/evidence=not_experimental complement(20308 . 20325)</pre>	<pre>complement(20025 . 20302) /rpt_family="AluSg"</pre>	<pre>/rpt_family~"AluY" /evidence=not_experimental</pre>	n d	<pre>complement(1946619612) /rpt_family="L2"</pre>	/rpt_family="AluJo" /evidence=not_experimental	/evidence=not_experimental 18300 18602	<pre>/rpt_family~"AluJo"</pre>	/rpc_ramity="(TTTTA)n" /evidence=not_experimental	18019. 18049	/rpt_family="AluJo"	/evidence=not_experimental complement(1786118018)	complement(1769617816) /rpt_family="FLAM_A"	/rpt_family="EIMB7" /evidence=not_experimental	/evidence=not_experimental 16231. 16940	/rpt_family="AluJo"	/+pt_romity = http://experimental /evidence=not_experimental comn!ement/15025 16230)	15911 15924 /rpt family="17MB7"	/rpt_family="L2" /rpt_family="L2" /evidence=not experimental	/evidence=not_experimental 1561815788	1515615239 /rpt_family="Charlie4"	/rpt_ramity="Alusx" /evidence=not_experimental	complement(1488715155)	/rpt_family="Charlie4"		<pre>complement(1475914875) /rpt_family="FLAM_C"</pre>	/rpt_family="AluJo" /evidence=not_experimental	$\sim a$	<pre>complement(1241812736) /rpt_family="AluSq"</pre>	<pre>/rpt_family="(TTAA)n" /evidence=not_experimental</pre>		/evidence=not_experimental 1105411343 /rot family="Almsx"
Query Match Best Local Simila Matches 422; Co	repeat_region		repeat_region	repeat_region		repeat_region	repeat_region		repeat_region	repeat_region		repeat_region		repeat region	repeat_region		repeat_region	repeat_region		repeat_region		repeat_region	repeat_region		repeat_region	norfar_radar		repeat_region		repeat_region	repeat_region		repeat_region	repeat_region	repeat_region
71.9%; Score 359.4; DB 9; Larity 86.3%; Pred. No. 1.le-24; Conservative 0; Mismatches 61;	39119391/3 /rpt_family="LlPA16"	/rpt_ramily="LiPA16" /evidence=not_experimental		/rpt_family="AluSg/x"	<pre>/rpt_family="MIR" /evidence=not_experimental</pre>	<pre>/evidence=not_experimental 3850638612</pre>	38069. 38351 /rpt_family="AluSg"	<pre>/rpt_family="Aluy" /evidence=not_experimental</pre>	/evidence=not_experimental 3748037793	/rpt_family="MLT1E2"	/rpc_id=ntiy= muit /evidence=not_experimental	/evidence-not_experimentar 37016, 37083	/rpt_family="Alusg"	/evidence=not_experimental 3642136721	complement(3583335996) /rpt_family="MER5B"	<pre>/rpt_family="AluSg/x" /evidence=not_experimental</pre>	/evidence=not_experimental 3555935661	complement(30/4831041) /rpt_family="AluJo"	/evidence-not_experimental	7630826508 /rot family="A});;To"	/rpt_family="(A)n" /ovidence=not experimental	/evidence=not_experimental 2585825885	25627. ,25853 ∕rpt familv="AluSx"	<pre>/rpt_family="AluYa8" /evidence=not_experimental</pre>	complement(2531025609)	/rpt_family="Aluxb8"	/evidence=not_experimental	complement(2467824968) /rot family="Alusx"	<pre>/rpt_family="Aluy" /evidence=not_experimental</pre>	/evidence=not_experimental 2443924588	<pre>complement(2175921862) /rpt_family="AluSp/q"</pre>	<pre>/rpt_family="AluSg" /evidence=not_experimental</pre>	/evidence=not_experimental complement(2148221758)	2118621481 /rpt_family="AluY"	<pre>complement(2088521149) /rpt_family="Alux" /evidence=not experimental</pre>
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                                                                                                                      4 (bases 1 to 150754)
5 (bases 1 to 150754)
6 (bases 1 to 150754)

OK 73019, USA

5 (bases 1 to 150754)

Hu,P., Wu,H., Yang,L., Morrow,B.E. and Roe,B.A
Direct Submission
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Submitted (26-JUN-2000) Department Of Chemistry And Biochemistry, Submitted (26-JUN-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hu,P., Wu,H., Yang,L., Morrow,B.E. and NUE,B.A. Direct Submission
Submitted (14-FEB-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 150754)

14, P., Wu, H., Yang, L., Morrow, B.E. and Roe, B.A.

140, P., Wu, H., Yang, C., Morrow, B.E. and Roe, B.A.

150, Homo sapiens Chromosome 22q11 BAC Clone 659m11 In BCRL2-GGT Region Unpublished
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Homo sapiens chromosome 22q11 clone unknown, complete sequence,
AC023491
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P., Wu, H., Yang, L.,
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RESULT 7 AP000550

ACCESSION VERSION

AP000550.1 GI:5931536

DEFINITION

Homo sapiens genomic DNA, chromosome 22q11.2, BCRL2 region, clone:KB1592A4.

PRI 01-0CT-1999

Snoor

KEYWORDS

ORGANISM

BAC library clone:KB1592A4.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens pre-pro-B cell cell_line:FLEB14-14 DNA, clone_lib:Keio

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                                                                                             Db 110813 GGCATCGCCAAGGAGGACGCCGCCCAGGGCATCGCCAAGGACGCCGCCCAGGGCATC 110754
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Direct Submission
Submitted (21-JUL-2000) Department Of Chemistry And Biochemistry,
Directify Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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On Jul 21, 20
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6 (bases 1 to 150754)
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/db_xref="taxon:9606"
/chromosome="22q11"
/clone="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.6%; Score 357.8; DB 9; Length 150754; 86.1%; Pred. No. 1.5e-24;
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/evidence-not_experimental /evidence-not_experimental complement(59425625) /rpt_family="LIM1"	/evidence-not_experimental /evidence-not_experimental complement(3535554) /rot family-will	/evidence=not_experimental /evidence=not_experimental complement(49635286) /rnf family="""" ""	/FPC_temily="Lift4" /evidence=not_experimental 4617.4637 /rot_fam;li_midalin		/ Price in the second of the s	/rpt_family="AluJb" /evidence=not_experimental 2578.2875	/rpt_family="12"/rpt_family="12" /rpt_family="12" /rpt_family="10" /r	Complement('5' 662) Trpt_family="MIR" Peridence-not_experimental	/complement(/1//32) /rpt_family="L2" /rpt_family="L2" /evidence-not_experimental	/rpt.family="(TCCA)n" /rpt.family="(TCCA)n" /evidence=not_experimental	/ryt_tamily="MIR" /ryt_tamily="MIR" /ryt_tamily="MIR" /ryt_tamily="MIR"	/evidence=not_experimental complement(572640)	complement(401. 570) /rpt_family="LTR33"	/complement(99399) /rpt_family="Alusg" /rpt_family="Alusg" /retdence=pot experiments)	complement(190) /rpt_family="Alus" /evidence=not_experimental	/clone_lib="Keio BAC library" /map="22q11.2"	/cell_type="pre-pro-m cell" /chromosome="22" /clone="Km1592A4"	/db_xref="fxxon:9606" /dell_line="FLEB14-14"	ocation/Qualifiers	This is a complete sequence of the insert of K81592A4 clone. The distal adjacent clone is KB876E2 (Acc.#AP000551) with 1196-bp	Nobuyoshi Shinaizu, Kelo University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan (E-mail:nshinizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370,	mission // 27-ceps-1000/ +o +be pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//pro//forpark databage // 27-ceps-1000/ +o +be pro//pro//pro//pro//pro//pro//pro//pro/	DNA sequence from clone KB1592A4 on chromosome 22q11.2 shed Only in DataBase (1999) In press ases 1 to 150724)	Eutheria; Primates; Catarrhini; Hominidae; Homo.
repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	To be considered to the second	reneat region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region
complement(1477114238) /rpt_family="MIT1E" /evidence=not_experimental	complement(13882: .14031) /rpt_family="MLT1E2" /evidence=not experimental	complement(1345913774) /rpt_family="Alux"	/evidence=noc_experimental complement(1290113183) /rpt_family="AluSg"	/evidence-not_experimentar complement(12640 .12746) /rpt_family="MIR"	/evidence-not_experimentar 12231. 12416 /rpt_family="L1P"	/evidence=not_experimental complement(11911 .12230) /rpt_family="LlPA6" /rpt_family="LlPA6"	/rpt_family="LIM2"	/rpt_iamliy="LIM/" /evidence=not_experimental 1154011728	/rpc_rdmily= hima/ /evidence=not_experimental 1133211537	/evidence-not_experimental complement (10867. 11330)	/evidence=not_experimental 1054810734	10013. 10508 /rpt_family="L1ME2"	<pre>/rpt_family="L1ME2" /evidence=not_experimental</pre>	<pre>/rpt_family="L1ME2" /evidence=not_experimental q324</pre>	<pre>/rpt_family="AluSx" /evidence=not_experimental 92249298</pre>	/evidence=not_experimental complement(86798980)	/evidence=not_experimental complement(80758296) /rpt family="L1PA8"	/evidence=not_experimental complement(67787721) /rpt_family="L1MA6"	complement (65586709) /rpt_family="L1"	complement (64866554) /rpt_family="AluJ/FRAM" /ruddonce-not experimental	/evidence=not_experimental complement(62366447) /rpt_family="LIM4"	/evidence=not_experimental 60256235 /rpt family="alwith"	/evidence=not_experimental complement(58836008) /rpt_family="LIM1"	/evidence=not_experimental complement(56265882) /rnt familv="Aludb"

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             84871 AGCGAGGACGCCACGGCATCGCCATCGCCACGACGACGACGAGGCATCGCCAACGAG
                                                                                                                                           84751 CAGGGCATCGCTAACGAGGCCGCCGACAAGGGCATCGCCAACGAGGATGCCGCCCACGGC 84810
                                                                                                                                                                                                                                                                        84691 GCCGCCCAGGGCATCGCCAACGAGGGCCCCCAGGGCATCGCCAAAGAGGACGCCGCC 84750
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                                                                                                             255 AACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGCATCGCCAACGGG 314
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                                                                                                                                                                                                                                                                                                      78 ACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCC---GAGGACGCCATC 134
                                                                                                                                                                                                                                                                                                                                                                                                                   Match 71.2%;
Local Similarity 85.9%;
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complement(29773..30076)
/rpt_family="Aluy"
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complement(25398. .25624)
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/rpt_family="Aluy"
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/evidence=not_experimental
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25945. .26235
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25642. .25941
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25366. .25393
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/rpt_family="Alusg"
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/evidence=not_experimental
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15255. .15418
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dence=no+
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 356.2; DB 9; Length 150724;
Pred. No. 2.1e-24;
0; Mismatches 63; Indels 6;
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Matches 419;
85111 GCCAACGAG 85119
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                                                                                                                                                     18 GAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCCATCGCTAATGAGGAC 77
                                                                                                                                                                                                                                                              Match 70.9%;
Local Similarity 85.7%;
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Fu.Y., Fang,F., Wang,Q., Pan,H., McDermid,H. and Roe,B.A.
Direct Submission
Submitted (19-DEC-1999) Department Of Chemistry And Blochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
(Kases 1 to 122364)
Fu.Y., Fang,F., Wang,Q., Pan,H., McDermid,H. and Roe,B.A.
Fu.Y., Fang,F., Wang,Q., Pan,H., McDermid,H. and Blochemistry,
Submitted (06-MAY-2000) Department Of Chemistry And Blochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OK 73019, USA
5 (bases 1 to 122364)
5 (bases 1 to 122364)
Fu,Y., Fang,F., Wang,Q., Pan,H., McDermid,H. and Roe,B.A.
Direct Submission
Submitted (18-MAY-2000) Department Of Chemistry And Biochemistry,
Submitted (18-MAY-2000) Department Of Chemistry And Biochemistry,
Proposersity Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122364)

1 (bases 1, Wang, O., Pan, H., McDermid, H. and Roe, B.A. Homo sapiens Chromosome 22q11 BAC Clone b293 In CES Region Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-APR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC007324 122364 bp DNA linear PRI 18.1 Homo sapiens chromosome 22q11 clone b293, complete sequence. AC007324
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On May 18, 20
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22q11"
/clone="7293"
/clone="7293"
31795 a 28253 c 28482 g 33834 t
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                                                                                                                                                                                                                                       0; Mismatches 64;
                                                                                                                                                                                                                                                              Score 354.6; DB 9;
Pred. No. 3.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Barown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocker, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Hehozzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morrown, J., Naylor, J., Necrano, C., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Tesfaye, S., Titreil, A., Vassilley, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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                                                                                                                                                                              Direct Submission
Submitted (09-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:6479088.
All repeats were identified using RepeatMasker:
Smit, A.F. A. 6 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 159550)
                                                                          Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
    Contact: sequence_submissions@genome.wi.mit.edu
                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                         Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * 17960 25939; contig of 8980 bp in length 26940 27039; gap of 100 bp in length 27040 36269; contig of 8980 bp in length 36270 36368; gap of 100 bp in length 48875 48674; contig of 12205 bp in length 48875 62315; contig of 13205 bp in length 62316 62415; gap of 100 bp in length 77558 7757; gap of 100 bp 5685 96844; contig of 1927 bp in length 96885 124230; contig of 1927 bp in length 124231 124330; gap of 100 bp 100 bp
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Center clone name: 278_E_23
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7051 9136: contig of 2086 bp in length
9137 9236: gap of 100 bp
9237 17859: contig of 8623 bp in length
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1730 1829; gap of 100 bp
1830 3716; contig of 1887 bp in length
3717 3816; gap of 100 bp
3817 6950; contig of 3134 bp in length
6951 7050; gap of 100 bp
7051 9136; contig of 2086 bp in length
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                                                                              /note="assembly_fragment"
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                                                                                                                                                                                                                               /note="assembly_fragment"
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RESULT 10
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 15950) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-278E23
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marguis, N.,

McEwan, P., Maylor, J., Norman, C., H., O'Connor, T., O'Donnell, P.,

Morrow, J., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stolanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pleces is not known and their order in this sequence record starbitrary, daps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: 12604

Center clone name: 278_E_23

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 144663 bases at least Q40
Consensus quality: 154318 bases at least Q30
Consensus quality: 153318 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 173000; agarose-fp
Quality coverage: 5.4 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 bases; sum-of-contigs
48575 480/3.
48575 62315; cont.
48675 62315; cont.
62316 62415: gap of 100 bp
62316 77457; contig of 15042 bp in length
77458 77557; gap of 100 bp
77558 96884; contig of 19327 bp in length
17558 96884; contig of 27246 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                      3717 3816: gap of 100 bp 6
3817 7050: gap of 100 bp 6
6950: contig of 3134 bp in length
6951 7050: gap of 100 bp
7051 9136: contig of 2086 bp in length
9137 17859: contig of 8623 bp in length
17860 17959: gap of 100 bp
17960 26939: contig of 8980 bp in length
17960 27039: gap of 100 bp
26940 27039: gap of 100 bp
27040 36269: contig of 8980 bp in length
27040 36269: contig of 9230 bp in length
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Contact: sequence submissions@genome.wi.mit.edu
------project Information
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1730 1829; gap of 100 bp
1830 3716: contig of 1887 bp in length
3717 3816: gap of 100 bp
3817 6950: contig of 3134 bp in length
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                                                                                                                                                                                                                                                                                  36369: gap of 100 bp in length 48574: contig of 12205 bp in length 48674: gap of 100 bp 62315: contig of 13641 bp in length
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                                                  Db 124579 GACTCCGCCCACGGAATCGCCAGCGAGGACGCCGCCCACGGCATCGCCAGCGAGGACGCC 124520
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                                                                                                                                                                                                                                                                                                           Db 124819 GCCGCCCAGGGCATCGCCAGCGAGGACGCCGCCCAGGGCATCGCCAGCGAGGACGCCGCC 124760
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315 GACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCC 374
                                                                                                                                   255 AACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCACGGCCATCGCCAACGGG
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48675. .62315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 349.8; DB 2; Length 159550; Pred. No. 7.6e-24;
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Db 124519 GTCCAGGGCATCGCCAAGGAGGACGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAG 124460
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Submitted (07-DEC-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
OK 73019, USA
Submitted (01-FEB-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA 9 (bases 1 to 98557) Wang, O., Fang, F., Fu, Y., Pan, H., Edelmann, L. and Roe, B.A. Birect Submission Submitted (03-FEB-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                             8 (bases 1 to 98557)
Wang,O., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang,Q., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A. Direct Submission
Submitted (26-JAN-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Direct Submission
Submitted (22-UUL-1999) Department Of Chemistry And Biochemistry.
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-DEC-1999) Department Of Chemistry And Blochemistry. The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-DEC-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,Q., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang,Q., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A Direct Submission
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Homo sapiens Chromosome 22q12 PAC Clone pac699j1 In CES-DGCR Region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9957)
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Fang, F., Fu, Y., Pan, H., Edelmann, L. and Roe, B.A.
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                                                              27796 CAGGGCATCGCCAAGGACGCCGCCCAGGGCATCGCCAAGGAGGGCGCCCCAGGGC 27737
                                                                                                                                               27856 GCCGCCCAGGGCATCGCCAGCGAGGACGCCCCAGGGCATCGCCAGGGAAGGACGCCGCC 27797
195 ATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGGACGCCGTCCACGGCTTCGCC 254
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                                                                                                      CAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGC 194
                                                                                                                                                                                                                                                                                                               415;
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Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

AC008132(pace9956) 136107 14570 (0) overlaps AC008103(pac69951) 13687 175338 (0) overlaps AC008103(pac69951) 138871 175338 (0) overlaps AC008103(pac69951) 14435 (54202) AC0097325(b48) 71505 165050 (0) overlaps AC008103(pac69951) 144364 (4413) AC008103(pac69951) 56194 (98557 (0) overlaps AC0087326(p423) 1 42365 (60533).
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Direct Submission
Submitted (10-FEB-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Direct Submission
Submitted (08-FEB-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Submitted (05-FEB-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang,Q., Fang,F., Fu,Y., Pan,H., Edelmann,L. and Roe,B.A. Direct Submission Submitted (27-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-MAR-2000) Department Of Chemistry And Biochemistry
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Direct Submission
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/chromosome="22q12"
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Zhan, M. and Roe, B.A.
Direct Submission
Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OK 73019, USD
4 (bases 1 to 106650)
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2han,M. and Roe,B.A.
Direct Submission
Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,
Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,
Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106650 bp DNA linear PRI 31-MAN Homo sapiens chromosome 22q11 clone b563b9, complete sequence AC007708 AC007708.13 GI:5923689
                                                                                                        on Sep 25, 1999 this sequence version replaced gi:5919292.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

ACO00018(b379nl1) 146090 180888 (0) overlaps ACO07708(b563b9) 1 34927 (71723) ACO07708(b563b9) 10650 (0) overlaps ACO09288(p413m7) 1 101851 (39025).
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Direct Submission
Submitted (02-UN-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106650)
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                        Hua,A., Emanuel,B. and Roe,B.A.

Direct Submission
Submitted (13-ANG-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Homo sapiens chromosome 22q11 clone p413m7, complete sequence.
AC009288
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Hua,A., Emanuel,B. and Roe,B.A.
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                     Hua, A., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (19-NOV-1999) Department Of Chemistry And Biochemistry.
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Hua, A., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (31-MAY-2000) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                    AC007981 175358 bp DNA linear PRI 27-M
Homo sapiens chromosome 22qll clone b291, complete sequence.
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                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 20, 2000 this sequence version replaced gi:7940350.

Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

ACO08132(pac99506) 4747 145670 (0) overlaps ACO07981(b291) 1 142425 (32936) AC007981(b291) 59901 175358 (0) overlaps AC007325(b48) 1 115948 (49102) AC007981(b291) 132871 175358 (0) overlaps AC007325(b48) 1 115948 (49102) AC007981(b291) 132871 175358 (0) overlaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 (bases 1 to 175358)
FU,Y., PBan,H., Shalkh,T., Kurahashi,H., Emanuel,B. and Roe,B.A. Direct Submission
Submitted (27-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
or 70110 mes
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Direct Submission
Submitted (18-MAY-2000) Department Of Chemistry And Biochemistry,
Submitted (18-MAY-2000) Department Of Chemistry,
Submitted (18-MAY-2000) Departm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pu,Y., Pan,H., Shalkh,T., Kuranasnı,n., Lamanasnı,n., Direct Submission
Submitted (07-JUL-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fu.Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A. Direct Submission
Submitted (12-MAR-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fu.Y., Pan, H., Shaikh, T., Kurahashi, H., Emanuel, B. and Roe, B.A. Direct Submission
Submitted (15-JAN-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                             OK 73019, USA
On May 20, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 (bases 1 to 175358)
9 (bases 1 to 175358)
Fu,Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A.
Direct Submission
Submitted (20-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fu.Y., Pan,H., Shaikh,T., Kurahashi,H., Emanuel,B. and Roe,B.A. Direct Submission
Submitted (08-JAN-2000) Department Of Chemistry And Biochemistry, Submitted (08-JAN-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175358)

1 (bases 1 to 175358)

Fu, Y., Pan, H., Shaikh, T., Kurahashi, H., Emanuel, B. and Roe, B.A.

Homo sapiens Chromosome 22q11 BAC Clone b291 In CES-DGCR Region
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                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22q11"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVA
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                                                                                   3 (bases 1 to 180884)
Zhan,M. and Roc,B.A.
Direct Submission
Submitted (01-NOV-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                    2 (bases 1 to 180884)
Zhan,M. and Roe,B.A.
Direct Submission
Submitted (10-7UL-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                      OK 73019, USA
4 (bases 1 to 180884)
Zhan, M. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens Chromosome 22q11 BAC Clone b379n11 In BCRL2-GGT Region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18084)
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Pred. No. 2.4e-23;
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PRI 31-MAY-2000

Qy 422 GGACC 	QY 362 TAACG Db 103453 CAACG	QY 302 CATCG Db 103393 CATCG	QY 242 CCACG 	Qy 182 CGCCG Db 103273 CGCCG	Qy 122 CGAGG 	Qy 65 CGCTA Db 103153 CGCCA	Qy 5 CTACG Db 103093 CGACA	Query Match Best Local Simi Matches 404;	REFERENCE 5 AUTHORS Zhai TITLE Subi TOURNAL THE AUTHORS EA AUTHORS DIX TOURNAL Subi TOURNAL Subi TOURNAL Subi TOURNAL Subi The OK COMMENT On I Bec: ACO	TITLE Direc
GACGCCGCCAGGGAATCGCCGAGGATGTCGCAC 	AACGAGGACGCCGTCCAGGCATCGCTAACGAGGTGGCCGACGGCCAGGGCATCGCCAACG 	NTCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACCGCCATCG 	GCTTCGCCAACGGGGACGCCGTCCTCA 	CACAGGGCATCGCCAATGAGGACGCCA {	ACGCCATCCAGGGCATCGCCAACGAGG. 	TAATGAGGACACCACCAGTGCATCGCCA 	TACGGCATTGCTGAGGACGCTGGCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCA 	65.1%; Score 325.4; milarity 81.0%; Pred. No. 1.1e Conservative 0; Mismatches	The University of Oklahoma, 620 Parri OK 73019, USA 5 (bases 1 to 180884) Zhan, M. and Roe, B.A. Direct Submission Submitted (20-MAY-2000) Department Of The University Of Oklahoma, 620 Parri OK 73019, USA 6 (bases 1 to 180884) Zhan, M. and Roe, B.A. Direct Submission Submitted (31-MAY-2000) Department Of The University Of Oklahoma, 620 Parri OK 73019, USA On May 20, 2000 this sequence version Because these overlapping clones came there are numerous instances of inser nuclectide polymorphisms in the overl AC002472(p.n5) 129927 147086 (0) over 1156723) AC007664(b453h4) 79011 16247 AC008018(b379n11) 183457 (97431) AC00 (130925) overlaps AC002054(clone88) 1 13707 22563 (158328) AC002054(clone88) 1 13707 22563 (15832	t Submission
CACAGGGCATCGCCAACGAGGACGCCGC 	AGGTGGCCGCCCAGGGCATCGCCAACGA 	GCAACGAGGTCACCATCCACGGCATCGC 	CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGACGCCGCCCAGGGCLI	GCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 	GAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGT 	GAGGACACCACCAGTGCATCGCCAACGAGGAGCAGCCCCAGGGCATCGC 	TCGCTAATGAGGACGCCGACCAGGGCAT 	5.4; DB 9; Length 180884; . 1.1e-21; tches 91; Indels 4; G	of Chemistry And Bioche rington Oval, Room 208, Of Chemistry And Bioche rington Oval, Room 208,	Chamistry and Div
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Match
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      Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/backfiles1.seq:*
/cgn2_6/ptcdata/2/ina/backfiles1.seq:*
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                5273901-6
US-08-655-227-17
US-08-655-227-17
US-08-655-227-17
US-09-144-759-17
US-09-144-759-17
US-09-144-759-17
US-09-144-759-19
US-08-209-165-264-1
US-08-9165-264-13
US-09-165-264-13
US-09-165-264-14
US-09-135-979-20
US-08-770-379-20
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US-09-135-994-1
US-09-135-994-1
      US-08-469-802B-3
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Patent No. 5273901
Sequence 17, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 31, Appl
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06 GCTGGGCTGANGCTGGGGCTGGGGCTGNNGCTG	46 GCTGAGGTTGGGGCTGGGGCTGGACG 	86 GTTGGGCTGGGACTGAGGCTGGGGCTANGGCTG	26 GCTGAGGCTGGGACTGGGACTGAGGCTGGGACTGAGGCTGGGGCTGAGCTGAGGCTGAGCTGAGGCTGAGGCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	66 GCTGGGGCTGAGGCTGGGGCTGGGGCT 	6 CCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGTGCTGC	Match 21.0%; Score 1 Local Similarity 56.3%; pred. N es 188; Conservative 0; Mism	90.8 18.2 2165 2 US-08 90.8 18.2 2165 4 US-09 90.8 18.2 26530 2 US-08 90.8 18.2 6530 3 US-08 90.8 18.2 6530 3 US-08 90.8 18.2 6530 5 US-08 90.8 18.0 9551 1 US-08 90.2 18.0 9551 2 US-09 91.4 17.0 6449 4 US-09 91.4 17.0 6449 4 US-09 91.4 16.9 152331 3 US-09 91.4 16.9 15202 3 US-09 91.5 16.9 15202	1.2 18.2 234 2 US-08
CTG 339	SCTGGGGCTGAGGCTNGGNCTGAGGCTG 	CTGGGGCTGAGGCTAGGGCTNAG CTGGTGCTGCTGCAGCTGGTGCTGCAGCT	CTGGGACTGAGGCTGGGGCT 	GGGGCTGGGACT 	CTGGGACTGAGGCTGGGGCT 	05.2; DB 6; Length lo. 4.1e-14; matches 146; Indels	21.2 44.2 44.2 44.2 30.1 30.1 30.9 33.7 11.6 16.7 16.7 16.7 16.7 1; RUFF, MICHAEL L.; RUFF COCCIDIOSIS	
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OTHER INFORMATION: /note= "domain = ecdysone receptor"
OTHER INFORMATION: ligand binding domain."
US-08-659-188-17
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US-08-659-188-17/c
. sequence 17, Application US/08659188
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US-08-655-227-17/c
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
ANAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE CAmpbell and Flores
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
                                                                                1161 GGGCTGGGGCTGAGGCTGATGCTGGGCC 1128
                                                                                                                                                           1221 AGGTTGTAGCTGCGGCTGTGTCTGGTGCTGGGAATCGTTCTGGGTCAGGGAGGAGGGTTG 1162
                                                                                                                                                                                                                                         1281 CGTCTGAAGCTGTGGTTGGAGCTGGGGTTGCAGTTGACCTTGCAGCTGAGGTGGTAGCTG 1222
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STATE: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
                                                                                                    190 GGGCTGGGGACTGAGGCTGGGGCC 223
                                                                                                                                                                                             130 AGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGACTGAGGCTGGGGCTGAGGTTG 189
                                                                                                                                                                                                                                                                                70 GGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGACTGAGGCTGGGGCTGGGGCTG 129
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TOPOLOGY: linear
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CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      145;
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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Pred. No. 8.2e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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US-08-655-241-17/c
Sequence 17, Application US/08655241
Patent No. 602543
GENERAL INFORMATION:
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: LOCATION: 1.1656
: OTHER INFORMATION: /note= "domain = ecdysone receptor
: OTHER INFORMATION: ligand binding domain."
US-08-655-227-17
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INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 1656 base ---
Types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                              1161 GGGCTGGGGCTGAGGCTGATGCTGGGCC 1128
                                                                                                                                                                                                                                                                                                          1281 CGTCTGAAGCTGTGGAGCTGGGGTTGCAGTTGACCTTGCAGCTGAGGTGGTAGCTG 122
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CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                     190 GGGCTGGGGACTGAGGCTGANGGCTGGGGC 223
                                                                                                                                                                                                                                                            130 AGGCTGGGGCTGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGAGGTTG 189
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nucleic acid
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Pred. No. 8.2e-14;
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APPLICANT:

Yanofsky, Martin F.

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               Sequence 17, Application US/09398326
Patent No. 6355863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants
TITLE OF INVENTION: Reproductive
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                      1161 GGGCTGGGGCTGAGGCTGATGCTGGGCC 1128
                                                                                                                                                                                                                                                                                                                                                                         1281 CGTCTGAAGCTGTGGTTGGAGCTTGGGGGTTGACCTTGCAGCTGAGGTGGTAGCTG 1222
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Development and Methods of Making Same
                                                                                                                                                                                                                                                                                               1221 AGGTTGTAGCTGCGGCTGTGTCTGGTGCTGGGAATCGTTCTGGGTCAGGGAGGAGGAGGTTG 1162
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CORRESPONDENCE ADDRESS:
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  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       190 GGGCTGGGGACTGAGGCTGGGGCC 223
                                                                                                                                                                                                                                                                                                                     130 AGGCTGGGGCTGGGGCTGGGGGCTGGGGACTGAGGCTGGGGGCTGAGGTTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                 70 GGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGGGGCCTGGGGCCTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GGGCTGGGGCTGGAGCTGGAGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1.1656
OTHER INFORMATION: /note- "domain - ecdysone receptor
OTHER INFORMATION: ligand binding domain."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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4370 La Jolla Village Drive, Suite 700
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N: CLASS 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%;
Seed Plants Exhibiting Inducible Early Reproductive Development and Methods of Making Same 26
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Pred. No. 8.2e-14;
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RESULT 6
US-09-144-759-17/c
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GENERAL INFORMATION:
APPLICANT: Hoock, Thomas
APPLICANT: Germann, Ursula
APPLICANT: Kwong, Ann
APPLICANT: Kwong, Ann
TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
TITLE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 1656 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                         Sequence 17, Application US/09144759 Patent No. 6117639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.8%;
Best Local Similarity 67.8%;
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NAME/KEY: misc_feature
LOCATION: 1..1656
OTHER INFORMATION: /note= "domain = ecdysone receptor
OTHER INFORMATION: ligand binding domain."
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                1161 GGGCTGGGGCTGAGGCTGATGCTGGGCC 1128
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                              1221 AGGTTGTAGCTGCGGCTGTGTCTGGTGCTGGGAATCGTTCTGGGTCAGGGAGGAGGGTTG 1162
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PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-1---
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CITY: San Diego
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4370 La Jolla Village Drive, Suite 700
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Pred. No. 8.2e-14;
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US-09-144-759-19/c
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US-09-144-759-17
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Patent No. 6117639
GENERAL INFORMATION:
APPLICANT: HOOCK, Thomas
APPLICANT: Germann, Ursula
APPLICANT: Kwong, Ann
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CURRENT APPLICATION NUMBER: US/09/144,759
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
SEQ ID NO 17
                                                                                                                                                                                                                           Matches 145;
                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS TITLE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY EILE REFERENCE: VPL/98-08 CURRENT APPLICATION NUMBER: US/09/144,759 CURRENT FILING DATE: 198-08-31 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                             1923 CGTCTGAAGCTGTGGAGCTGGGGGTTGCAGTTGACCTTGCAGCTGAGGTGGTAGCTG 1864
                                                                                                                                          1983 GGGCACGGGAGCGGAACGGGAAGGAGCTGTGGCTGTGGTTGAATCTGTGGCTGGAGTTG 1924
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                      130 AGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGGTTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 19
ENGTH: 2295
                                                                                   70 GGGCTGAGGCTGGGGCTGGGGCCTGGGGCTGGGGCTGGGGCTGGGGCTG 129
                                                                                                                                                                                10 GGGCTGGGGCTGAGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTG 69
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                                                                                                                                                                                                                                             Local Similarity
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Similarity
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                                                                                                                                                                                                                                         20.8%; Score 104.2;
67.8%; Pred. No. 8.7
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Pred. No. 8.6
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US-08-209-747-1
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                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08209747 Patent No. 5733771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS FILTE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY FILE REFERENCE: VPL/98-08 CURRENT APPLICATION NUMBER: US/09/144,759 CURRENT FILING DATE: 198-08-31 NUMBER OF FEC ID NOS: 24 SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 23
TYPE: DNA
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                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                             TITLE OF INVENTION: cDNAs Encodin
                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                               1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1929 CGTCTGAAGCTGTGGAGCTGGGGGTTGCAGTTGACCTTGCAGCTGAGGTGGTAGCTG 1870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1869 AGGTTGTAGCTGCGGCTGTGTCTGGTGCTGGGAATCGTTCTGGGTCAGGGAGGAGGGTTG 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGC 223
                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTG
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                                                                             ZIP:
                                                                               COUNTRY: USA
ZIP: 22040-3487
  OPERATING SYSTEM:
                                                                                                                    STATE:
                     COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCTGGGGCTGAGGCTGATGCTGGGCC 1776
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                                                                                                               Virginia
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                cDNAs Encoding Minor Ampullate Spider
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                                                                                                                         Sequence 1, Application US/08458298 Patent No. 5756677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 222;
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                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                  APPLICANT: Lewis, Randolph V. APPLICANT: Colgin, Mark TITLE OF INVENTION: CONAS EncuTITLE OF INVENTION: Silk Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            724 GTGCTGGCGGTTACGGTAGAGGTGCTGGTGCTGGAGCAGGAGCCGCTGCGGGTGCTGGAG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 GCGGATATGGTGCCGGAGCAGGAGCTGGTGCGGCTGCTGCTGGTGCAGGAGCAGGAG
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                                                                                                                                                                                                                                                                                       360 CTGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCT 398
                                                                                                                                                                                                                                                                                                                                844 CTGCTGCTGGAGCAGGATCTGGAGGCGCTGGCGGTTACGGTAGAGGTGCTGGTGCTGGAG 903
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LOCATION: 183..2675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       CTGGAGCTGGGGCTGANGCTGG-GGCTGGGGGCTGANCTGGGGGCTGAGGCTCCNG 359
                                                                                                                                                                                                                                                                                                                                                                                                                CTGGAGGCTACGGTGGTCAAGGTGGGTACGGTGCCGGAGCAGGAGCTGGTGCCGGCTGCTG
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EDNESS: double
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                      Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.5%;
                                      cDNAs Encoding Minor Ampullate Spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "N. clavipes minor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102.6; DB 1; Length 2793; Pred. No. 1.9e-13; 0; Mismatches 173; Indels 4;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 CAGCTGCTGGAGCAGGAGCCGGAGGCGCTGGTGGTTACGGTAGAGGTGCTGGTGCTGGAG 606
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STREET: P.O. Box 747
CITY: Falls Church
    360 CTGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCT 398
                                             844 CTGCTGCTGGAGCAGGATCTGGAGGGGGGGTGGCGGTTACGGTAGAGGTGCTGGTGCTGGAG
                                                                                                                           784 CTGGAGGCTACGGTGGTCAAGGTGGGTACGGTGCCGGAGCAGGAGCTGGTGCGGCTGCTG 843
                                                                                                                                                                                                              724 GTGCTGGCGTTACGGTAGAGGTGCTGGTGCTGGAGCAGGAGCCGCTGCGGGTGCTGGAG
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                                                                                  301 CTGGAGCTGGGGCTGANGCTGG-GGCTGGGGGCTGNNGCTGANCTGGGGCTGAGGCTCCNG
                                                                                                                                                                  241 CTNAGGCTGAGGTTGGGGCTGGGGCTGGNGCTGACGCTGGGGCTGAGGCTNGGNCTGAGG 300
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REGISTRATION NUMBER: 28,97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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LOCATION: 183..2675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: minor ampullate gland
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                                                                                                                                                                                                                                                                                                                                                                                                                61 CTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGACTGAGGCTGGGG 120
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RESULT 12
US-08-998-416-915/c
: Sequence 915, Application US/08998416
: Patent No. 6239264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 144; Conserv
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                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2398 GGGCACGGGAGCGGGAGCGGGAAGGAGCTGTGGCTGTGGTTGAATCTGTGGCTGGAGTTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
                                                                                                                                                                                                2218 GGGCTGGGGCTGAGGCTGATGCTGGGCC 2185
                                                                                                                                                                                                                                                                            2278 AGGTTGTAGCTGCGGCTGTGTGTGCTGCGAATCGTTCTGGGTCAGGGAGGAGGATTG 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATIN (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Ecdysteroid Dependent Regulation of TITLE OF INVENTION: Genes In Mammalian Cells
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MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                         190 GGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGC 223
                                                                                                                                                                                                                                                                                                                    130 AGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGGTTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904 CTGGAGCCGCTGCAGGTGCAGGAGCAGGAGCTGGAAGCT 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitts, Renee A. REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: POFILING DATE: 19920803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.5%; Score 102.6; DB 5; 67.3%; Pred. No. 1.9e-13; ative 0; Mismatches 70;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 688 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: GENOMIC DNA SEQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
361 TGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATG 408
                                     301 CTGGAGCTGGGGCTGANGCTGGGGCTGGGGCTGANCTGGGGCTGAGGCTCCNGC 360
                                                                                                                 369 CAGTTGTGGCTGATGAGGCTGTAAACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGG
                                                                                                                                                      241 CTNAGGCTGAGGTTGGGGCTGGGGCTGACGCTGAGGCTGAGGCTNGGNCTGAGG
                                                                                                                                                                                              429 CIGCIGCGICIGCIGCGCTCTGCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGC 370
                                                                                                                                                                                                                                      181 CTGAGGTTGGGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGCTGGGGCTAGGG 240
                                                                                                                                                                                                                                                                            121 CTGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGGGG 180
                                                                                                                                                                                                                                                                                                                                                       549 CTGGACTTGCTGGAACCGGTTGTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                     609 CTGTGAAAGTTGCTGAGGCTGTGGTTGTTGTTGAGACTGGACTTGCTGGTTGTTGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local 211;
                                                                                                                                                                                                                                                                                                                                                                                61 CTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTGAGGCTGGGGCTGGGGCTGGAGCTGGAGCTGAGGCTGGGGCTGGGG 60
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Wendtle, Philipp
Rebischung, Corinne
REDISCHUNG, CORING DNA SEQUENCES OF ASHBYA GOSSYPII
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Pred. No. 2.2e-13;
0; Mismatches 197;
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; Sequence 7, Application US/09165264
; Patent No. 6197510
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US-09-165-264-7
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US-09-165-264-8
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-8
                                                            SOFTWARE: Pat
SEQ ID NO 8
LENGTH: 319
TYPE: DNA
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CURRENT FILING DATE: 1998:10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 320
TYPE: DNA
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                                                                                                                                                                                                                                        Sequence 8, Application US/09165264 Patent No. 6197510
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Best Local Similarity
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                                                                                                                        CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                        APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic
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                               ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                        GGAGCTG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176;
                                                                                                              PatentIn Ver. 2.1
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Pred. No. 3.7e-13;
0; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09165264 Patent No. 6197510
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                     Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 320
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                                                   GGGACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTAGGGCTNAGGCTGAGGTT 254
                                                                                                       GGGGCTGGGACTGAGGCTGGGGCTGGGGACTGAGGCTGGGGCTGGGGCTGAGGTTGGGGCCT 194
                                                                                                                                                           GAGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGCTGAGGCT 134
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                 Genoscope
                                                                     Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H.,
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Direct Submission
                                                    Unpublished
                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CTGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGAGCTGGGGCTGANGCTGGGGCTGNNGCTGA-NCTGGGGCTGAGGCTCCNG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGGCTGAGGCTGGGGCTGGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGGCTGAGTCCGGGGCTGAGGCCGGGGCTGAGGCCGAGGCTGAGG
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                                                                                                                                                                                                                                                                                                           GSS;
                                                                                                                                                                                                                                                                                                                         sequence.
AL191876
AL191876.1 GI:7829980
Roest-Crollius, H., Jaillon, O., Dasilva, C.,
                                       Unpublished
                                                                           Charaterization and repeat analysis of the compact genome of the
                                                                                                                                            Roest-Crollius, H.,
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Actanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                    Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                      GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon
256B21 of
                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS02D1N
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                                                              freshwater pufferfish
                                                                                                       Weissenbach,J
                                                                                                                   Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
                                                                                                                                                                                   Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                       (bases 1 to 613)
                                                                                                                                                              (bases 1 to 613)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUC-Ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="197624"
/clone_ib="G"
/note="Genoscope sequence ID : COAG197BD12SP1-end
                                                                                                                                                                                                                                                                                                                                                                                       613 bp DNA linear GSS 13-MAY: nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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79.2%;
                                                                                                                                                                                   Tetraodon
                                                                                                                                          Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                           Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 250; DB 12;
Pred. No. 3.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 t
                                                                                                                                                                                                                   Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 723;
Bouneau, L., Fisher, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                            end of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ORIGIN
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VERSION
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                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CTNAGGCTGAGGTTGGGGCTGGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTNGGNCTGAGG 300
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                                                                                                                                       AL265983.1 GI:7987741
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS03Y86 1061 bp DNA linear GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
063J24 of library G from Tetraodon nigroviridis, genomic survey
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Tetraodontidae; Tetraodon.
1 (bases 1 to 1061)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL265983
AL265983.1
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12; Conservative
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/Ob_xref="taxon:9983"
/Clone="556821"
/Clone=1bb="G"
/Clone_lib="G"
/note="Genoscope sequence ID : COAG256CA11LP1-end : T7"
/note="Genoscope sequence ID t 12 others
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Pred. No. 8.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 613;
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REFERENCE
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/db_xref="taxon:99883"
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RESULT 6 CNS031R8	Qy 301 CTGGAGCTGGGGCTGANGCTGGGGCTGNNGCTGA-NCTGGGGCTGAGGCTCCNG 359	Oy 181 CTGAGGTTGGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTAAGGCTGAGGCTAAGGCTGAGGCTAAGGCTGAGGCTAAGGCTGAGGCTGAAGAAAAAAAA	Qy 61 CTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGG	Query Match 47.4%; Score 237; DB 12; Length 880; Best Local Similarity 74.9%; Pred, No. 3.1e-27; Matches 299; Conservative 0; Mismatches 99; Indels 1; Gaps 1; Matches 299; Conservative 0; Mismatches 99; Indels 1; Gaps 1; Qy 1 Graaggc	<pre>n="Tetraodon nigroviridis" "taxon:99883" 199ED1" 1b="G" snoscope sequence ID : COAG199AC01SP1~end : 223 g 172 t 1 others</pre>	000) to the EMBL/GenBank/DDBJ databases single read and was generated as part of a large usnoing project of the Tetraodon nigroviridis formation, please take a look at e.cns.fr/Tetraodon.	
Db 840 CTGARGCCGGGCTGARGCTGARGCCGGGGCTGAGCCTGAAGAAGCTGAAGACTGAAGCTGAAGAGTAGAAGCTGAAGGTGAAGCTGAAGCTGAAGCTGAAGAGAGGAGAGAGGAGAGGAGAGAGA			Query Match 47.4%; Score 237; DB 12; Length 949; Best Local Similarity 73.8%; Pred. No. 3.1e-27; Matches 296; Conservative 5; Mismatches 99; Indels 1; Gaps 1; Matches 296; Conservative 5; Mismatches 99; Indels 1; Gaps 1; Qy 1 CTGAGGCTGGGGCTGGGGCTGAGGCTGGAGCTGGAGCTGGAGCTGAGGCT	/db_xref="thaxon:99883" /clone="205022" /clone_llb="G" /note="Genoscope sequence ID : CO 205 a 202 c 390 g 144 t	Direct Subirect Submitted Submitted This seque scale clo genome. Finttp://www.ce	REFERENCE 2 (bases 1 to 949) REFERENCE 2 (bases 1 to 949) AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. TITLE Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence JOURNAL Unpublished AUTHORS Genoscope AUTHORS Genoscope AUTHORS Genoscope	LOCUS CNS031R8 DEFINITION Tetracdon nigroviridis genome survey sequence T7 end of clone 20502 of library G from Tetracdon nigroviridis, genomic survey sequence. ACCESSION AL223901 VERSION AL223901 AL223901 KEYWORDS GS: genome survey sequence. Tetracdon nigroviridis. ORGANISM Tetracdon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at
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Charaterization and repeat analysis of the compact genome of the
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
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PUC-Oxi"
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/db_xref="taxon:99883"
/clone="162H05"
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/clone=116-2H05"
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CTGAGGCTGGGGCTGGGGCTGAGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGG 60	Watch 44.9%; Score 224.6; DB 12; Length 890; Local Similarity 70.9%; Pred. No. 2.4e-25; hes 292; Conservative 5; Mismatches 114; Indels 1; Gaps 1;	/db_wref="taxon:99883" /db_wref="taxon:99883" /clone="214G09" /clone="1b="G" /note="Genoscope sequence ID : C0AG214AD05SP1-end : PUC-Ori" 139 a 368 c 203 g 154 t 26 others	etraodon nigrovirid look at	Unpublished Unpublished (bases 1 to 890) Genoscope. Birect Submission Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases Submitted (12-APR-2000) to the Was generated as part of a large	llius, Fiza and W	Noest-Crolling, H., Jaillon, C., Masilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished Unpublished Unpublished	AL22835.1 GI:7887828 GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Tetraodon. Tetraodontidae; Tetraodon.	CNS035KB 890 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 214G09 of library G from Tetraodon nigroviridis, genomic survey sequence. AL228836	CTGAAGCTGAGGCTGAGCTGAGCT 391	CTGGAGCTGGGGCTGANGCTGGGGCTGANGCTGA-NCTGGGGCTGAGGCTCCNG 359	CTNAGGCTGAGGTTGGGGCTGGAGGCTGACGCTGAGGCTNGGNCTGAGG 300	CTGAGGTTGGGGCTGGGGCTGAGGCTANGGCTGGGGCTGAGGCTAGGG 240
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/note="Genoscope sequence ID : CURGZZVAHUJIPI-end 170 a 335 c 224 g 232 t 4 others	yiri	Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a la scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers 1.965	Human gene number estimate provided by genome wide analysis Tetraodon nigroviridis DNA sequence Unpublished 3 (bases 1 to 965)	freshwater pufferfish Tetraodon nigroviridis Unpublished 2 (bases 1 to 965) Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fis Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F Saurin, W. and Weissenbach, J.	l (bases I to 965) Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizames, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. Weissenbach, J. Charaterization and repeat analysis of the compact genome	GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis Tetraodon nigroviridis Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae: Tetraodon.	CNS012DK 965 bp DNA linear GSS 12-MAY-Tetraodon nigroviridis genome survey sequence T7 end of clone 220005 of library G from Tetraodon nigroviridis, genomic survey sequence. AL174161.1 GI:7812218	IGGAGCTGAGGCTGAGGCTGGGGCTGNNGCTGA-NCTGGGGCTGAGGCTCCNG	TNAGGCTGAGGTTGGGGCTGGGGCTGACGCTGAGGCTGAGGCTNAGGNCTGAGG	TGAGGTTGGGGCTGGGACTGAGGCTGGGGCTAGGGCTGAGGCTAGGGCTAGGGCTAGGGCTAGGGCTAGGGCTAGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGACGCGGA	TGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGG 180	TGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGAGGCTGGGG

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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                       Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission Submitted (12-Apr-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large
                                                                                                                                                                                                                                                   2 (bases 1 to 986)
Roest-Crollius, M., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                      Unpublished
3 (bases 1
                                                                                                                                                                                       Tetraodon nigroviridis DNA sequence
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                                                                                                                           (bases 1 to 986)
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                                                                                                                                                                                                                       gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="G"
/note="Genoscope sequence ID : COAG131CE06SP1-end : PUC-Ori"
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Pred. No. 6.7e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285;
                                                                                                                                                                                                                             Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                 CNS028QT 791 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 245G14 of library G from Tetraodon nigroviridis, genomic survey
                       Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                           2 (bases 1 to 791)
Roest-Crollius, H., Jaillon, O., Dasilva, C.,
                                                                                               Unpublished
                                                                                                                                   Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                         Weissenbach, J
                                                                                                                                                                       Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizames, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
                                                                                                                                                                                                          Tetraodontidae; Teti
1 (bases 1 to 791)
                                                                                                                                                                                                                                                                                                                      GSS; genome survey sequence. Tetraodon nigroviridis.
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                                                                                                                freshwater pufferfish Tetraodon nigroviridis
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gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/db_xref="taxon:99883"
/clone="19103"
/clone_1ib="G"
/note="Genoscope sequence ID : COAG219AE02LP1-end :
/note="Genoscope sequence ID : 4 others
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73.58;
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Pred. No. 1.4
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                                                           Bouneau, L., Fisher, C.,
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                                                                                                                                                                                                                                                                     Neoteleostei;
                                                                                                                                                                                             Fisher, C.,
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                            Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chopterygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii, Neopterygii; Percomorpha; Tetraodontiformes;
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AL214842.1 GI:7873661
GSS; genome survey seq
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                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis genome survey sequence T7 167F12 of library G from Tetraodon nigroviridis,
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                                                                                       Roest-Crollius, H.,
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/db_xref="taxon:99883"
/clone='245G14"
/clone='15="G"
/clone_ib="G"
/note="Genoscope sequence ID : COAG245BD07LP1-end : T7"
/note="Tenoscope sequence ID : COAG245BD07LP1-end : T7"
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                                                                                       Jaillon, O.,
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             sequence.
AL296008 1 GI:8034588
AL296008.1 GI:8034588
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon ingroviridis.
Eukaryota: Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/clone_lib="G"
/note="Genoscope sequence ID : COAG167DC06LP1~end
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/db_xref="taxon:99883"
/clone="167F12"
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Neopterygii;
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Pred. No. 2.1e-23;
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                                                             GCTGGAGCTGGGGCTGANGCTGGGGCTGGGGCTGNNGCTGA-NCTGGGGCTGAGGCTCCN
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                                                                                                                              GCTGAGGCTGAGGCTGAGGCCGGRACTGAGTCTGAGTCCGGGGCTGAGGCCGAGGCTGAG
                                                                                                                                                                                             GCCGGGGCTGAGGCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGTCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1101)
1 (bases 1 to 1101)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Queties Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the compact genome of the freshwater pufferfish {\tt Tetraodon} nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
Direct Submission
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Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="118102"
/clone="118102"
/clone="fenoscope sequence ID : C0BG118BE01SP1~end pUC-Ori"
3 355 c 282 g 245 t 21 others
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74.7%;
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Pred. No. 3.6e-23;
3; Mismatches 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                       score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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AAQ03665
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                          Human small cell l
Sequence homologou
Human foetal liver
Probe #7022 for ge
Human bone marrow
Probe #6667 for ge
Probe #8847 used t
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DNA encoding novel
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AAA05548	AAV52505	AAQ88690	AAQ88689	092412	AAK75409	Q03665	AAD23836	AAZ45602	AAV52497	AAS86600	AAS20005	AAZ45597	AAC84677	AAF75507	ABI99802	AAD23837	AAH34279	AAC66020	AAA44382	AAD23835	AAQ13864	ABL24559	AAQ13868	AAS84306	AAS69141	ABL24558	AAI53240	AAI25929	AAK47401	AAK21244	ABA38433	ABA72813	AAF28060	AAS81401	580389
Streptococcus pneu	Streptococcus pneu		terminal pac)22 4-kb	Human immune/haema	Sequence homologou	Sugarcane proline	cDNA sequence of a	Streptococcus pneu	DNA encoding novel	fat-		DNA sequence of hu	Polyglutamine trac	Mouse ischaemic co	Sugarcane proline	Human colon cancer	Human lung cancer-	Human secreted exp	Sugarcane proline	PRP 378 gene and r	Drosophila melanog	Insert from clone	DNA encoding novel	DNA encoding novel	Drosophila melanog	6 used	Probe #15862 for g	D)	Human brain expres	Probe #16899 for g			DNA encoding novel	DNW encouring nover

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ALIGNMENTS

DR XX	XX	PT	v.:	40	PA	PA	××	PR	×x	J PF	xx	PD	- xx	PN	xx	os	××	KW	KW	KW	××	DE	××	Ta	xx	AC	××	AAD ID	RES
WPI; 2001-457597/49.		Stockert E. Scanlan MJ, Jager D. Old LJ, Gure AO, Chen Y;	`	٠,		(LUDW-) LUDWIG INST CANCER RES.		21-JAN-2000; 2000US-0489101.		19-JAN-2001; 2001WO-US02015.		26~JUL-2001.		WO200153349-A2.		Homo sapiens.		leimyosarcoma; synovial sarcoma; cytostatic; ds.	melanoma; cancer; colon; breast; head; neck; transitional cancer;	Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA;		Human small cell lung cancer associated gene, Novel-2.		24-SEP-2001 (first entry)		AAD11124;		AADIII24 ID AADII124 standard; DNA; 1232 BP.	RESULT 1

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RESULT 2
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                   Sequence homologous to Drosophila Per gene
                                                     07-AUG-1989
                                                                                      AAQ03665;
                                                                                                                     AAQ03665 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
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                                                   (first entry)
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01-FEB-2002

(first entry)

ABA60274;

ABA60274 standard;

DNA; 564

ВP

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Query Match
Best Local :
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1701 CTGTGCCTGTGCCTGTGCCTGTGCCTGTGCCTGTGACTTTGGCT 1652
                                                                                                                           1761 CTGAGCCTGAGCCTGAGCCTGTGCCTGTGCCTGTGCCTGTGCCTGTGCCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; fig 1; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-1988;
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                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                       361 TGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATGCT 410
                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 62.2 es 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGAGGCTGGGGCTGGGGCTGGGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGG 60
                                                                                                                                                                                      CTGGAGCTGGGGCTGANGCTGGGGGCTGNNGCTGANCTGGGGCTGAGGCTCCNGC
                                                                                                                                                                                                                                                      CTGAGCCTGAGCCTAGGCCTGTGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGC 1762
                                                                                                                                                                                                                                                                                                                     CTNAGGCTGAGGTTGGGGGCTGGGGCTGACGCTGAGGCTGAGGCTNGGNCTGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGGTTGGGGCTGGGGACTGAGGCTGGGGCTGAGGCTGGGGCTAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGTGCCTGTGC 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGGCTGAGGCTGGGGACTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171; DB 11;
Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumont J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2465;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 564 BP; 75 A; 103 C; 227 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 8579; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #8579.
                                                                                                                                                     195
                                                                                                                                                                                 181
                                                                                                                                                                                                             135
361 TGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATG 408
                                                         301 CTGGAGCTGGAGCTGANGCTGGGGCTGGGGCTGANGCTGANCTGGGGCTGAGGCTCCNGC 360
                                                                                                                                                                                                                                         121
                                                                                        254 CTGTGGCTCTGACTGGCCTGTGGCTGCTGCTGTGGATGTAGCTGGCACTGTGG 313
                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                   76 CTGTGGCTGTGAGTGGCACTGTGGCTGTGGCTATGACTGATACTGTGTCT-TGG 134
                                                                                                                                                                                                                                                                                                                                                            1 CTGAGGCTGGGGCTGGGGGCTGAGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                           Loca.
                             CTGAGGTTGGGGCTGGGGCTGGGGCTANGGCTGGGGCTGGGGCTAGGG 240
                                                                                                                                                                                                                                                                                                                               CTNAGGCTGAGGTTGGGGCTGGGGCTGACGCTGGGGCTGAGGCTNGGNCTGAGG 300
                                                                                                                                                  CTATGACTGGTACTGTCT-TGGCTGGTGCTATGGCTGTAGCTGGCACTGTGGCTGTGG 253
                                                                                                                                                                                                             CTGGTGCTATGGCTGGCTGGCACTGTGGCTGTGAGTGGCACTGTGGCTGTGG 194
                                                                                                                                                                                                                                         CT6666CTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTGGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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2000US-0608408.
2000US-06323667.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                   33.2%; 5c.
64.7%; Pre/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                         Score 165.8;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           9.5e-21
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 564;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA28556 standard; DNA; 564 BP
                                                                                                                                                                                                                                   Sequence 564 BP; 75 A; 103 C; 227 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                     congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; seQ ID No 7022; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #7022 for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 -JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA28556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
 121 CTGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTGGGG 180
                                                    61 CTGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 120
                                                                                                   16 CTGTGGCTATGGCTGGCACTGTGACTGTGGCTGTGGCTGTGGCTGTGGCTCTGACTGGCC 75
                                                                                                                                  1 CTGAGGCTGGGGCTGGGGCTGAGGCTGGAGCTGAGGCTGGGGCTGGGG 60
                                                                                                                                                                                      Cocal
                                    CTGTGGCTGTGGCTGTGAGTGGCACTGTGGCTGTGGCTATGACTGATACTGTGTCT-TGG 134
                                                                                                                                                                   264; Conservative
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-0024263.
                                                                                                                                                                                   33.2%; Score 165.8; DB 22; Length 64.7%; Pred. No. 9.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                   0; Mismatches 142; Indels
                                                                                                                                                                   2;
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RESULT 5
AAKOB55 5
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Query Match
Best Local Similarity
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human prain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                        Sequence 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 8543; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 8543.
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                                                                                                                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 CTGGTGCTATGGCTGTGGCACTGTGGCTGTGGCTGTGGCTGTGGCACTGTGGCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 CTGTGGCTATGACTGGCACCGTGGCCGTGGCTGGTGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CTGAGGTTGGGGCTGGGGACTGAGGCTGAGGCTAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTNAGGCTGAGGTTGGGGCTGGGGGCTGGGGCTGGGGCTGAGGCTNGGNCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTAGCTGGTGACTGTGGCTGTGGCTGGTGGCTCTGACTGGCCCTGTGG
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2000US-0207495
2000US-0608408
2000US-0632366
2000US-0234687
2000US-023659
2000US-023659
2000US-023659
                                                                                 BP; 75 A; 103 C; 227 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00667
   33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
Score 165.8; DB 22; Length 564; Pred. No. 9.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
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1

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human

Example 4; SEQ ID NO: 8992; 658pp + Sequence Listing; English.

analyzing gene expression in human bone marrow

Human genome-derived single exon nucleic acid probes useful for

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RESULT 6
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                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                        WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed single exon probe SEQ ID NO: 8992.
                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
                                                                                                               Penn
                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                               WO200157276-A2
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAK34435;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK34435 standard; DNA; 564 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264; Conservative
                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                             Hanzel DK,
                                                                                                                                                          2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0632365
2000US-0236559
2000US-0236559
2000US-0236553
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                             Chen W, Rank DR;
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WPI; 2001-488901/53.

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                                                                                          04-EEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-02007456.
30-JUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 564 BP; 75 A; 103 C; 227 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Probe #6667 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
              Penn SG,
                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                 WO200157278-A2
                                                                                                                                                                                                                                                                                                                            cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                        Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI16734 standard; DNA; 564 BP
                                            (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 CTGTGGCTGTGGCTGTGAGTGGCACTGTGGCTGTGGCTATGACTGATACTGTGTCT-TGG 134
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              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                             2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.2%;
              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 165.8;
Pred. No. 9.5
              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5e-21
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ID AAI
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AC AAI
XX AAI
XX T7-
XX T7-
XX P10
XX P10
XX Gen
XX Gen
XX Hom
XX Hom
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 6667; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells \dot{\cdot}
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                                                                                                                                                                                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                            09-AUG-2001
                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #8847 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI40161 standard; DNA; 564 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 TGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 CTGTAGCTGGTGTGACTGTGGCTGTGGCTGTGTGGCTCTGACTGGCCCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 CTATGACTGGTACTGTGTCT-TGGCTGGTGCTATGGCTGTAGCTGGCACTGTGGCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 180
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Similarity 64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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30-JAN-2001; 2001WO-US00663.

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RESULT 9
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ID AS8
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AC AAS8
XT TAS8
XX
DT 13-F
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DE DNA
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KW Huma:
KW food
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                           DNA encoding novel human diagnostic protein #20107
    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                     13-FEB-2002
                                                                                                                                     AAS84303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 8847; 654pp; English.
                                                                                                                                                                         AAS84303 standard; cDNA; 569 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                   374 CTGTGGCTATGACTGGCACCGTGGCCGTGGCTGGTGGTGCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                 CTGGAGCTGGGGCTGANGCTGGGGCTGGGGCTGANCTGGGGCTGAGGCTCCNGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTGGCTATGGCTGGCACTGTGACTGTGGCTGTGGCACTGTGGCTCTGACTGGCC 75
                                                                                                                                                                                                                                                                                                                                         CTGTAGCTGGTGTGACTGTGGCTGTGGCTGGTGGCTCTGACTGGCCCCTGTGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGGCTCTGACTGGCCTGTGGCTGTGGCTGCTGTGGATGTAGCTGGCACTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTGGCTGTGGCTGTGGCACTGTGGCTGTGGCTATGACTGATACTGTGTCT-TGG 134
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                                                                                                  (first entry)
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The C polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful in gene therapy techniques CC another the polynucleotide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating a polypeptide in the expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and no produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC and tro minor infinity with and not accompanies.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 569 BP; 163 A; 96 C; 211 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 20107; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
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    268
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                                                                                                                                                                                                                                                                                                                                       18 GCTGGGGCTGAGGCTGGAGCTGAGGCTGGGGCTGGGGCTGGGGCTGAG
GCTGAGGTTGAGGCCAGAACTGGAGCTAAAGTTGAGGCTGGAACCGGAGCTGAGGTTGAG
                        GCTGGGGCTGGNGCTGACGCTGGGGCTGAGGCTNGGNCTGGAGGCTGGGGGCTGAN 317
                                                                                                ACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTAGGGCTNAGGCTGAGGTTGGG 257
                                                                                                                                                   GCTGGGGCTGAGGCTGAAGCTGAAGAAGAGGTTATAGCTGCAGCTGAAGTAGAGGCTGGA
                                                                                                                                                                           GCTGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGGGGCTGAGGTTGGGGCTGGG 197
                                                                                                                                                                                                                                                                                                      GCTGGGGCTGGCGTTGGAAGCTGAAGTTGATGCTAGGGCTGAAGCAAGAATGGGAATTGAG
                                                                        ACTGAAGCTGAGACTGAGGCTGAGGCTGAAACTGGAGCTAAGGGTGAGGCTGGAACTGGA 267
                                                                                                                                                                                                                           GCTGAGGCAAGAATGGTGACAGAAGCTGGGGGTTGAAACTGAGGCAAGGATGGGGGTTGGA 147
                                                                                                                                                                                                                                                              GCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                 268;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 163.4; D
Pred. No. 2.5e-
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 569;
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AAS80389
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                The invention relates to isolated polynucleotide (I) and CC polymerase chair reaction (PCR) primers, oligomers, and for chromosome complymerase chair reaction (PCR) primers, oligomers, and for chromosome complymerase chair reaction (PCR) primers, oligomers, and for chromosome complymerase chair recombinant production of (II). The call of the complymerase chair and in recombinant production of (II). The call of the complymerase chair and in several control of the complymerase chair and the complymerase control of the complymerase
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food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 16193; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess haddron-time.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #16193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 GTGGGGCTGGGGTGNNG----CTGANCTGGGGCTGAAGCTGAGCTGAAGCTGAGGCT

18 GTGGGGCTGGGGTGANG----CTGANCTGGGGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 GGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATGCTTGNCTNANAATGNGNATGNNCTG 433
  ftp.wipo.int/pub/published_pct_sequences.
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations {\bf r}
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
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                                                             WPI; 2001-639362/73
P-PSDB; ABG17214.
                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                       11-OCT-2001.
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                      DNA encoding novel human diagnostic protein #17205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 ACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTAGGGCTAAGGCTGAGGTTGGG 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and CC polymerpide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The C2 polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polymeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of the invention.

CC stefer wire invention as obtained in electronic format directly from WIPO or after wire invention that and not appear in the printed continues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 268
                                              AAF28060;
    23-MAY-2001
                                                                                    AAF28060 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 17205; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGAGGCTGGGGCTANGGCTGGGGCTGGGGCTAGGGCTNAGGCTGAGGTTGGG 257
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    (first entry)
                                                                                    CDNA; 10347 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of the human 07CG27 oncogene. This gene is found at the HPC1 region of chromosome 1. The sequences can be used in the diagnosis and identification of treatments for prostate cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5866 GCTGGGGCTTGGAGCTGAAGTTGATGCTAGGGCTGAAGCAAGAATGGGAATTGAG 5807
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                                                               5566 GCTGGAACTGGAGTTAAGGTTGCCGGAAGTGGAGCTGAGGTTGAGGCTGGAACTGAAGCT 5501
                                                                                                                                                 5626 GCTGAGGTTGAGGCCAGAACTGGAGCTAAAGTTGAGGCTGGAACCGGAGCTGAGGTTGAG 5567
                                                                                                                                                                                                                              5686 ACTGAAGCTGAGACTGAGGCTGAAGCTGAAACTGGAGCTAAGGGTGAGGCTGGAACTGGA 562
                                                                                                                                                                                                                                                                                                                 5746 GCTGGGGCTGAGGCTGGAGCTGAAGAAGAGGTTATAGCTGCAGCTGAAGTAGAGGCTGGA 5687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 07CG27 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 79-91; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tavtigian SV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human prostate cancer marker gene termed as 07CG27 gene, useful for screening mutations in the gene in diagnosis of a predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB35408
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(HOSP-) HOSPITAL FOR SICK CHILDREN.
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374 GGGGCNTAACGCTGAGCTNGNNGC 397
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225..8684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "07CG27 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%;
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); Mismatches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                   probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal liver single exon nucleic acid probe #21118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA72813 standard; DNA; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 21118; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA72813;
                                                                                                                                                                                                                                                                                                              Sequence 368 BP; 29 A; 76 C; 149 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00669.
                                                                                           121
 195
                            181 CTGAGGTTGGGGCTGGGGACTGAGGCTGGGGCTAAGGCTGGGGCTGAGGCTAGGG 240
                                                                                                                                                    61 CTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGACTGAGGCTGGGG 120
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                  1 CTGAGGCTGGGGCTGGGGCTGGGGCTGGAGCTGGGGACTGAGGCTGGGGCTGGGG 60
                                                                            CTGGGGCTGAGGCTGGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGGGGC 180
CTGTGGCTCTGACTGGCCTGTGGCTGTGGCTGCTGTGGATGTAGCTGGCACTGTGG
                                                                                                                        CTGGTGCTATGGCTGTAGCTGGCACTGTGGCTGTGGCTGTGGCAGTGGCACTGTGGCTGTGG 135
                                                          CTATGACTGGTACTGTGTCTTGG-CTGGTGCTATGGCTGTAGCTGGCACTGTGGCTGTGG
                                                                                                                                                                                    CTGTGGCTGTGGCTGTGGCACTGTGGCTGTGGCTATGACTGATACTGTGTCT-TGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                              Conservative
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2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.
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                                                                                                                                                                                                                                                            29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                              Score 148.4;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                       1e-17;
                                                                                                                                                                                                                                                  115; Indels
                                                                                                                                                                                                                                                                              Length 368;
                                                            194
                                                                                                                                                                                    75
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Query Match Best Local : Matches

234;

Conservative

0;

Mismatches

115; Indels

2; Gaps

2

Similarity

29.78;

Score 148.4; Pred. No. 1e-

DB 22;

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RESULT 14
ABA38433
ID ABA38
XX ABA38
XX Probe
XX Probe
XX Human
KW Cardi
KW Cardi
KW Conge
XX WO200
XX WO1-FE
PR 03-AU
PR 30-JA
PF 30-JB
PR 04-OC
XX WPI;
FR 17-SE
PR 04-OC
XX WPI;
XX WPI;
XX WPI;
XX Sing)
PT heart
XX Clain
XX CC Grobe
CC Grobe
CC Grobe
CC Speciol
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멍
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #16899 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA38433;
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Sequence 368 BP; 29 A; 76 C; 149 G; 114 T; 0 other;
                                                                                              congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID No 16899; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease; ss.
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                                                                at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIGIAGCIGGTGCIGTGACTGTGCTGTGCTGTGCTCTGACTGGCCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTGGCTATGACTGGCACCGTGGCCGTGGCTGGTGGTGGTGA 365
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2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
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RRESULT 15
AAK21244
ID AAK21
XX AAK21
AC AAK21
XX Human
XW Human
XW Human
XW Human
XW Homo
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 21235; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe SEQ ID NO: 21235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 CTATGACTGGTACTGTGTCTTGG-CTGGTGCTATGGCTGTAGCTGGCACTGTGGCTGTGG 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGACTGAGGCTGGGGCTGGGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTNAGGCTGAGGTTGGGGCTGGGGCTGACGCTGGGGCTGAGGCTNGGNCTGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTGGCTCTGACTGGCCTGTGGCTGCTGCTGCTGGATGTAGCTGGCACTGTGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0236359
2000US-0224263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
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Sequence 368 BP; 29 A;

76 C; 149 G; 114 T; 0 other;

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Best Local Similarity
Matches 234; Conserv
                                                           255 CIGTAGCIGGTGCTGTGACTGTGGCTGTGGCTGTGGCTGTGGCTCTGACTGGCCCTGTGG
                                                                                                                          195 CTGTGGCTCTGACTGGCCTGTGGCTGTGGCTGCTGTGGATGTAGCTGGCACTGTGG
                                                                                                                                                         181
                                                                                                                                                                                         136
                                                                                                                                                                                                                         121
                                                                                          241 CTNAGGCTGAGGTTGGGGCTGGGGCTGGNGCTGACGCTGGGGGCTGAGGCTNGGNCTGAGG 300
                                                                                                                                                                                                                                                      61 CTGGGGCTGGGGCTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGG 120
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CTGTGGCTATGACTGGCACCGTGGCCGTGGCTGGTGGTGGTGTGA
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Search completed: October 10, 2002, 15:18:11 Job time : 91 secs

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                                                                         Small cell lung cancer associated antigens and uses therefor patent: WO 0153349-A 17 26-JUL-2001; LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL SLOAN-KETTERING CANCER CENTER (US); CORNELL RESEARCH FOUNDATION,
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1232)
                                                                                                                                                                                                                                                              AX201596 1232 bp
Sequence 17 from Patent W00153349.
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                                                                                                                                                      Stockert, E., Scanlan, M.J., Jager, D., Old, L.J., Gure, A.O. and
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E 1 (bases 1 to 54987)

E Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, T., Balsovoks, S.L., Amaratunge, H.C., Are, J.R., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bryant, N.P., Buhay, C., Burell, K.L., Byrd, N.C., Carron, T.F., Cher, S., Cher, R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Eslaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Fare, Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guaratte, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGAGGCTGGGGCTGGGGCTGGAGGCTGGAGCTGAGGCTGAGGCTGGGGCTGGGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGAGCTGGGGCTGANGCTGGGGCTGGGGCTGANCTGGGGCTGAGGCTCCNGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAGGTTGGGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTGGGGCTAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGGTTGGGGCTGGGGCTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTGGGGCTAGGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC094895.3 GI:17941690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU94895 54987 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus clone CH230-6Cl, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTGS_PHASE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%; Score 460;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                      Hale, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              findPhrapList
Consensus quality: 43361 bases at least Q40
Consensus quality: 47831 bases at least Q30
Consensus quality: 51743 bases at least Q20
Estimated insert size: 42188; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.

Direct Submission

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department Submitted (15-SEP-2001) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA

On Dec 20, 2001 this sequence version replaced gi:15667954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Senbank draft/data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 54987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GBQZ
Center clone name: CH230-6C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
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                                                                                        2220
2320
4534
4634
7599
7699
10268
10368
10368
                                                                                                                                                                                                                                                                                                   2219: contig of 2219 bp in length
2319: gap of unknown length
4533: contig of 2214 bp in length
4633: gap of unknown length
7598: contig of 2965 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Center
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spap of unknown contig of 2214 is gap of unknown; contig of 2965 k gap of unknown och gap of unknown is contig of 223 k gap of unknown is contig of 2892 k gap of unknown is contig of 2892 k gap of unknown is contig of u
                                                                                                                                                                                                                                                                                              f unknown leng of 2214 bp f unknown leng of 2965 bp
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bp in length
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Б QV

SOURCE KEYWORDS В Q 밁 Qγ 멍 QY

Qy

Д QΥ 망 Qy В γQ

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BASE COUNT
                                                                                                                                                     Query Match
Best Local :
                                                                                                                                            Matches 346;
                                                                                                     61 CTGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
                           source
181 CTGAGGTTGGGGCTGGGGCTGAGGCTGGGGCTGAGGCTGAGGCTGGGGCTAAGG 240
                                                                                                                                           Similarity 82.8
46; Conservative
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47785
4885
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26354
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33144
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34994
36301
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36301
38405
40094
420186
420186
                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                     /clone="CH230-6C1"
                                                                                                                                                                                         12393 c 12031 g 13918 t 2973 others
                                                                                                                                           57.9%; Score 289.4; DB 2; Length 54987; 82.8%; Pred. No. 1.7e-40; tive 0; Mismatches 66; Indels 6;
                                                                                                                                                                                                                                                53715: contig of 1061 bp in length 53815: gap of unknown length 54987: contig of 1172 bp in length
                                                                                                                                                                                                                                         /Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-FEB-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
4 (bases 1 to 143720)
Han,J., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M., Goltz,J., Haider,A., Hall,L., Toshikhes,T.P., Lee,E., Long,J., Direct, Submission

Direct, Submission
                                                                                                                                                                                                                                                        5 (bases 1 to 143720)
Han,J., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M., Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J., Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.
Direct Submission
Submitted (25-JAN-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St., Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-DEC-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave. Bronx, NY 10461, USA
3 (bases I to 143720)
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Mus Musculus Chromosome 2 RP23-58L18, complete sequence
AC087332
                                                                                                                                                                                02139, USA
On Feb 1, 2001 this sequence version replaced gi:12484303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02139,
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 143720)
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Center Code: HPGC
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                                                       //wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                          Harvard Partners Genome Center
gnktm@capecod.bwh.harvard.edu
                                                                                                                                                                         Genome Center
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Sequencing vector: pv018; L08752
Chemistry: Dye-terminator Big Dye; 100%
Assembly program: Phrap version 0.990319
Contig length: 143720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatWasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low coverage linkages are vertified by ECR product size verification or verification of forward and reverse reads from clones which span
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contig length: 143720 Fraction of Phrap value < 40: 8.349e-05 Error Rate in Consed: 0.00 per 10,000 bases Number of N's in consensus: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than I per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.
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                                   /rpt_family="(TTC)n"
complement(3946, .40)
                                                                                                                                             /rpt_family="L1MB7"
3265. .3380
                                                                       /rpt_family="L1MB7" 3834. .3914
/rpt_family="B4A"
                                                                                                           /rpt_family="(TATATG)n"
complement(3381. .3819)
                                                                                                                                                                                                     rpt_family="L3"
                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
2373. .2464
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                                                                                                                        /rpt_family="B3A" 39771. 40266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_famil
                                                 /rpt_family="(TG)n"
complement(40705. .40894)
                                                                                  /rpt_family="L1M4"
40273 . .40321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="B2_Mm1" 33687. .33709
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complement(19924. .2004
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38396, .38754
                                                                                                                                                                                                                                                                                                                                                           /rpt_fami
36830. .3
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36558. .3
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33524. .33686
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29704...2
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27887. .2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(CAGAGA)n"
complement(10946. .1109
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/rpt_family="B3A"
complement(4233 . .4449)
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10774. .10795
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/rpt_family="B1_MM"
complement(4957...5065)
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27851. .27887
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26227, .26602
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7862. .7906
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7137. 7206
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                                                                                                                                                                                                                                                          _fami
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2. .17361
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                                                                                                                                                                                                                                                                                                                                       _family="PB1D7"
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           57.0%; Score 285; DB 10; Length 143720;
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AL670227/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26348 CTGGGGCTGGGCCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 26407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26288 CTGGGGCTGGGGCTGGGGCTGGGGCTGGGCCTGGGGCTGGGGCTGGGG 26347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26228 CTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGCCTGGGCCTGGGGC 26287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26588 CTGGGGCTGGCTCCTTGCTCCAAGTTAAGTGGT 26626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26528 CTGGGGCTGGGGCTGGGCCTGGGGCTGGGGCTGGGGCCTGGGGCTGGGGCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 CTGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CTGAGGTTGGGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CTGGGGCTGAGGCTGGGGCTGGGACTGAGGCTGGGGACTGAGGCTGGGGCTGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CTGGAGCTGGGGCTGANGCTGGGGCTGGGGCTGNNGCT-GANCTGGGGCTGAGGCTCCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGGGGCTGGGGCTGGGGCTGGGGGCTGGGGGCTGGGGCTGGGGCTGAGGCTGGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGAGGCTGGGGCTGGGGCTGGGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGG 60
                                                                                                                                                              Assembly program: XGAPA; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 219697 bases at least Q40
Consensus quality: 229081 bases at least Q20
Consensus quality: 220081 bases at least Q20
Insert size: 220261; sum-of-contigs
Insert size: 213159; 11.3% error; agarose-fp
Quality coverage: 13.01x in Q20 bases; sum-of-contigs
Coverage: 13.51x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:18307364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL670227 220761 bp DNA linear HTG 30-JAN MUS musculus chromosome 4 clone RP23-317N1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: bM317N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL670227.2 GI:18477084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: humquery@sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                   NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number will
as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG 30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                             RESULT 5
AF218784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 240 GCTMAGGCTGAGGTTGGGGCTGGGGCTGAGGCTGAGGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OY 1 CTANGGCTGGGGCTGGGGCTGAGGCTGAGGCTGGAGCTGGAGGCTGAGGCTGGGG 60
Db 119954 CTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGGGGTGAGGGGGTGAGGGCTGAGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 119774 GCTGAGGCTGGGGCTGGGGCTGGGGCTGAGGCTGAGGCTGAGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 119834 GCTGAGGCTGGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 119775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 119894 CTGGGGCTGGGGCTGGGGCTGGGGGCTGAGGCTGAGGCTGAGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                              ACCESSION
                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                       Db 119594 GCTGGGGGCTGAGGCTGGGGGC-TGGGGCTGAGGCTGGGGGCTGGGGCT 119544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pb 119654 GCTGAGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGAGGCTGGG 119595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
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                                                                               KEYWORDS
                                                                                                              VERSION
               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GCTGGGGCTGAGGCTGGGGCTGGGACTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 GCTGAGGTTGGGGCTGGGACTGAGGCTGGGGCTANGGCTGGGGCTGAGGCTGGGGCTAGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 GCTGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATGCT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTGGGGCTGGGGCTGAGGCTGGGG-CTGGGGCTGGGGCTGGGGCTGGAGGCTGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGGAGCTGGGGCTGANGCTGGGGGCTGGGGCTGNNGCT-GANCTGGGGCTGAGGCTCCN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344;
           Gallus gallus
                                                                                                                                                                      AF218784 2801 bp DNA linear VRT 05-MAR Gallus gallus MHC Rfp-Y class I alpha chain (YFVI) pseudogene, YFV-Y-FVw*7 allele, complete sequence.
                                                                                                              AF218784
AF218784.1
                                               chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
57530 a 54793 c 52961 g 54975 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:02733 fragment_chain:1" 20014. .220761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:03451
fragment_chain:1"
130096. 133380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:SP6
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fragment_chain:1"
156640. .208913
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fragment_chain:1"
150271. .156539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:02708
fragment_chain:1"
133481 . 150170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-317N1"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:05258
                                                                                                              GI:13195166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.1%; Score 280.4; DB 2; Length 220761; 83.5%; Pred. No. 5.4e-39;
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Guillemot, F., Billault, A., Pourquie, O., Behar, G., Chausse, A.M.,
Zoorob, R., Kreibich, G. and Auffray, C.
A molecular map of the chicken major histocompatibility complex:
the class II beta genes are closely linked to the class I genes and
the nucleolar organizer
EMBO J. 7 (9), 2775-2785 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-DEC-1999) Department of Molecular Biology, Beckma Research Institute of the City of Hope National Medical Center, 1450 E. Duarte Road, Duarte, CA 91010-3011, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen Binding Region
J. Immunol. 166 (5), 3324-3333 (2001)
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Afanassieff,M., Goto,R.M., Ha,J., Sherman,M.A., Zhong,L.,
Anfanassieff,M., Goto,R.M., Zoorob,R. and Miller,M.M.
Auffray,C., Coudert,F., Zoorob,R. and Miller,M.M.
At Least One Class I Gene in Restriction Fragment Pattern-Y
At Least One Class I Gene Cluster in the Chicken, Is
Transcribed, Polymorphic, and Shows Divergent Specialization in
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Afanassieff, M., Zoor
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/gene="YFVI"
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/allele="Y-EVIw*7"
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Pred. No. 3.9e-35;
0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 160964 bases at least Q40
Consensus quality: 164326 bases at least Q30
Consensus quality: 164426 bases at least Q30
Consensus quality: 164482 bases at least Q30
Estimated insert size: 200000; agarose-fp estimation
Estimated insert size: 170624; sum-of-contigs estimation
Quality coverage: 10.97 in Q20 bases; sum-of-contigs estimation
Quality coverage: 12.86 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Submitted (19-DEC-2000) Production Sequencing Facility, DOE Joint
Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                              BOE
                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118562)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC026443 118562 bp DNA linear PRI 15-AUG-
Homo sapiens chromosome 5 clone CTD-2296H22, complete sequence
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Direct Submission
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Joint Genome Institute
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/db_xref="taxon:10090"
/clone="rep3-3310f"
/clone="frecI mouse BaC library 23"
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                                                                                                                                                         Homo sapiens chromosome 5 clone CTD-2194D22, SEQUENCE, 11 ordered pieces.
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4 (Dases 1 to 118562)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Quality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 0.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finishing Completed at Stanford Human Genome Center
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 126080 bases at least Q40
Consensus quality: 131684 bases at least Q30
Consensus quality: 131684 bases at least Q30
Consensus quality: 133080 bases at least Q20
Estimated insert size: 151790; agarose-fp estimation
Estimated insert size: 151790; agarose-fp estimation
Quality coverage: 5.58 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.33 in Q20 bases; sum-of-contigs estimation.
*NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs estimation.
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the arccession number will be preserved.
                                          Similarity 74.(
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 19, 2001 this sequence version replaced gi:9256458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project Information
Center Project Name: 702139
Center clone name: CITB-H1_2194D22
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13490)
DDE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center Code: JGI
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DOE Joint Genome Institute.
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Unpublished
2 (bases 1 to 134909)
                                                                                                                                                                                                                                                                                                                                                                                                                         the accession number will be preserved.

1 1795: contig of 1795 bp in length
1896 30803: contig of 28908 bp in length
30804 30903: gap of unknown length
30904 34172: contig of 28908 bp in length
34173 34272: gap of unknown length
34173 40069: contig of 5797 bp in length
40170 40169: gap of unknown length
40170 40169: gap of unknown length
62854: contig of 2968 bp in length
62855 62954: contig of 20640 bp in length
62855 83594: contig of 20640 bp in length
83595 83694: gap of unknown length
83695 84926: contig of 1232 bp in length
84927 102731: contig of 17705 bp in length
102832 116522: contig of 18691 bp in length
102832 116522: contig of 18691 bp in length
116523 116522: gap of unknown length
116523 116522: gap of unknown length
1131921 132020: gap of unknown length
131921 132020: gap of unknown length
132021: gap of unknown length
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82855
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102732
                                                                                                                                                                                       /clone="CTD-2194D22"
/clone_lib="CalTech human BAC library D"
/35747 c 36124 g 30727 t 1000 others
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 134909
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                      45.0%; Score 225; DB 2; 74.0%; Pred. No. 1.6e-29; tive 0; Mismatches 101
                                                                                                  Length 134909;
                                          Indels
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AUTHORS
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AC104515
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AL Unpublished (1998)

CE 2 (bases 1 to 179386)

CE 2 (bases 1 to 179386)

CE 2 (bases 1 to 179386)

RS Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

ROGLES,Y. An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,

Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,

Ferriera,S., Frise,E., Galle,R.F., Gargy,N.S., George,R.A.,

Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,

Ibeyvam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,

McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J.,

Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,

Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,

Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.E., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hostlin, S.R.A., Hostlin, D., Howland, T.J.,
Ibeywam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Woshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Patragas, V., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.,
Sequencing of Drosophila chromosome X, region 20B-20C
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BACR27K09, complete sequence.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 179386)
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AC104515.1 GI:17646880
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (http://www.fruitfly.org/sequence/) or send email
                                                                                  ACO11760 182421 bp DNA linear HTG 18-FEB-2000 Drosophila melanogaster chromosome X clone BACRO5K22 (D1132) RPCI-98 05.K.22 map 20C-20C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 116 unordered pieces.
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Sequence submitted by:
Berkeley Drosophila Ge
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AC011760
AC011760.8 GI:6996986
HTG; HTGS_PHASE1.
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Lawrence Berkeley National Laboratory, MS 64-121
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02; Conservative
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/clone=ib="ReCI-98 (Roswell Park Cancer Institute
/clone_lib="ReCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
pBACe3.6) 5 36862 g 54093 t
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'Strain-"y; cn bw sp"

/db_xref-"taxon:7227"

/chromosome-"X"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CE 1 (bases 1 to 182421)

RS Celniker, S.E., Adpayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Humnasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Woshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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Direct Submission

AL Submitted (14-OCT-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, Ms 64-121, Berkeley, CA 94720, USA,

On Feb 18, 2000 this sequence version replaced gi:6980168.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruiffly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence . It currently

* consists of 116 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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2: contig of 449 bp in length
2: gap of unknown length
3: contig of 624 bp in length
4: gap of unknown length
5: gap of unknown length
6: gap of unknown length
7: contig of 647 bp in length
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RATEURS.

RATEURS
                     Submitted (23 OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062358.
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Rattus norvegicus
Eukaryota; Metazo
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AC098110.3 GI:17969661
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findPhrapList
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Contact: hgsc-help@bcm.tmc.edu

------- Project Information

Center project name: GGHX

Center clone name: CH230-158N10

------ Slumnary Statistics

Assembly program: Phrap; version 0.990329First call to
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165046:
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154120:
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6: gap of unknown length
1: contig of 2155 bp in length
7: contig of 2056 bp in length
7: contig of 2056 bp in length
7: gap of unknown length
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7: gap of unknown length
7: contig of 1688 bp in length
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                                               Score 217.6; DB Pred. No. 2.8e-28
                                      Mismatches
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AF189263/c
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97286 CTGGGTCTGGGTCTGGGTACTGGTCTAGGACTGGGACT 9732:
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Sinkkonen, S. T., Hanna, M.C., Kirkness, E.F. and Korpi, E.R., GABA(A) receptor epsilon and theta subunits display unusu structural variation between species and are enriched in locus ceruleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (24-SEP-1999) Dept. of Functional Genomics, The Institute
for Genomic Research, 9712 Medical Center Drive, Rockville, MD
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Hanna, M.C. and Kirkness, E.F.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21. .2753
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/db_xref="taxon:10090"
1. .2773
EPQPEPQPEPQPEPKPEPEPQPEPEPQPEPQPEPQPEPXPEPQPEPXPEPQPEPXPEPQPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Epsilon"
/note="similar to GABA-A receptor subunit family members"
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1. .2773
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JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS RESULT 13 AF131866 KEYWORDS SOURCE ORGANISM BASE COUNT FEATURES DEFINITION VERSION ACCESSION Query Match TITLE JOURNAL 1085 CTCCGGCTGGGGCTCCGGCTTGGGCTCGGGCTCAGGCTCAGGCTCAGGCTCAGG 1026 1145 CTCAGGCTCCGGCTCAGGCTCCAGGCTCCGGCTCAGGCTCAGGCTCAGG 1086 181 CTGAGGTTGGGGCTGGGGCTGGGGCTANGGCTGGGGCTGAGGCTGGGGCTAGGG 240 726 GTCTGGGTCGGGGTTGGCGCCCAGCCTGGACCTGGGCTGGGGTCTGGGGCT 676 420 ATGNGNATGNNCTGNGGCTNNCNTCCNNGACAAANANTTNNAACTTGNGGT 470 301 CTGGAGCTGGGGCTGANGCTGGGGCTGNNGCTGA-NCTGGGGCTGAGGCTCCNG 359 241 CTNAGGCTGAGGTTGGGGCTGGGGCTGACGCTGGGGCTGAGGCTNGGNCTGAGG 300 61 CTGGGGCTGGGGCTGAGGCTGGGGCTGGGGGCTGGGGCTGGGACTGAGGCTGGGG 120 1 CTGAGGCTGGGGCTGGGGCTGAGGCTGGAGCTGAGGCTGGGGCTGGGG 60 Local ${\tt CTGTGGCTCAGGCTGGGGC-TCAGGCTGAGGCTCAGGCTGGGGCTCAGGCTGAGGGCTGAGGGCTGAGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT$ CTGAAGCTGAGGCTGGGGCNTAACGCTGAGCTNGNNGCTGGTGCTNATGCTTGNCTNANA 419 CTCAGGCTGGGGCTCAGGCTCCGGCTGGGGCTCAGGCTGAGGCTCAGGCTGTGG CTCAGGCTCCGGCTTGGGTTCTGGCTGGGGCTCCGGCTGGGGCTCCGGCTGAGGCTCAGG Mus musculus BAC 271B7 chromosome X Gabre gene, complete sequence. AF131866.1 GI:6651043 Direct Submission
Submitted (26-FEB-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 110312)
Platzer,M., Zhao,W., Nordsiek,G., Herman,G.E. and Rosenthal,A. Genomic analysis of mouse X chromosomal regions corresponding to been scales. Platzer, M Unpublished Mus musculus house mouse Similarity 610 (bases 1 to 110312) Conservative נם YLTALDEYLAICEYULCFCTLLBEAVLMELTYNNIKROASLKYYOLDTNSRANAHTRAR ARTRARARAROOQEVFVCEIVTYBENABEGYQWSPRSRRPQCPWRRCGRSYVCFRV LRKYECMAÞGCEGGSWQRGRICHHYRLDNYSRVLFPITFFFNVLXWLICLNL" 1904 c 683 g 576 t 43.0%; 0; Mismatches 157; Pred. No. 9.8e-28; 110312 bp DNA Length 2773; Indels linear ROD 01-JAN-2000 Gaps 846 misc_feature repeat_region repeat_region repeat_region polyA_signal repeat_region 21338. .21484,2 /gene="Gabre" /codon_start=1 /rpt_family="L1" 2888. .3141 /rpt_family="ID3"
complement(1490. .2634)
/rpt_family="ID3" /note="CpG island: 66.6 %GC, o/e=0.60, *CpGs= 55" /note="Region: CpG Island" complement(23063. .23106) /rpt_family 19674. .198 /rpt_family="L1"
complement(17215. /rpt_family="PB1"
complement(14063..141)
/rpt_family="(CAGGA)n" complement(10476...10533)
/rpt_family="L2"
complement(10573...10814)
/rpt_family="L2" complement(4369. .4422)
/rpt_family="(CA)n" __mprement(3412. .3417)
/gene="Gabre"
comple: /gene-"Gabre"
/gene-"exons 2,3 predicted by procrustes"
/product="GABA receptor epsilon subunit"
/product="GABA receptor epsilon subunit"
complement(3398. .>22146) /rpt_family="purine-rich"
complement(1071. .1157) /rpt_family="RSINE1" 214. .345 /clone~"BAC 271B7" 77. .186 /organism="Mus musculus" /db_xref="taxon:10090" /chromosome="X" /product="GABA receptor epsilon subunit" /protein_id="AAF22143.1" /db_xref="GI:6651044" /rpt_family="LlME3A" 21533. 21572 /rpt_f 16548. complement(13500. .13566)
/rpt_family="MIR"
13657. .13807 /rpt_family-"L2" 21703. .22547 /rpt_family="LlM3e" 19123. 19156 /gene="Gabre" /rpt_family="Lx8" /rpt_family-"L1_MM" /rpt_family="(TAA)n" 19477. .19625 /rpt_family-"RLTR13D" "LIMC5" .14107)

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RESULT 14 AC015260/c	pb 17879 Grendegreegegrigececchaderadaceregeertegegreer 17929	QY 420 ATGNGNATGNUCTGNGGCTNNCNTCCNNGACAAANANTTNNAACTTGNGGT 470	Db 17820 CTGTGGCTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG	VINTAMONOMMONOMONOMONOMONANONANONANONANONANO	301 CTGGAGCTGGAGGCTGGAGGCTGGGGGCTGNUGCTGA-NCTGGGGCTGAGGCTCCNG	QY 241 CTNAGGCTGAGGCTGGGGCTGGGGCTGACGCTGAGGCTGAGGCTGAGG 300	QY 181 CTGAGGTTGGGGCTGGGACTGAGGCTGAGGCTAANGGCTGAGGCTGAGGCTGAGGCTAAGGCTGA	OY 121 CTGGGGCTGAGGCTGGGGCTGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCCAGGCTCAGGCTCCAGGCTCAGGCTCCAGGCTCAGGCTCCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCCAGGCTCAGGCTCCAGGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGAGCTCAGAG	QY 61 CTGGGGCTGGGGCTGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 120	OY 1 CTGAGGCTGGGGCTGGGGCTGGAGCTGGGACTGAGGCTGGGGCTGGGG 60	Query Match 43.0%; Score 215; DB 10; Length 110312; Best Local Similarity 66.2%; Pred. No. 8e-28; Matches 312; Conservative 0; Mismatches 157; Indels 2; Gaps 2	repeat_region 4814449165	repeat_region complement(4608848144)	repeat_region complement(4427)44452) repeat_region 4450144652 repeat_region 4450144652	repeat_region 43294. 43443 repeat_region 43294. 43443	4177 /rpt	complem /rpt_fa	repeat_region complementaly="Laxas" (40873)		repear_region 40195 40325	39918 /rpt	repeat_region 3975539896 /rpt_family="B1_MM"

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                                                                                                                                                                                                      274388 bp DNA linear INV 12-OCT-200. Drosophila melanogaster genomic scaffold 142000013386033 section 1 of 2, complete sequence. AE003574 AE002529
fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 274388)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
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* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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1 (bases 1 to 7085)
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On Oct 16, 2000 this sequence version replaced gi:10726352.
Location/Qualifiers
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         Search completed: October 10, 2002, 19:01:38 Job time: 1301.87 secs
                                                                                                                                                                          Db 177782 CTGGGACTGGGACTGGGACTGGGACTGGGACTGGGATTGGG 177736
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Best Local
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                                                                                                                                                                                                                                                301 CTGGAGCTGGGGCTGANGCTGGGGCTGNNGCTGANCTGGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                      241 CTNAGGCTGAGGTTGGGGGCTGGGGCTGACGCTGGGGCTGAGGCTNGGNCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTGGGCCTGGGGCTGAGGCTGGGGCTTGGGGCTGGGGACTGAGGCTGGGG 120
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28782. .296
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4 US-09-025-556-167
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6 US-09-105-537-1
7 US-09-385-028-1
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Sequence 2, Appli
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Sequence 176, App
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Sequence 11, Appli
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Sequence 2,
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Best Local Similarity
Matches 213; Conserv
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ORGANISM: Artificial Sequence
FEATURE:
 293 CGCCCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCA 352
                                                                    233 GGACGCCGTCCACCGGCTTCGCCAACGGGGACGC 292
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0; Mismatches 161; Indels Score 116.4; DB 4; Pred. No. 4.9e-13;

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Length 390;

23.38;

RESULT 1 US-09-197-649- ; Sequence 7, ; Sequence 7, ; Sequence 7, ; Sequence 7, ; Patent No. 6 ; GENERAL INFO ; APPLICANT:	00000000000000000000000000000000000000	
SULT 1 -09-197-649-7 Sequence 7, Application US/0919: Batent No. 6194550 GENERAL INFORMATION: APPLICANT: GOId, Larry APPLICANT: Tuerk, Craig APPLICANT: FILDNOW, DAVId APPLICANT: FILDNOW, DAVId APPLICANT: FILDNOW, DAVId APPLICANT: FILDNOW, Systematic FILE REFERENCE: NEXOZ/CI-CON CURRENT APPLICATION NUMBER: US. CURRENT FILING DATE: 1998-11-2 EARLIER FILING DATE: 1992-01-3 EARLIER FILING DATE: 1991-08-0 EARLIER FILING DATE: 1991-08-0 EARLIER FILING DATE: 1990-08-0 NUMBER OF SEQ ID NOS: 26 SOFTMARE: PATENTIN Ver. 2.0 SEO ID NO7 LENGTH: 390	5 5 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	70.8 70.2
49-7 7, Application US 6194550 16194550 17: Gold, Larry 17: Gold, Larry 17: Tuerk, Craid 17: Smith, Jonatha 1 NVENTION: Syste ERENCE: NEXOZ/C1- APPLICATION NUMBE FILING DATE: 1992 APPLICATION NUMBE FILING DATE: 1992 APPLICATION NUMBE FILING DATE: 1991 17: BATCHION STEP 1992 10 NOS: 26 10 NOS: 26 11 D NOS: 26 11 D NOS: 26 11 D NOS: 26 11 D NOS: 26	11333333334 113333333333333333333333333	14.2
49-7 7, Application US/09197649 . 6194550 . 6194550 . 6194550 . File Craid T: Gold, Larry T: Toerk, Craid T: Smith Jonathan D. INVENTION: Systematic Poly ERENCE: NEXO2/C1-CON APPLICATION NUMBER: US/09/1 FILING DATE: 1998-11-23 APPLICATION NUMBER: 07/829, FILING DATE: 1992-01-31 APPLICATION NUMBER: 07/739, FILING DATE: 1991-08-01 FILING DATE: 1991-08-02	30001 12585 11585 1193 352 352 352 1187 639 639 639 637 647 653 2123 2123	4411529 30001
091: 00 00 00 00 00 00 00 00 00 00 00 00 00	242421222223	1 4
49-7 7, Application US/09197649 . 6194550 . 6194550 . 6194550 . File Control T: Gold, Larry T: Tuerk, Craid T: Prichow, David T: Smith, Jonathan D. INVENTION: Systematic Polypeptide Evolution by INVENTION: Systematic Polypeptide Evolution by FILING DATE: 1998-11-23 APPLICATION NUMBER: 07/7829,461 FILING DATE: 1992-01-31 APPLICATION NUMBER: 07/739,055 FILING DATE: 1991-08-01 FILING DATE: 1991-08-01 FILING DATE: 1991-08-02 FEST ID NOS: 26 FILING DATE: 1991-08-02 FEST ID NOS: 26	0474-933-387-9420-387-9420-419-075-419-075-419-075-419-075-419-075-419-075-419-075-5248-419-075-	US-09-103-840A-1 US-08-125-468-1
Reverse Translation	31, 25, 27, 27, 28, 27, 28, 27, 28, 27, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28	Sequence 1, Appli Sequence 1, Appli

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                                                                                                                                                                                                                                    Db 3937927 GCCGCCTCGCCGCCGGTACCGCCGTTGCCGCCGTTGCCGCCATCGCCCAGTGTCGCC 3937868
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US-09-103-840A-2/c
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                                               Db 3937807 CCCGTTGCCGCCGGGGTCGTCAGTGAGTGGGCCGTGGCCGGATGGCCCCGTTGCCGCC 3937748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-2007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 NUMBER OF SEQ ID NOS: 2 SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: YENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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  453 GCACAGGGCATCGCCAACGAGGACGCCCCCAGGGCCATCGCCAAC 497
                                                                                         393 GAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGAATCGCCGAGGATGTC 452
                                                                                                                                                                                     333 GGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAAC 392
                                                                                                                                                                                                                                                                              273 AGCTTCGCCAACGGGGACGCCGCCCCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATG 332
                                                                                                                                                                                                                                                                                                                                                                     213 ACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACGGGGACGCCGTCCTC 272
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Local Similarity 49.2%;
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0; Mismatches 236;
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FILE REFERENCE: NEXO2/C1-CON
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: U5/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
FEARLIER FILING DATE: 1992-01-31
FEARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/7561,968
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER PLING DATE: 1991-08-02
SEC ID NO 7
SEC ID NO 7
SEC ID NO 7
; Sequence 4, Application US/09023173 ; Patent No. 6066781 ; GENERAL INFORMATION:
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Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gold, Larry APPLICANT: Tuerk, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Sequ
OTHER INFORMATION: having a 120 repeat of ACG flanked by fi
OTHER INFORMATION: fragments having NCOI restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 390
                                                                                                                                                                          481 CCCAGGGCATCGCC 494
                                                                                                                                                                                                                                                                                            361 CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCGAGGACGCCATCCAGGGCATCGCCAACGAGGGTTGCCCAGGGCCATCGCCAATGGGG 180
                                                                                                                                                                                                                                                     421 AGGACGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCG 480
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                                                                                                                                      TCGTCGTCGTC
                                                                                                                                                                                                                   GCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCG 360
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Similarity 51.3%;
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Pred. No. 3.7e-07;
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; CLONE: US-09-023-173-4
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Best Local Similarity 48.8
Matches 239; Conservative
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APPLICATION NUMBER: 60/038,168
EILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: PELILINORY, Joanne R
REGISTRATION NUMBER: 0665-000
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
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APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of Mature Proteins
TITLE OF INVENTION: in Plants
NUMBER OF ESQUENCES: 23
CORRESPONDENCE ADDRESS:
                                               368 GGACGCCGTCCA---GGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGA 424
                                                                                                                                                                                                               510 CGCCGGCACCGTCGCCCTCACCAACAGCATCGGCGTCCTCGGCGTCGCCCCGAGCGC 569
                                                                                                                                                                                                                                                           248 CTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCCAGGGCATCGC 307
                                                                                                                                                                                                                                                                                                          450 TAGCATGGTCCCGAGCGAGACCAACCCGTTCCAGGACACCAACAGCCATGGCACCCACGT 509
                                                                                                                                                                                                                                                                                                                                                       188 ACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 CGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCCATCGCCAATGGGGTCGCCGC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 CGCCTACGTCGAGGAGGACCACGTCGCCCACGCATATGCACAGAGCGTCCCGTACGGCGT 329
                      630 CAACGGCATCGAGTGGGCCATCGCCAACAACATGGACGTCATCACCATGAGCCTCGGCGG 689
                                                                                                              570 CAGCCTCTACGCCGTCAAGGTACTCGGCGCCGACGGCAGCGGCCAGTACAGCTGGATCAT 629
                                                                                                                                                             308 CAACGGGGACGCCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGA 367
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FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCCAGGGCATCGCCGAGGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                      CGCCGTCATCGACAGCGGCATCGACAGCAGCCACCCGGACCTCAAGGTCGCCGGCGGAGC 449
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US-09-056-556-176
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; Patent No. 6350456
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                           278 CGCCAACGGGGACGCCCACCCCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 CGCCGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCGCCCA 484
256 CTTTGCCGGTGCCGGCGGCCAGGGCGGCCTCGGTGGGCAGGGCGGCAATGGCGGCGGCTC 315
                                                                                           218 GGGCATCGCCAACTGGGACGCCGTCCACGGGCTTCGCCAACGGGGACGCCGTCCTCAGCTT 277
                                                                                                                                                                                         136 CGGCAAGGGCGGCTTCGGCGGCGACGGCGGTCAGGGCGGCCCCAACGGCGGCGGTACCGT 195
                                                                                                                                                                                                                                  158 TGCCCAGGGCATCGCCAATGGGGTCGCCCGCACAGGGCATCGCCAATGAGGACGCCACCCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 CCITY: Seattle STATE: Washing
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                                                                                                                                                                                                                                                                                                                              98 CGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGT 157
                                                                                                                                                                                                                                                                                                                                                                             16 CGGCAAGGGCGGCGACGGTGGCCACGGCGTGACGGCGTCGGCGACAGTTCCGTCAC 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 15.4%; Score 77; DB 4; Length 494
al Similarity 49.6%; Pred No. 3.8e-06;
197; Conservative 0; Mismatches 200; Indels
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SYSTEM: PC-DOS/MS-DOS
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-- NO: 176:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: EUKARYOTIC Cells Stably Expressing Genes
TITLE OF INVENTION: EVKARYOTIC Cells Stably Expressing Genes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
US-09-056-556-167

Sequence 167, Application US/09056556

Patent No. 6350456

; GENERAL INFORMATION:
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Patent No. 5976807
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                                                                                                                                                                   316 GACGAGGACGGGGACGAGGACGAGGACGAGGACGAGGACGAGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 ACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCCATCCAG 137
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION UNBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 632-4900
TELEFAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 1439 base pairs
TYPE: 1139 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 07-APR-199
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
PC-DOS/MS-DOS
PC-POS/MS-DOS
PC-POS/MS-DOS
                                              1357 GTGCCGCCAGCGGCTCAGGCGTCAACGTCACCGCCGCCACGGCCAACGGCGAACGGCGCA
                                                                                                                                          1297 GCGGCCACGGCGGTGCCACCGGCGGCGACGGCAACGGCACCAGCG 1356
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                        1237 GCGGCAACGGCTCCGCGGGCGCCGGCGGCGAGGGCGCGGCAGCGCCGGCAACG 1296
                                                                                                                                                                                                                                                                                                                                      1177 GCTCAGGCGTCGTCAACGTCACCGCCGGCCACGGCGAACGGCGGCAATGGCGGCAACG 1236
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499 A 499
                                                                                        379 AGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGAA 438
                                                                                                                                                                                                                                                                                    319 CCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCC 378
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Similarity 48.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30
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US-09-056-556-167/c

; Sequence 167, Application US/09056556

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APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.9
Best Local Similarity 49.9
Matches 220; Conservative
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 12
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1417 A 1417
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES; 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         804 CAACCACGCCGCCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .416 CAACGAGGACGCCGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 CGCCGCCATGGGCCTCACCTCCACGTCGACGCGTTTCCCGAGGTCATCGACCGGAACCGGCG 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 CATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           684 CTTCGACCTGCCCGGCGGCAGCCCCGCCGGCGGACCAACGCCAAGATGAGCGAGGCCGC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 CCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 CGCCGTCGTCACCGACGACGCCGACCTCGCCGCCCGGATCCGCGCCCTCCACAACTTCGG 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 CGTCCACGGCTTCGCCAACGGGGA----CGCCGTCCTCAGCTTCGCCAACGGGGACGCCC6C 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 CGGCGACGCCGAGGTCTTCAGCTTCCACGCCACGAGGCCGTCAACGCCTTCGAGGGCGG 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; Score 74.4; DB 4; Length 1248; 49.5%; Pred. No. 1.1e-05; htive 0; Mismatches 221; Indels 3
                                                      TREAT
     RESULT 10
US-09-105-537-3/c
; Sequence 3, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
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Best Local (
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1439 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1353 TGGTGCCGTTGCCGCCTTGCCGCTGGCGCGCCGCTGGCACCGCCGTGGCCGCCGT 1294
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                                                                                                                                                                                                                                                                                      1113 CGCCGTGGCCGCTTGCCGCCGTTGCCGCCGTCGCCGACAGCGTTGCCGAAGGACA 1054
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STREET: 6300 C
CITY: Seattle
STATE: Washing
                                                                                                                                                                                          993 TGCCCCCATTACCGCCGGCACCACCGGAGCCGGCGTTGCC 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 ACAGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 CGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGC 187
                                                                                                                                                                                                                                      428 CGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCC 467
                                                                                                                                                                                                                                                                                                                                  368 GGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                           308 CAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 CTTCGCCAACGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCCAGGGCATCGC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/177,349
CURRENT FILING DATE: 198-10-23
UNMBER OF SEQ ID NOS: 14
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5036
TYPE: DNA
DRGANIZM: Mycobacterium tuberculosis
US-09-177-349-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-177-349-2/c
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-3
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09177349 Patent No. 6268201 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 220; Conservative
                                                                                                                                                                                                                                         APPLICANT: Bloom, Bavid
APPLICANT: Bloom, Barry R.
APPLICANT: Jacobs Jr., William R.
TITLE OF INVENTION: Inib, iniA AND iniC GENES OF MYCOBACTERIA AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 96700/491
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APPLICANT: Xue, Y.
APPLICANT: Zhao, I.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12080 CAACCACGCCTACCGCGAGCACCTCGCGGGGACCTCCCCGGGCGTCGTCGTCGACCA 12021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12140 CGCCGCCATGGGCCTCACCTCCCTCGACGCGTTTCCCGAGGTCATCGACCGGAACCGGCG 12081
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Similarity 49.5%;
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; Pred. No. 1.1e-05;
0; Mismatches 221; Indels 3; Gaps
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TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLLER REPLICATION NUMBER: CIP OF 09/141,908
EARLLER REPLICATION NUMBER: CIP OF 09/073,538
EARLLER RILING DATE: 1998-05-06
EARLLER APPLICATION NUMBER: CIP OF 08/846,247
EARLLER FILING DATE: 1998-05-06
EARLLER RAPLICATION NUMBER: CIP OF 08/846,247
EARLLER RAPLICATION NUMBER: CO19 OF 08/846,247
EARLLER RAPLICATION NUMBER: 60/119,139
EARLLER RAPLICATION NUMBER: 60/119,139
EARLLER RAPLICATION NUMBER: 60/10,880
EARLLER RILING DATE: 1999-02-08
EARLLER RILING DATE: 1998-09-22
EARLLER RILING DATE: 1998-09-29
EARLLER RILING DATE: 1998-09-29
EARLLER FILING DATE: 1998-0
                                                                                                                                             ; ORGANISM: Streptomyces venezuelae US-09-320-878-21
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                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver
SEQ ID NO 21
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09320878A Patent No. 6117659
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APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, ROBERT
APPLICANT: TANG, Li
                                                                                                                                                                                                                                   TYPE: DNA
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14.8%; Score 74; DB 3; 49.3%; Pred. No. 1.3e-05;
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GENERAL INFORMATION:
                                                                                      PILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                  TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-SRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: BUNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O.BOX 74
CITY: FALLS CHURCH
STATE: VA
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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12588 base pairs
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin;
FILE REFERENCE: 600.438US1
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                                                                                                                                                               Sequence 1, Application US/09105537A Patent No. 6265202
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Best Local S
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ORIGINAL SOURCE:
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STRANDEDNESS: single
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nes 230; Conserv
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RESULT 15
US-09-025-691-2
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09025691
Patent No. 6069299
GENERAL INFORMATION:
APPLICANT: Broadway, Roxanne M.
APPLICANT: Harman, Gary E.
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5032 GATCGCCGCGCACGTCGCCGGTGTCCTCTCCCTCGACGCCGCACGTCTCGTCAC 5091
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5212 CGTCAACGGACCCACCGCCGTGGTCGTCTCCGGCGACGCGGACGCCGCCG 5261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5152 GGGCGAGGCCGAGGTCGTCGAGTCCCTGAAGGGCTACGAGGGCAGGGTCGCCGTCGCCGC 5211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4912 GGAGCTGGACCTCACCGCGTACACCCAGCCCGCCCTTTCGCCTTTCGAGGTGGCGCTGTT 4971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4792 CGCCATGGGCGAGGAACTGCGCGCCGCGCACCCCGTGTTCGCCGCCGCCGCCCTCGACACCGT 4851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 15872
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                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                          STREET: Clinton
CITY: Rochester
                      APPLICATION NUMBER: FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                              Nixon, Hargrave, Devans & Doyle LLP inton Square, P.O. Box 1051
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Search completed: October 10, 2002, 20:05:06 Job time: 1144.73 secs

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Best Local s
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668 CTTCGCCGACA 678
                                                                              608 CATCTCGGTCGGCGGCGAGAAGGGCGCGGTCGCCGTCAACGACAGCGCCTCCGCCCAGCG 667
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                                    488 CATCGCCAACA 498
                                                                                                                   428 CGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCCAGGG 487
                                                                                                                                                       557 G-----CAGTTCCGCGCCGACCTCGCCGCCAAGCAGGCCGACGCCAAGTCGGTGAT 607
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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16) 263-1600
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Pred. No. 2.3e-05;
0; Mismatches 169; Indels 9
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                 153.4
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Match Length DB
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/db_xref="taxon:5606" /clone="bKr2p434E0731" /clone="bKr2p434E0731" /clone=lib="434 (synonym: htes3)" /tissue_type="testis" /dev_stage="adult" /lab_host="pH10B" /lab_host="pH10B" /note="vector: pSport1; Site_1: Not1; Site_2: Sal1" 217 a 181 c 180 g 119 t	Am Klopferspitz 18a D-82152 Martinsried, Germany Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. No sl sequence available. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. 1. 697 1. 697 1. 697 1. 697 1. 697	ALI10383 ALI10383 ALI10383 ACT 29-FEB-2000 DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731_5', mRNA sequence. ALI10383.1 GI:5865991 EST. EST. ALI10383.1 GI:5865991 EST. ALI10383.1 GI:5865991 EST. ALI10383.1 GI:5865991 ELWARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 697) Elum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Blum, et al.) Unpublished (1999) COntact: Blum H

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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
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                                                                                                                                                                                                                                                                                          No s1 sequence available.
This clone (NKFZp434C1116) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Henbnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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63 c 60 g 16 t 2 others
                                                                   /lab_host="DH10B"
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                                                                                  122 CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCCAGGGCATCGCCAATGGGGT 181
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                                        8 CGAGGACGCTGTATACGACATCGCTAATGAGGACGTTGTATATGACATCGCTAATGAGGA 67
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                                                                                                                               190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11425 row: f column: 07
High quality sequence stop: 758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI829297.1 GI:15940847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603079427F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170950 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                           215
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                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop:
                                                                                                                                                                                                                                 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NH MCC Library."

a 159 c 167 g 217 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5170950"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nttp://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                 Score 118.6; DB 10; Length 758; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124.6; DB 9;
Pred. No. 3.4e-08;
0; Mismatches 31;
                                                                                                                               Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 bp
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                                                                                                                               0;
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REFERENCE
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BI561135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                      Query Match
Best Local :
                                                              Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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199 CCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 AGAAGATGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 CATCGCTAATGAGGACGCTGTATATGGCATCGCTAATGAGGATGCTGTATACGAATTCGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 ATATGACATCACTAATGAGGACGCTCTATACGACATCACTAATGAGGACGCTGTATACAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCCAGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TGCTTTACAAGACATAGCGAATGAGGTTGCTGTATATGACATCGCTAATGAGGACATTGT 127
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAATAAGGATGCTGTATATGACATTGCTAATGAGGACACTGTACAAGACATCTGTAAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACGCCGC 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI561135
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1749 row: k column: 15
                                                                                                                                                                    172
                                                              Conservative
                                                                                                                                                     /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI_XhoI (gtcgag); Oligo-df primed using primer 5'.-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 185 c 185 g 131 t
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5296262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                             22.6%;
                                                            Score 113; DB 10;
Pred. No. 1.1e-06;
0; Mismatches 65;
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                                                                                                   Length 673;
                                                              Indels
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AUTHORS
TITLE
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BG724320
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BG724320.1 GI:14003507
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Plate: LLAM10750 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                  183 a
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4829993"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                             19.7%;
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319 CARCAAAGGCAMTGGCAACGAGGTCACAAGGCATGCCTAACGAGGAGGCCGTCC 378
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                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 582) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG724320 582 bp mrNA linear EST 08-MAY-2001 602697968F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4829993 5', mRNA sequence.
                                                                                                                                                                                                                                      row: g column: 18 ence stop: 580.
                                                                                                                                                 Score 98.6; DB 10;
Pred. No. 9e-05;
0; Mismatches 94;
                                                                                                                                                   Indels
                                                                                                                                                                                   Length 582;
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RESULT 6 AI904151

SOURCE

KEYWORDS VERSION δÃ Вþ ρ Дb γQ Db

В

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BASE COUNT
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ACCESSION
                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 CATGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 CGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACGGGGACGCCGT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 CGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCGCCAATGAGGA 208
                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AAGGCACGCTAACGTGGACGCTGTACACGACATTGCTAATGAGGACAGCGTATAAGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTGTACAAGACATCACCAATGAGGGCGCTTTATACGACATTGCTAATGGCACCGAC-- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGGACACCCTACAAGCCGTCGCTAACAAGTACACTGTACACAACATCGCTAATGAGGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 241)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagali,M.A., de Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvelho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1904151 241 bp mRNA linear EST 30-
CM-BT043-090299-075 BT043 Homo sapiens cDNA, mRNA sequence
A1904151
                                                                                                                                                                                                                                                                                                                                                                                                                                                        \label{linear_constraints} $$ \frac{http://www.ludwig.org.br/seq/gethtml.pl?tl=CMst2=CM-BT043-075.html&t3=090299&t4=1)$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Empall: asimpson@ludwig.org_br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
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                                                                                                        /note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                              /clone_lib="BT043"
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/db_xref="taxon:9606"
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                         18.8%;
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                                           Length 241;
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16 CTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGG 75
                                                                                      TOCST
                                                                    240;
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Durham, NC 27708-1000
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919 613 8177
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187 GCTGTATATGGCATCGCTAATGAGGATGCTGTATACGAATTCGCTAATAAGGATG 241
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
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1024015H06.y2 C. reinhardtii CC-1690, normaliz
Chlamydomonas reinhardtii cDNA, mRNA seguence.
                                                                                                                                                                                    Anote-"vector: pBluescript II SK-; Site_1: EcoRI; Site_2: Xhol; This library, constructed by John Davies and Jeffrey McDermott, combines coNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light. TAP medium in the dark. HS (minimal) medium in the light. TAP medium in the dark. HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the BcoRI (5') and XDOI (3') sites. PBLuescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
                                       Score 85.4; DB 10; Length 780; Pred. No. 0.0051;
231; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 822)
                                                                                                              Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                       Genoscope.
                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                              Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fish Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F., Saurin,W. and Weissebbach,J.

Human gene number estimate provided by genome wide analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H.
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GSS; genome survey seq
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007M14 of library H from Tetraodon nigroviridis, genomic survey
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                  /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone-"007M14"
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                                                                                                                                                                                                               TITLE
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Contact: Bailey P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACAC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGCATCGCCAACGGGGA 316
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                                                                                                                                                                                                                                                                                                                                                                                          Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Clouting, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G., Sorrells, M., Warburton, M. and Wenzel, G., International Triticeae EST Cooperative (TEC): Production of
                                                                            Cereals Group, John Innes Centre
Norfolk, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 455571 ext. 2587
Fax: 44 1603 502241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
Email: paul.bailey@bbsrc.ac.uk
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITEC PSR Wheat Endosperm Library Triticum aestivum cDNA
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/note="Genoscope sequence ID : C0BH007BG07XE1-end : PUC-Ori"
a 262 c 203 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                 onal Triticeae EST Cooperative (ITEC): Production of Sequence Tags for Species of the Triticeae
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rocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 CCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 TCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCGCCCAGGGCCATCGCCAACA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 AGCACAAGGGCAACAAGGTCAGCAGCTAGGACAAGGGCAACAAGGTCAGCAGCCAGTGA-536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AACTTCTCCGTTGCAGCCAGGACAAGGGCAACCAGGGTACGACCCAACTTCTCCGCAACA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 ACAAGGGCAACAGCCAGGACAATGGCAACAACCAGGACAAGGGCAACCAGGATACTACCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCG 198
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i (bases l to 884)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Kannangara,G., von
Wetstein,D., Akhunov,E., Chin,A., Choi,D.W., Fenton,R.D., Kianian
,P., Otto,C., Simons,K., Zhang,D., Begum,D., Frisch,D., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                  BG417341 884 bp mRNA linear EST 23-OCT-2001
HVSWEk0017J12f Hordeum vulgare testa/pericarp EST library
HVCDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEK0017J12f, mRNA
                                                                                                                                                    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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Location/Qualifiers
                                                                                                                                 Triticeae;
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/dev_stage="1:1 mix 10:20 days post anthesis"
/note="vector: Lambda ZAP II (Stratagene)"
/note="vector: Lambda ZAP II (Stratagene)"
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/clone_lib="ITEC PSR Wheat Endosperm Library"
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/cultivar="Soleil"
                                                                                                                                 Hordeum.
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Pred. No. 0.031;
0; Mismatches 226; Indels 11
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                                           288 GACGACGCCACACATCAACAAGCACACTTCCGCGTCCCCTTCGTCTGCGGCTGCCGC 347
                                                                                               195 ATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCC 254
                                                                                                                                                                                                                135 CAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGC 194
                                                                                                                                                                                                                                                                                                                                                                                         237 GAGTCCATCGGCGTCGACTACGTGGACGAGAGC-----GAGGTCCTCACACTCGCC
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                                                                                                                                                                                                                                                                                                                             75 GACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATC 134
                                                                                                                                                                                                                                                                        GTCACCATCCCGGTCATGGCCCAAGGCCCGCATCGGGCACTTCGTCGAGGCCCAGATCCTC 236
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100 Jordan Hall, C
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On Mar 13, 2001 this sequence version replaced q1:13322988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 686.
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Total hq bases = 467
Seq primer: AATTAACCCTCACTAAAGGG
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Fax: 864 656 4293
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Similarity 50.4%;
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//lab_bost="TyCl21"
//lab_bost="TyCl21"
//note="Yector| lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
//note="Yector: lambdaZAP; Site_1: EcoR1; Site_1: Xho1;
//note="Yector: lambdaZAP; Site_1: Ronangara, Indition of the state of the state; And I million pfu dest and periodarp were dissected from developing kernels at Washington State University, Pullman WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was purified, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagenids in the Ty Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Xianian, Otto, Simons, Zhang). Phagenids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/genedes/bun/3/Coover.html)"
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HVcDNa0013 (normal)"
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/clone="HVSMEk0017J12f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 GTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AACCTGGGCGAGGCCCTCCGCCGCATCCGCGAGGGCGCCGCCATGATCCGCACCAAGGGC 407
183 GCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTC 242
                                                                                     123 GAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTC 182
                                                                                                                             201 ATCAAGCGCGCCGTCACCATCCCAGTCATGGCCCAAGGCCCGCATCGGGCACTTCGTCGAG 260
                                                                                                                                                                                                                      141 GCCTATATCCGCGCCCAGGGCGGCGTCGCCCGCATGTCCGACCCGGGCCTCATCCGCGAA 200
                                             261 GCCCAGATCCTCGAGTCCATCGGCGTCGACTACGTGGACGAGAGC-----GAGGTC 311
                                                                                                                                                                           63 ATCGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGGCATCGCC 122
                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                            3 GTCTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGC 62
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EST0477 Triticum aestivum Lambda Zap Triticum aestivum cDNA clone
JA1_5B_H05_T3 5′, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Anderson, J.M.
Crop Production & Pest Control Research Unit
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Analysis of an EST database reveals a probable CF2 resistance gene
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4565"
/clone="th=15B_H05_T3"
/clone_lib="Triticum aestivum Lambda Zap"
/tissue_type="leaf"
/dev_stage="9 day old seedlings"
/dev_stage="9 day old seedlings"
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179 TGTGGCCGACGCCAGCAACCAGACTGTGGCCGACGCCAGCAACCAGACTGTGGC 238
                                                                                            119 CCAGACTGTGGCCGACGCCGCCAGCAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCAGAC 178
                             89 CATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGC---CATCCAGGGCATCGC 145
                                                                                                                                     29 CCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACCCAGTG 88
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1 (bases 1 to 602)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences Graduate School of Science, University of Tokyo Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan Tel: 81-3-5841-4443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Kiyoshi I
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EST.
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Medaka EST Project in University of Tokyo (2001)
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                  /clone_"0La14.06c"
/clone_lib="Sugano-Kawakami 5' end enriched cDNA library
/OLA) from HNI"
/tissue_type="whoie body"
/dev_stage="adult"
/dev_stage="adult" 49 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryzias latipes"
/strain="HNI"
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                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasliva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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Tetraodon nigroviridis genome survey sequence T7 end of clone
262H14 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                        /clone_lib="G"
/note="Genoscope sequence ID : C0AG262DD07LP1-end
                                                                                                                                                   /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRACGGCAGCGACGACGACGACGACAACAAAAAACRGCAACRACGACGGCGACRACAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                            genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases I to 915)

1 (bases I to 915)

1 (bases I to 915)

Roost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 044F19 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissenbach, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS03P82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 915)
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Conservative
                                                                                       Location/Qualifiers
1. .915
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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l; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          915 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 17-MAY-2000
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                                    BASE COUNT
ORIGIN
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AV438522/c
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ORIGIN
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      629 CAACGGCAACAACGACGGCAAAACGACGACAACGACAACGACAACGA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 CATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 CAACAA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 CAACAA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 GGGAATCGCCGAGGATGTCGCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 CGATGACGACAACGGCAACGACAACAACAACAACAACAACAATGACAACGACGACAA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 TGACAACGACAACGACAGCGACAGCG-----ANCAACGACGACGGCAACAACGGCAACAA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 GGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 CAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGACGCCCCAGGGCATCGCCAACGG 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168;
                                                                                                                                                                                                                     The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV438522 AV438522 Porphyra yezoensis TU-1 Porphyra yezoensis CDNA clone PS033d03_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                       Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyra yezoensis. Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV438522.1 GI:8593747
                                                                                                                                                                                                                                                                                                                      Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                Nikaido, I., Asamizu, E., Nakajima, M., Nakamura, Y., Saga, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 401)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="044F19"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG044CC10SP1-end : PUC-Ox1"
                                                                                      /clone="PS037d03_r"
/clone_lib="Porphyra yezoensis TU-1"
/clote="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
//clote="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                /organism="Porphyra yezoensis"
/strain="TU-1"
/db_xref="taxon:2788"
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                                                     187 c
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  14.78;
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                                                     124 g
Score 73.4;
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DB
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Length 401;
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Search completed: October 10, 2002, 20:28:30 Job time: 698.733 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 CGCCGGCGCGCGTAGGAGACGCAGTCGGGACGTACGGCACCGGCGTCGGCGACGCGGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGGACGCCGT 241
                                                                                                                                                                                               419 CGAGGACGCCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC 478
                                                                                                                                                                                                                                       132 CGCGGTCGCCGGCGCGTGGGCGACGCGGTCGGGACGTACGGCACCGGCGTCGGCGA 73
                                                                                                                                                                                                                                                                         359 CGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAA 418
                                                                                                                                                                                                                                                                                                                      192 GGGCACGTACGGCACGGGAGTGGGCGACGCACGTACGGCACCGGCGCGCGGGGGCGA 133
                                                                                                                                                                                                                                                                                                                                                                                                242 CCACGGCTTCGCCAACGG-~-GGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCA 298
                                                                                                                    479 CGCCCAGGGCA 489
                                                                                                                                                                                                                                                                                                                                                       299 GGGCATCGCCAACGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCAT 358
                                                                                12 CGCGGTGGGAA 2
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.8%;
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DNA encoding

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Result
No.
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    500
500
307.8
302.4
269.6
257.6
257.6
257.6
                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_032802:*

1: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*

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8: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1989.DAT:*

9: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1989.DAT:*

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21: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*

22: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*

23: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*

24: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd
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  AAD11123
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                 Human small cell l
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Human brain expres
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Human brain expres
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                   WPI; 2001-457597/49
                                                                                                                                                                                                                                                                                                                                                          Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; lelmyosarcoma; synovial sarcoma; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human small cell lung cancer associated gene, DKFZp434C196 #2.
                                                        Stockert E, Scanlan MJ,
                                                                                           (SLOK ) SLOAN KETTERING INST C
                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                    21-JAN-2000; 2000US-0489101.
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                                                                                                                CANCER RES.
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                                                        Old LJ,
                                                          Gure AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel probe #14922 for g Probe #14318 for g Human breast cell probe #3704 for ge Human foetal liver Human bone marrow Probe #8606 used t Human foetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel Human foetal liver probe #1522 for ge Human brain expres Probe #1635 used t Human brain expres Human brain express Human brain express #14376 for g
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Chen

Human foetal liver Human brain expres Human bone marrow Probe #21755 used

Human Human Probe Probe

brain expres bone marrow #8675 used t #5050 for ge

Human Human Probe

bone marrow #10096 used foetal liver #12924 for g brain expres #23134 used

Human Probe Human

Human Probe Probe

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RESULT 2
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          Human small cell lung cancer associated gene, DKFZp434C196 #1
                                             24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 57; Page 116; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                    AAD11122 standard; DNA; 1201 BP
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(SLOK ) SLOAN KETTERING INST C.
(CORR ) CORNELL RES FOUND INC.
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                          GCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCG
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Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; ds.

old LJ, Gure AO, Chen

Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encodisolated nucleic acid comprising an NA Group 3 or 4 molecule is encoded by an

are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, lelmyosarcoma or synovial sarcoma. The present sequence is human DKTZP43C196 DAA. This small cell lung The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with cancer associated gene is designated as NY-SCLC-13.

Sequence 1201 BP; 255 A; 377 C; 349 G; 178 T; 42 other;

100.0%; Score 500; DB 22; 100.0%; Pred. No. 1.3e-67; Mismatches 0 Indels Length 1201; 0; Gaps

0,

181 TCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCG TCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCG 240

TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGG 300 240

GCATCGCCAACGGGGACGCCAACGAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCG TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGG 360

361 CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCCAGGGCATCGCCAACG

Length 1593;

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                                                                                   The invention relates to isolated polynucleotide (I) and CC polymeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPR primers of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess the contract of the contract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 8481; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #8481.
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Sequence 1593 BP; 444 A; 429 C; 434 G; 286 T; 0 other;
                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
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Best Local Similarity
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                                       P-PSDB; ABG08491
                                                                    WPI; 2001-639362/73
                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                               (HYSE-) HYSEQ INC
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCAGGGCCCAGGGCTCAGCGTTCGCCAACGGGGACGCCCAGGGCATCGCCAACGAGGACGCCCAACGGAGGACGCCCCAGGGCATCGCCAACGAGGACGCCCTCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1173 CATCGCCAACGAGGACGCCACCCATGGCATCGCCAACGAGGACGCTGCCCACGGCATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #8482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 CATCGCCAACGGGACGCCAACGAGGGCATGGGCAACGAGGTCACCATCCACCGCCATCGC 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933 CGCCAACGAGGACGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCACGGAATCGCCAG 992
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AAS72679
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CC the formal sequence and for this patent did not appear in the printed content of the sequence data for this patent did not appear in the printed content of the products of the invention.
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AAS72679;
                                                    AAS72679 standard; cDNA; 2922 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               2290 GCCCAGGGCATCGCCAACGAGGGCGCCGCCCAGGGCATCGCCAAGGAGGACGCCGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 GACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGGCATCGCCAACGGGGGACGCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACCGGCTTCGCCAACGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 CAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC---CGAGGACGCCCATCCAGGGC 140
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                                                                                                                                                                                               GC---CGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCGCCAGGGCATCGCCAAC 497
                                                                                                                                                                                                                                                                                                               GGCATCGCCAAAGAGGGCCCCGCCCACGGCATCGCCAACGAGGACGCCCCCAGGGCATC
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                                                                                                                                                                                                                                                                                                                                                                       GGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGAATC 440
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                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags cf for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in set therapy techniques (II). (II) and its binding partners are useful in medical canding of sites expressing (II). (II) and (II) are useful in medical consisting of sites expressing (II). (II) and (II) are useful for treating consisting of sites expressing (II). (II) and (II) are useful for treating consisting the polypeptide and polynucleotide sequences have applications in consisting forensis, gene mapping, identification of mutations for the polypeptide and polynucleotide sequences have applications of mutations of data and products dependent on DNA and canding acquences. AAS64197-AAS94564 represent novel human canding sequence so if the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                          1966 CACGATATCACTAACGAGGACGCTGTCCACGGCATCGCTAACGAGGCCGCCGCCCAGGGC 2025
                                                                                                                                                                                                                                                       1906 GATGCCAAGAAAGCTCCCCATGAGGACACCGTACACAACATCACTAACGAGGATGCCTCA 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2922 BP; 833 A; 829 C; 806 G; 454 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 8483; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
                                                 141 ATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCCGCACAGGGCATCGCC 200
                                                                                                                                                                        84 CAGTGCATCGCCAAGGAGGAAGCCGCCCAGGGCATCGC---CGAGGACGCCCATCCAGGC 140
                                                                                                                                                                                                                                                                                                                  24 GCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                          362;
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     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human foetal liver single exon nucleic acid probe #15166.
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                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 15166; 639pp + sequence listing; English.
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                                                 Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
                                                                                                                   Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                              from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-063234687.
2000US-0236359.
2000US-0236359.
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  Score 257.6;
     DB 22;
Length 518;
                                                                                                                      format directly
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                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #12396 for gene expression analysis in human heart cell sample.
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     Penn SG,
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                                               (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 TCTACAAGCCGTCGCTAACA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 TA---ATGACACCGTACAAGGCA-CGCTAACGAGGATGCTGTACACGACATCGCTAATGA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CATCGCCAACGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 CCATGGCATCGCCAACGAGGACGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 CGCCGCCCAGGGCATCGCCAACGAGGACGCCCCCAGGGCATCGCCAACGAGGACGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 CTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCAT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
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     Hanzel DK,
                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                 2000GB-0024263
     Chen W,
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0; Mismatches 114;
       Rank DR;
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AAK1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
  Human brain expressed single exon
                           05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                           AAK15297 standard; DNA; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID No 12396; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 CGCTAACGAGGCCGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                        TCTACAAGCCGTCGCTAACA 518
                                                                                                                                                                                                             GGACGCCCCAGGGAATCG----CCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC 478
                                                                                                                                                                                                                                                                                                                                  CGCCCAGGGCATCGCCAACA 498
                                                                                                                                                                                     GGACACCATACAAGGCATCGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC
                                                                                                                                                                                                                                     TA---ATGACACCGTACAAGGCA-CGCTAACGAGGATGCTGTACACGACATCGCTAATGA
                                                                                                                                                                                                                                                                                    CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
                                                                                                                                                                                                                                                                                                          CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                   CGCCGCCCAGGGCATCGCCAACGAGGACGCCCCGCCCAGGGCATCGCCAACGAGGACGCCGT
                                                                                                                                                                                                                                                             TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCCATCGCCAACGA 421
                                                                                                                                                                                                                                                                                                                                                                                                          CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGACGCCGCCCACGGAATCGCCAGCGAGGACGCCCCGCCCAGGGCATCGCCAACGAGGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 257.6; DB 22; Length 518; Pred. No. 5.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
  probe SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114;
    NO: 15288
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Best Local :
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 383
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TA---ATGACACCGTACAAGGCA-CGCTAACGAGGATGCTGTACACGACATCGCTAATGA 438
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                    (MOLE-) MOLECULAR DYNAMICS
Hanzel DK,
                                                                         2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234387
2000US-0236359
2000US-0236353
                                                                                                                                                                                                                                    2001WO-US00667
Chen W, Rank DR;
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exon nucleic acid probes for analyzing gene expression ij human

Example 4; SEQ ID NO: 15288; 650pp + Sequence Listing; English

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, muntiple scherosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the

Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;

362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421 302 CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC 143 CGAGGACGCCGCCCACGGAATCGCCAGGGACGCCCCAGGGCCATCGCCAACGAGGT 5 CTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCAT CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGG CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC CCATGGCATCGCCAACGAGGACGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCCAGGGCCATCGCCAATGGGGT 181 CGCTAACGAGGCCGCCGCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGCCAA 142 CGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC--- 121 CAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGGACGCTGTCCACGGCAT Similarity Conservative 51.5%; 75.2%; 0; Score 257.6; DB 22; Length 518; Pred. No. 5.1e-31; Mismatches 114; Indels 10; Gaps 241 82 361 322 301 262 202 64 4

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301

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; hu
genetic disorder; ss
                                                                                                                                                                                                                                                          Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 15758; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2001
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     143 CGAGGACGCCGCCCACGGAATCGCCAGCGAGGACGCCCCAGGGCATCGCCAACGAGGT 202
                       122 CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGGTTGCCCAGGGCATCGCCAATGGGGT 181
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                                                                                                 CGCTAATGAGGACACCCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCCATCGC--- 121
                                                                    CGCTAACGAGGCCGCCGAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGCCAA 142
                                                                                                                                                                                              376;
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; placenta; antenatal diagnosis;
                                                                                                                                                                                                           51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                              0;
                                                                                                                                                                                             Score 257.6; DB 22; Length Pred. No. 5.1e-31; 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                           DB 22; Length 518;
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AAS72676
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #8480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS72676 standard; cDNA; 3345 BP
                                                                                                                                                              Claim 1; SEQ ID No 8480; 103pp; English.
                                                                                                                                                                                              biodiversity
                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 GGACACCATACAAGGCATCGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 GGACGCCGCCCAGGGAATCG----CCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 TA---ATGACACCGTACAAGGCA-CGCTAACGAGGATGCTGTACACGACATCGCTAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 CATCGCCAACGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 CCATGGCATCGCCAACGAGGACGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT
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                                                                                                                                                                                                                                                                                            2001-639362/73.
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                  DNA encoding novel human diagnostic protein #8125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2196
                                          Homo sapiens.
                                                                                                                                                13-FEB-2002 (first entry)
                                                                                                                                                                                                            AAS72321 standard; cDNA; 3522 BP
                                                                                                                                                                                                                                                                                       2552 TCTACAAGCCGTCGCTAACAAG 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2256
                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                  2492 GGACACCATACAAGGCATTGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2136 CGCTAACGAGGCCGCCGACAAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGCCAA 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2076 CAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGGACGCTGTCCACGGCAT 2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3345 BP; 954 A; 940 C; 913 G; 538 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2376 CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                     479 CGCCCAGGGCATCGCCAACAAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                           362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGACGTCACCATCCACGGCATCGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 CTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCAT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                               GGACGCCGCCCAGGGAATCG---CCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC 478
                                                                                                                                                                                                                                                                                                                                                                                                             TA---ATGACACCGTACAAGGCA-CACTAACGAGGACGCTGTACACGACATCGCTAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACGGCATCGCCAACGAGGATGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCGCCCAGGGCATCGCCAACGAGGACGCCCCAGGGCATCGCCAAGGAGGACGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGGACGCCGCCCACGGAATCGCCAGCGAGGACGCCCAGGGCCATCGCCAACGAGGT
                                                                                    chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250; DB 23; Pred. No. 5.6e-30;
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                                      302 CATCGCCAACGGGGACGCCAACGAGGGCATGGGCAACGAGGTCACCATCCCACGGCATCGC 361
                                                                                                  242
                                                                                                                                                              182
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65 CGCTAATGAGGACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC--- 121

CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC

CCACGGCATCGCCAACGAGGATGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG CCACGCCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCCAGGG 301

2552

CGCCGCACAGGGCATCGCCAATGAGGACGCCCACCCAGGGCATCGCCAACTGGGACGCCGT 241

CGCCGCCCAGGGCATCGCCAACGAGGACGCCCCCAGGGCATCGCCAAGGAGGACGCCGC 2491

CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGT 181 CGCTAACGAGGCCGCCGACAAGGGCATCGCCAACGAGGACGCCCCAGGGCCATCGCCAA 2372 Local

372;

Conservative

0:

Mismatches 120;

Indels 10;

Gaps

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cc polypertide (II) sequences. (I) is useful as hypridisation probes, cc polyperase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cplynucleotides are also used in diagnostics as expressed sequence tags cf for identifying expressed genes. (I) is useful in gene therapy techniques cc for identifying expressed genes. (I) is useful in gene therapy techniques cc (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical cimaging of sites expressing (II). (II) and (II) are useful for treating cc imaging of sites expressing (II). (II) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polyuclectide sequences have applications in cc diagnostics forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and cc anino acid sequences. AAS64197-AAS94564 represent novel human cc diagnostic coding sequences of the invention.

CC rependence data for this patent did not appear in the printed content that was obtained in electronic format directly from WIPO as for the represent movel human can be a formation of the products dependence of the twenthence to the products of the products dependence of the products depende
                                                            Query Match
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                                                                                                                                                                                                      Sequence 3522 BP; 1005 A; 1006 C; 959 G; 552 T; 0 other;
                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
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       Similarity
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50.0%; score 250; DB 23; 74.1%; Pred. No. 5.6e-30;
                                                            Length 3522;
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RESULT 12
ABA54299
ID ABA54
XX ABA54
XX ABA54
XX O1-FE
XX Human
XX Homo
XX Homo
XX Homo
XX O9-AU
XX 09-AU
XX 09-AU
XX 01-FE
XX 09-AU
XX 10-AU
PR 01-SE
PR 04-FE
PR 04-GC
XX 10-AU
XX Thai
XX Thai
CC measu
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CC fetal
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                                                                                                                                               Matches 299;
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2613 TA---ATGACACCGTACAAGGCA-CACTAACGAGGACGCTGTACACGACATCGCTAATGA 2668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human foetal liver single exon nucleic acid probe #2604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2669 GGACACCATACAAGGCATTGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC 2728
                                                                                                                                                                                                                                     Sequence 495 BP; 121 A; 174 C; 129 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2604; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 CGCCCAGGGCATCGCCAACAAG 500
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        103 AAGCCGCCCAGGGCATCGC----CGAGGACGCCATCCCAGGGCATCGCCAACGAGGAGGTTG 159
                                                108 ATGAGGACACCGTACACAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGG 167
                                                                           43 ATGAGGACGCCGAGGGGATCGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGG 102
                                                                                                                                                                    Loca
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                                                                                                                                            Similarity 77.3
99; Conservative
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2000US-0207456.
2000US-0508408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236553.
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                                                                                                                                                                  47.08;
77.38;
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                                                                                                                                            0;
                                                                                                                                                                  Score 235; DB 22;
Pred. No. 1.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                            Mismatches
                                                                                                                                            85;
                                                                                                                                                                                       Length 495;
                                                                                                                                            Indels
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                Claim 1; SEQ ID No 2522; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
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04-FEB-2000; 2000US-0180312.

26-MAX-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023559.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; probe;
cardiovascular disease; hypertension; cardiac arrhythmia;
Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #2522 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA24056 standard; DNA; 495 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 CCATATATGACATCGCTAATGACACCG 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 GCATCGCCAACGAGGTCGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCCAGGGCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 ACGCTGTCCACGGCATCGCTAACGAGGCCGCCGCCCAGGGCATCGCCAACGAGGACGCCG
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                                                                                                                                                                                      MOLECULAR DYNAMICS INC.
                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279
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                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
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   Penn SG,
                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                                                     30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe SEQ ID NO: 2574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK02583 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
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   Hanzel DK,
                                                                                                                                           ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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                                                                                                                    2000GB-0024263.
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77.3%;
   Chen W,
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Pred. No. 1.3e-27;
   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                Probe #2635 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 495 BP; 121 A; 174 C; 129 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human brains \boldsymbol{\cdot}
                                                              30-JAN-2001; 2001WO-US00663.
                                                                                                                             09-AUG-2001.
                                                                                                                                                                                     WO200157272-A2
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                               genetic disorder;
                                                                                                                                                                                                                                                                                                                                           Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI33949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI33949 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                           human; placenta; antenatal diagnosis
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04-FEB-2000; 2000US-0180312

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30-JUN-2000; 2000US-0609408.
03-AUG-2000; 2000US-0233667.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234635.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 2635; 654pp; English.
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                                                                                           400 CCGCCCAGGGCATCGCCAACGAGGACG 426
                                                                                                                          408 AGGATGCCGTGCACGGCATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATG 467
                                                                                                                                                       340 AGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGG 399
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Sequence 4, Appli
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173 62	Query M Best Lo Matches , 113	APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF TI FILE REFER CURRENT FI CURRENT FI EARLIER FI OTHER INF OTHER INF OTHER INF	RESULT 1 US-09-197-1 ; Sequence ; Sequence	22250000000000000000000000000000000000
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GGGTCGC ACGACGJ	ch Similarity Similarity Similarity Conservat GCATCGCCGAGGAC	NT: Gold, Larr NT: Tyerk, Cra NT: Pribnow, D NT: Smith, Jon F INVENTION: S FERENCE: NEXO2 APPLICATION N FILLING DATE: APPLICATION: D INFORMATION: f 649-7	649-7 0.7, Applicat 0.6194550	114. 114. 113.4. 113.4. 113.3.
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CARTGGGGTCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTG	tch 23.3%; Score 116.4; DB 4; Length 390; all Similarity 57.0%; Pred, No. 4.9e-13; 213; Conservative 0; Mismatches 161; Indels 0; G GGGCATCGCGAGGACGACGACGACGACGACGACGACGACGACGACG	Polypeptide (709/197,649 3 3 7829,461 1 7739,055 1 7561,968 2 2 8 2 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALIGNMENTS 97649	US-09-103-840A-1 US-08-125-468-1 US-08-125-468-1 US-08-125-468-1 US-09-056-556-182 US-09-056-556-182 US-08-387-942C-1 US-09-372-422A-23 US-08-419-075-24 US-08-419-075-22 US-08-419-075-22 US-08-419-075-28
GCCACCCAG GACGACGAC	DB 4; I 9e-13; ss 161; I .CGAGGAGGTT CGACGACGAC	olution Sequen G flank		25 5 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
GGCATCGCCA GACGACGACG	Length 390; Indels 0 TGCCCAGGGCA 1 CGACGACGACG	y Reve		Sequence Sequence
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Patent No. 6294328
GENERAL INFORMATION:
ADDITORNAL PROPERTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT ENTLING DATE: 1998-05-24
CURRENT FILLING DATE: 1998-05-24
                                            3937807 CCCGTTGCCGCCGGGGTCGTCAGTGAGTGGGCCGTTGGCCGCCGATGGCCCCGTTGCCGCC 3937748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                  393 GAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGAATCGCCGAGGATGTC 452
                                                                                                                                                                  333 GGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAAC 392
                                                                                                                                                                                                                                                273 AGCTTCGCCAACGGGGACGCCGCCCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATG 332
                                                                                                                                                                                                                                                                                                                                213 ACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACGGGGACGCCGTCCTC 272
                                                                                                                                                                                                                                                                                                                                                                                                                153 GAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCGCCAATGAGGACGCC 212
       453 GCACAGGGCATCGCCAACGAGGACGCCGCCCAGGGCCATCGCCAAC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 CGCCAACGAGGACGCCCCCCCCCAGGGAATCGCCGAGGGATCGCCAACGA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111 |||| ||
362 CGACGACGCCATGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 CGGCATCGCTAACGAGGCGCCGCCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 GGACGCCGCCCAGG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 GCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATCCAGGGCATCGCCAACGAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 GGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCAACCCAGTGCATC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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Similarity 49.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87.4; DB 4; Length 4403765;
Pred. No. 6.5e-08;
0; Mismatches 236; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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; Sequence 4, Application US/09023173 ; Patent No. 6066781 ; GENERAL INFORMATION:
                                                             RESULT 4
US-09-023-173-4
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US-09-197-649-7/c
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Db 3937747 ATCGCCCCGCCGCCGCCCCCCCCCCGCTGCCGCTGCCGCCAGC 3937703
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CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-02
NUMBER OF SEQ ID NOS: 26
SOFTMARE: Patentin Ver. 2.0
15 ENTER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gold, Larry
APPLICANT: Tuerk, Crai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 7, Application US/09197649
Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pribnow, David APPLICANT: Smith, Jonathan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed OTHER INFORMATION: fragments having Ncol restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGG 180
                                              481 CCCAGGGCATCGCC 494
                                                                                                                                                 421 AGGACGCCGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCG 480
                                                                                                                                                                                                            361 CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACG
                                                                                                                                                                                                                                                                                                                  301 GCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGG
28 TCGTCGTCGTCGTC 15
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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; IMMEDIATE SOURCE: COCOn-optimized RAmy3D signal-prosubtilisin BPN' US-09-023-173-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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FILING DATE: 13-FEB-1997
ATTORNEY_AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: 042995
REFERENCE/DOCKET NUMBER: 066:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/038,168
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CORRESPONDENCE ADDRESS:
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APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of Mature Proteins
TITLE OF INVENTION: in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 330 Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 CAGCCAGATCAAGGCCCCGGCCCTCCACAGCCAGGGCTACACCGGCAGCAACGTCAAGGT 389
630 CAACGGCATCGAGTGGGCCATCGCCAACAACATGGACGTCATCACCATGAGCCTCGGCGG 689
                                                    368 GGACGCCGTCCA---GGGCATCGCTAACGAGGTGGCCCAGGGCCATCGCCAACGAGGA 424
                                                                                                            570 CAGCCTCTACGCCGTCAAGGTACTCGGCGCCGACGGCAGCGGCCAGTACAGCTGGATCAT 629
                                                                                                                                                                308 CAACGGGGACGCCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGA 367
                                                                                                                                                                                                                              510 CGCCGGCACCGTCGCCGCCCTCACCAACAGCATCGGCGTCCTCGGCGTCGCCCCGAGCGC 569
                                                                                                                                                                                                                                                                               248 CTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGCATCGC 307
                                                                                                                                                                                                                                                                                                                                       450 TAGCATGGTCCCGAGCGAGACCAACCCGTTCCAGGACCAACAGCCATGGCACCCACGT 509
                                                                                                                                                                                                                                                                                                                                                                                               188 ACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 CGCCGTCATCGACAGCGGCATCGACAGCAGCCACCCGGACCTCAAGGTCGCCGGCGGAGC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 CGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 CGCCTACGTCGAGGAGGACCACGTCGCCCACGCATATGCACAGAGCGTCCCGTACGGCGT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 15.4%;
Similarity 48.8%;
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350 Cambridge Ave., Suite 250
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RESULT 5
US-09-056-556-176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SED ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.4%;
Best Local Similarity 49.6%;
Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PAI-ENTIN Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 CCCGAGCGGCAGCGCCCTCAAGGCCGCCGTCGACAAGGCCGTCGCCAGCGGCGTCGT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 CGCCGCCCAGGGAATCGCCGAGGATGTCGCAACGAGGCATCGCCAACGAGGACGCCGCCCA 484
196 CGGCACCGTGGCCGGTGGCGGCGACGGCGGTGTCGGCGGCCGGGGCGGCGACGGCGT 255
                                                                                                                                                                    136 CGGCAAGGGCGGCTTCGGCGGCGGCGACGGCGGTAGGGCGGCGGCGGCGGTACCGT 195
                                                                                                                                                                                                          158 TGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: 63
                                                                                                                           218 GGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                           98 CGAGGAAGCCGCCAGGGCATCGCCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGT 157
                                                                                                                                                                                                                                                                                                                                    16 CGGCAAGGGCGACGGTGGCCACGGCGGTGACGGCGTCGGCGGCAACAGTTCCGTCAC 75
                                                                                                                                                                                                                                                                                                                                                                          38 CGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACCCAGTGCATCGCCAA 97
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                                                                                                                                                                                                                                                     76 CCAAGGCGGCAGCGGCGGTGGCGGCGGCGGCGGCGGCGGCGGCAGCGGCTTTTTCGG 135
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 4; Length 494
Pred. No. 3.8e-06;
0; Mismatches 200; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 494;
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
US-09-056-556-167

Sequence 167, Application US/09056556

Patent NO. 6350456

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 2, Application US/09130114
Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D93US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                              496
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                                                                                                                                                   316 GACGAGGACGGGGAGGACGAGGACGGAGGACGAGGACGAGGACA 265
                                                                                                                                                                                          438 ATCGCCGAGGATGTCGCACGGGGCATCGCCAACGAGGACGCCGCCCAGGGCA 489
                                                                                                                                                                                                                                  378 CAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGA 437
                                                                                                                                                                                                                                                                                                                        198 GCCAATGAGGACGCCAGCGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GGCATCGCCAACGAGGAGGTTGCCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 GGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 CACCGGCGAACGGCGGCCTTGGCGGCGCGGGCGGTGGCGAAGGCAACGCCCCGGCTCG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 TGCCGAATCCGGGCTGACCATGGACAGCGCGGCCGAAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCCATCGCTAATGAGGAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 ACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATCCAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCAGGGCCATCGCCAACGGGGAC 317
                                                                                                                                                                                                                                                                                                                                                                    GCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTC 377
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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47.7%; Pred. No. 4.2e-06;
vative 0; Mismatches 247; Indels 0
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Best Local Similarity 48.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (205),622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                             1297
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LENGTH: 1439 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                         1357 GTGCCGCCAGCGGCTCAGGCGTCATCAACGTCACCGCCGGCCACGGCGGCAACGGCGGCA 1416
                                                                                                                                                                                                                1237 GCGGCAACGGCTCCGCGGGCGGCGGCGGCCAGGGCGGTGCCGGCGAGCGCCAGCGAACG 1296
                                                                                 199 CCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GCATCGCCAACGAGGAGGTTGCCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Concerns: Seattle STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 ACGCGAGCACCACCGGCAACGCCGGCTCCGGTGGTGCCGGCGGTAATGGGGGGCACTG 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 CCCAGTGCATCGCCAACGAGGAAGCC---GCCCAGGGCATCGCCGAGGACGCCATCCAGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TENGTH: 1455 LENGTH: 1455 LENGTH: 1455 LENGTH: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACGCTGCCCAGGGCATCGCTAATGAGGACGCCCGACCAGGGCATCGCTAATGAGGACACCA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                             GCGGCCACGGCGGCGCTGCCACCGGCGGCGCCAGCGCCAAGGGCGCCAACGGCACCAGCG 1356
                                                                                                                                                                       AGGGCATCGCTAACGAGGTGGCCGCCCAGGGGCATCGCCAACGAGGACGCCGCCCCAGGGAA 438
                                                                                                                                                                                                                                                        CCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCC 378
                                                                                                                                                                                                                                                                                                  GCTCAGGCGTCGTCAACGTCACCGCCGGCCACGGCGCAACGGCGGCAATGGCGGCAACG 1236
                                                                                                                                                                                                                                                                                                                               GGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGGCATCGCCAACGGGGACG 318
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US-09-105-537-7

(Sequence 7, Application US/09105537A

Patent No. 6265202

(GENERAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: LABO, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600 438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF ESQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 7

SEQ ID NO 7

LENGTH: 1248
                                                                                             RESULT 9
US-09-056-556-167/c
US-09-056-556-167/c
; Sequence 167, Application US/09056556
; Patent No. 6350456
; Patent No. 6350456
; Patent No. Reed, Steven G.
ADDLICANT: Reed, Steven G.
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Best Local Similarity 49.5
Matches 220; Conservative
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GGTCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 CGCCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGG 178
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                                                                                                                                                                                                                                                                                                                                                        476 CGCCGCCCAGGGCATCGCCAACAA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 CAACGAGGACGCCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 CATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 CTTCGACCTGCCCGGCGGCAGCCCCGGCGGGGACCAACGCCAAGATGAGCGAGGCCGC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 CCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 CGACCGCCACGGCCTCAACAACCA 887
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                                                           TREAT
           ; Sequence 3, Application US/09105537A
, Patent No. 6265202
, GENERAL INFORMATION:
, APPLICANT: Sherman, D.H.
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                                                                                                           RESULT 10
US-09-105-537-3/c
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INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 1439 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 219; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY MAKI, DAVID J.
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1413 CGCCGTTGCCGCCGTGGCCGGCGGTGACGTTGATGACGCCTGAGCCGCTGGCGGCACCGC 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1233 TGCCGCCATTGCCGCCGTTGCCGCCGTGGCCGTGACGTTGACGACGCCTGAGCCGC 1174
                                                                                                                                                                                                                                                                                                        1113 CGCCGTGGCCGCCGTTGCCGCCGTTGCCGCCGTCGCCCACAGCGTTGCCGAAGGACA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1173 TGGCGGCACCGCTGCCGTTGCCGCCGTCGCCGCCGGCGCGCCGTCGTGCCGTCGC 1114
                                                                                                                                                                                                        993 TGCCCCCATTACCGCCGCCACCACCGGAGCCGGCGTTGCC 954
                                                                                                                                                                                                                                                        428 CGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCC 467
                                                                                                                                                                                                                                                                                                                                                     368 GGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 CAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 CTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGGGCATCGC 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER FILING DATE: 07-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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07-APR-1998
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) 682-6031
-- NO: 167:
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47.6%; Pred. No. 1.1e-05;
ative 0; Mismatches 241; Indels 0
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; LENGTH: 5036
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-177-349-2
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US-09-177-349-2/c
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-3
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Alland, David
APPLICANT: Alland, David
APPLICANT: Bloom, Barry R.
APPLICANT: Jacobs Jr., William R.
APPLICANT: Jacobs Jr., William R.
APPLICANT: TOURNTION: iniB, iniA AND iniC GENES OF MYCOBACTERIA AND METHODS
                                                                                               TITLE OF INVENTION: 1018, 101A AND 101C GETILE OF INVENTION. OF USE FILE REFERENCE: 96700/491
CURRENT ENLING DATE: 1980-10-23
CURRENT FILING DATE: 1980-10-23
NUMBER OF SEO ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 2
SEO ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09177349
Patent No. 6268201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 14.9%; Score 74.4; DB 4; Length 13613; Best Local Similarity 49.5%; pred. No. 1.1e-05; Matches 220; Conservative 0; Mismatches 221; Indels 3;
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LENGTH: 13613
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APPLICANT: Xue, K.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION UNMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 CGTCCACGGCTTCGCCAACGGGGA---CGCCGTCCTCAGCTTCGCCAACGGGGACGCCGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 CGCCGCCCAGGGCATCGCCAACAA 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 CCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGG 355
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EARLIER APPLICATION NUMBER: 60/087,08
EARLIER FILING DATE: 198-05-28
ENUMBER OF SED ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 270
LENGTH: 5970
TYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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Query Match 14.8%;
Best Local Similarity 49.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 14.8%; Score 74; DB 4; Length 5036; Best Local Similarity 48.2%; Pred. No. 1.3e-05; Matches 209; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 CCGGCTGAGACACCGATCTGGCTAGCGATGCCCGGCCTGGCCGCCGACACCAGCGCCGACA 816
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   Score 74; DB 3;
Pred. No. 1.3e-05;
                               Length 5970;
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US-08-387-942C-1
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                                                                                 APPLICATION NUMBER: US/08/387
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN ReLease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 CGCCGTCGTCACCGACGCCGACCTCGCCCGCCCGGATCCGCCCCTCCACACTTCGG 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 CAACCACGCCGSCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 CAACGAGGACGCCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGA 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 CATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGC 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                  703-205-8050
                                                                                                                                                                                                                            US/08/387,942C
09-MAY-1995
V. //27
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                                                                                                                                   1809-106P
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                                                                                                                                                                                                                       RESULT 14
              Sequence 1, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xie, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: DAA encoding methymycin and pikromycin
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  FILE REFERENCE: 600.438US1
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ORIGINAL SOURCE:
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2227..6438
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09025691 Patent No. 6069299
GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAYDAN, GATY E.
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5152
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                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                               AUDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051 CITY: Rochester
                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGA 127
CLASSIFICATION:
                        FILING DATE:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                       STATE:
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Y: U.S.A.
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                                         us/09/025,691
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Pred. No. 1.8e-05;
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Search completed: October 10, 2002, 19:46:20 Job time: 1097.73 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1294 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael I
                                                                                                                                                        557
668 CTTCGCCGACA 678
                                     488 CATCGCCAACA 498
                                                                           368 GGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGC 427
                                                                                                                                                                                                                                                                         308 CAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGA 367
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                                                                                                              428 CGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCCCAGGG 487
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                                                                                                                                                                                                                                    CAACGCGGGCGAGATCACCTTCACCCTCGACTCGGTCGGGCTCGGCGGCTACACCGACGA 556
                                                                                                                                                      G-----CAGTTCCGCGCGCGACCTCGCCGCCAAGCAGGCCGACGGCAAGTCGGTGAT
                                                                                                                                                                                                                                                                                                               CCTCGCCGACGTGCCGGACGCCTACGACATCATCGCCGTCTCCCTTCGCCGACGCCACGGC 496
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Match Length DB
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gb_est1:*
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AL041090 DKFZP444C
BIB2927 603079427
BI561135 603253662
BG724320 602697968
A1904151 CM-BT003-BG847089 102401540
AL305165 Tetraodon
BE427000 PSR6561 I
BG417341 HVSMEK001
BE216934 EST0477 T
AU176645 AU176645
AL193990 Tetraodon
AL254315 Tetraodon
AV438522 AV438522
BG739444 EM1_81_A0
BG773077 602721380
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AUTHORS
TITLE
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VERSION
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AL110383
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ORGANISM
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No s1 sequence available.

This clone (DKFZp434E0731) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Can-
Research Center (DKF2); Email s.wiemann@dKfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S. EST (Blum, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL110383

DKFZp434E0731_rl 434 (synonym: h
DKFZp434E0731 5', mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 697)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Blum H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL110383.1 GI:5865991
217 a
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=nkEpg43kD731"
/clone_11b="434 (synonym: htes3)"
/fissue_type="test1s"
/dev_stage="adult"
/lab_host="BH0B"
/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
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AU088571
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BF612759 HVSMEC001
BG314481 WHE2445_D
BG874723 RC1-BF025
BE213813 HV_CED000
BG906607 Talx1151A
AL053013 Drosophil
AU088578 AU088578
BE517259 WHE0615_F
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AU222996 AU222996
BF47493 WHE2104_E
BE470936 WHE0282_H
AV91690 AV916390
AV941861 AV941861
BE350540 DG1_64_E1
BF2560540 WHE1701-1
BE605180 WHE1701-1
BE605180 WHE1701-1
BC006062 AV438522
AV438522 AV438522
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BG9907710 TB1r1162C
BM178959 Saj61608.
AL506812 AL506812
BF360740 HVSMEE002
BG36745 HVSME1001
BF483260 WHE1787_G
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                                                                                                                                                                                                                                                             No sl sequence available.
This clone (DKFZp434C1116) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 5, 140; Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                    Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5 sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz heidelberg.de;
sequenced by BMFZ (Blomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cataniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cataniata; Hominidae; Homo.

Louises 1 to 179)
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DKFZp434C1116 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                             Project.
                                     /Clone="bKFZp434Cil6"
/Clone=1b="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="pht10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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lonym: htes3) Homo sapiens cDNA clone
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Best Local Similarity 82.1%;
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122 CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGT 181
182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
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67 GGCATCGCTAACGAGGTCGCCCCCCCACGCATCCCCAAACGAGGACGCCCCCCACGCATC 126
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                                                                                                 8 CGAGGACGCTGTATACGACATCGCTAATGAGGACGTTGTATATGACATCGCTAATGAGGA 67
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 758)
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/db_xref="taxon:9606"
/clone="IMAGE:517050"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla fra anonymous male age 27. Library is Oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Invitrogen). Research Gene
this is a NIH_MGC Library."
159 c 167 g 217 t
                                                                                                                                                                                                                                                                                                          Score 118.6; DB 10; Length Pred. No. 1.9e-07; 0; Mismatches 119; Indels
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199 CCAATGAGGACGCCACCCAGGGGATCGGCAACTGGGACGCCGTCCACGGCTTCGCCAACG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 AGAAGATGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 GGACGCCGC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 TAATAAGGATGCTGTATATGACATTGCTAATGAGGACACTGTACAAGACATCTGTAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 CATCGCTAATGAGGACGCTGTATATGGCATCGCTAATGAGGATGCTGTATACGAATTCGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 CATCGCCAACGGGGACGCCAACGAAGGCCAACGAGGTCACCATCCACGGCATCGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ATATGACATCACTAATGAGGACGCTCTATACGACATCACTAATGAGGACGCTGTATACAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Pakkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 630.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 673)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
plate: LLAM11749 row: k column: 15
                                                                                                      Similarity
                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5296262"
/clone_lib="NIH_MGC_97"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                      22.6%;
                                                                               Mismatches
                                                                                                   Score 113;
Pred. No. 1
                                                                                                      DB 10;
1.1e-06;
                                                                                                                             Length 673;
                                                                               Indels
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ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 CCGTCCACGGCATCGCTGACTGGGACGCC-TCCATGTCCTCGCTGACGAGGACGCCGCCA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 CCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 AGGACGCCGTCCATGGCACCGCCGACGAGGACGCCGTCCAGGGCATCGCCGACGACGAGGACG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 GGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCCCAGGGCATCGCCAACGGGGACG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 CCCATGGGGACACCATCCACGACATCACGAACGAGGACGCCGTCCACGACACCACCGACG 502
        76 CATCGCCAAAGAGGACGCCGCCCACGGCATCGCCAACGA-GCTGTATACGACATCGCTAA 134
                                                                                                                                89 CATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATCCAGGGCATCGCCAA 148
                                                                                                      18 CCCAGGCATCGCCAACGAGGACGCCCCCA-GGCATCGCCAACGAGGACGCCGCCCAG-G 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG724320 582 bp mRNA linear EST 08-MAY-2001
602697968E1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4829993 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CINA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CONA Library Preparation: (RIKEN)
TOShiyuki and Piero Carninci (RIKEN)
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CONA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llni.gov
plate: LLAM10750 row: g column: 18
High quality sequence stop: 580.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG724320.1 GI:14003507
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                               183 a
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                         /note=*Organ: testis; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag pBluescript RS+); Size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.*

a 147 c 151 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4829993"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                              19.7%;
                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                       Score 98.6; DB 10;
Pred. No. 9e-05;
0; Mismatches 94;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                        Length 582;
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RESULT 6
AI904151
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                   Matches
                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 CATGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 CCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGCATCGCCAACGGGGACGCCACCAAGGG 328
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           Local Similarity es 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 24.)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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CM-BT043-090299-075 BT043 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/seq/gethtml.pl?tl=CMst2=CM-BT043-075.html
st3=090299st4=1)
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                   Conservative
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                                                                                                                                                                           'dev_stage="Adult"

/dev_Stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 . The puck of the pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="BT043"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                           18.8%;
           0;
                                       Pred. No. 0.00038;
           Mismatches
                                                                           Length 241;
           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 GAGGACGCTCTATACGACATCGCTAATGAGGACGCTGTATACAACATCGCTAATGAGGAC
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                                   16 CTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGG 75
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                                                                                                                                               Loca
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                                                                                                               240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG847089 780 bp mRNA lin 1024015H06.y2 C. reinhardtii CC-1690, normaliz Chlamydomonas reinhardtii cDNA, mRNA sequence. BG847089 GT:14228273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydomonadaceae; Chlamydomonas
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Fax: 919 613 8177
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                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                      208
                                                                                                           Conservative
                                                                                                                                                                                                                                                                          /note="vector: pBluescript II SK-; Site_1: EcoRI; Site_2: Xhol; This library, constructed by John Davies and Jeffrey Xhol; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark. HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wiid type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
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                                                                                                                                       17.1%;
50.3%;
                                                                                                           0; Mismatches 231;
                                                                                                                                               Score 85.4; DB 10; Pred. No. 0.0051;
normalized, Lambda Zap II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCGTCCGACGACGACGATGACGACGAGGAGGACGACGATGACAGCGAGGAGG - - 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodontidae; Tetraodon.

1 (bases 1 to 822)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNSU4SGK 822 bp DNA linear GSS 24-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone OCTA (1) of library H from Tetraodon nigroviridis, genomic survey
                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Bernot, A., Fizame
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Unpublished 
2 (bases 1 to 822)
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                                                                                                                                                                                                                                                                     Submission
      /clone="007M14"
                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CTAAGGTGATGCTAACCTGGAGTCAGGCTAAGTCGACGCTAACCCGGAGTCAGGCTAAGG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 CCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGACGACGCCCCAGGG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GTCAGGCTAAGGTGATGCTAACCCGGAGTCAGGCTAAGTCGACGCTAACCCGGAGTCAGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 CGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 CCTGGAGTCAGGCTAAGGTGATGCTAACCCGGAGTCAGGCTAAGGTGATGCTAACCCGGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 CGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGGCCATCGCCAACGGGGA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 CGCTAACCTGGAGTCAGGCTAAGGTGATGCTAACCTGGAGTCAGGCTAAGGTGATGCTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 CGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCCACGGCTTCCCCAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 AGGTGACGCTAACCCGGAGTCAGGCTAAGACGACGCTAACCCGGAGTCAGGCTAAGGTGA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 GGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 AGGCTAAGTCGACGCTAACCCGGAGTCAGGCTAAGGTGACGCTAACCCGGAGTCAGGCTA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556 GGAGTCAGGCTAAGGTGACGCTAACCCGGAGTCAGGCTAAGTCGACGCTAACCCGGAGTC 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACAC 79
                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
Riticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
                                                                                                                                                                                                         Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutie, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P. Herrmann, R. G., Holton, T., Jacquemin, J. M., Jia, J., Joudrier, P., Lazo, G. R., Lin, J. J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSR6561 ITEC PSR Wheat Endosperm Library Triticum aestivum cDNA clone PSR6561, mRNA sequence.
Unpublished (2000)
Contact: Bailey P
Cereals Group, John Innes Centre
Norfolk, Norwich NR4 70H UNITED KINGDOM
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
Email: paul bailey@bbsrc.ac.uk
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE427000.1 GI:9424933
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a 262 c
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/note="Genoscope sequence ID : COBH007BG07XE1~end
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Pred. No. 0.021;
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                                                                                                    REFERENCE
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                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 AG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 AGCACAAGGGCAACAAGGTCAGCAGCTAGGACAAGGGCAACAAGGTCAGCAGCCAGTGA- 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 GCCAGGACAAGGGCAACCAGGACAATTGCAACAACCAGCACAAGGGCAACAAGGGCA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 TCGCCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGCCCCCCCAGGGCATCGCCAACA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 GCATCGCCAACGAGGATGCCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AGGTCAACAGCCAGGGCAAGGGCAACAAGGTCAGCAGCCAGGACAAGGGCAACAAGGTCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AACTTCTCCGTTGCAGCCAGGACAAGGGCAACCAGGGTACGACCCAACTTCTCCGCAACA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 CCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGCCATCCAGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCCCCAGGGAA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAACTAGCACAAGGGCAACAAGGGCAGCAGCAGCAGCAGTGCAACAAGGGCAGCAGCC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGGGGCATCGCCAACGGGGACG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAAGGGCAACAGCCAGGACAATGGCAACAACCAGGACAAGGGCAACCAGGATACTACCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAACCGGGGCAAGGGCAGCCAGGGTACTACCCAACTTCTC------CGCAGCAATCAGG 237
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245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           BG417341 884 bp mRNA linear EST 23-OCT-2001
HVSMER0017J12f Hordeum vulgare testa/pericarp EST library
HVCDNA0013 (normal) Hordeum vulgare cDNA cione HVSMER0017J12f, mRNA
1 (bases 1 to 884)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Kannangara,G., von
Wetstein,D., Akhunov,E., Chin,A., Choi,D.W., Fenton,R.D., Kianian
,P., Otto,C., Simons,K., Zhang,D., Begum,D., Frisch,D., Yu,Y.,
                                                                                                                         Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Agmoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                            BG417341.2
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Organism-"Triticum aestivum"
/Gultivar="Soleil"
/db_xref="faxon:456;"
/db_xref="faxon:456;"
/clone="198656!"
/clone="198656!"
/clone="198656!"
/clone="198656!"
/clone="198656!"
/clone="1980 PSR Wheat Endosperm Library"
/tissue_tye="endosperm"
/dev_stage="1:1 mix 10:20 days post anthesis"
/note="Vector: Lambda ZAP II (Stratagene)"
/note="Vector: Lambda ZAP II (Stratagene)"
185 c 180 g 45 t 4 others
                                                                                                                                                                                                                                                                                                               GI:16333154
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Pred. No. 0.031;

^ Mismatches 226; Indels 11; Gaps
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                                                                                         195 ATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCC 254
                            288 GACGACGCCCACCACCACCAACAACCAACTTCCGCGTCCCCTTCGTCTGCGGCTGCCGC
                                                                                                                                                                                                               135 CAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGC 194
                                                                                                                                                                                                                                                                        177 GTCACCATCCCGGTCATGGCCAAGGCCCGCATCGGGCACTTCGTCGAGGCCCAGATCCTC 236
                                                                                                                                                                                                                                                                                                                                                                                                     117 GCCCAGGGCGGCGTCGCCCGCATGTCGGACCCGGGCCTCATCCGCGAAATTAAGCGCGCC 176
                                                                                                                                                      237 GAGTCCATCGGCGTCGACTACGTGGACGAGAGC-----GAGGTCCTCACACTCGCC
                                                                                                                                                                                                                                                                                                            75 GACACCACCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCCAGGACGACGCCATC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226;
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Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cDNA library Unpublished (2001)
On Mar 13, 2001 this sequence version replaced gi:13322988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plants were raised from seeds in a Controlled Environments growth chamber maintained in continuous light at 180C, and testa and pericarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was purified, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the Ty Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Phagemids were plated and plicked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close Ty, Wing R, Xleinbofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gypages/bgn/3/2cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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HVcDNA0013 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="testa/pericarp"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="HVSMEk0017J12f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism≠"Hordeum vulgare"
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Gaps

B Q g Q В δÃ Вb δÃ

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RESULT 11
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183 GCCGCACAGGGCATCGCCAATGAGGACGCCCACCCAGGGCATCGCCAACTGGGACGCCGTC 242
                                            261 GCCCAGATCCTCGAGTCCATCGGCGTCGACTACGTGGACGAGAGC------GAGGTC 311
                                                                                           123 GAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTC 182
                                                                                                                                             201 ATCAAGCGCGCCGTCACCCATCCCAGTCATGGCCAAGGCCCGCATCGGGCACTTCGTCGAG 260
                                                                                                                                                                                            63 ATCGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGCC 122
                                                                                                                                                                                                                                                                       3 GTCTACGGCATTGCTGAGGACGCCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGC 62
                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                             230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 990
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Anderson, J.M.
Crop Production & Pest Control Research Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, J.M., Williams, C.E. and Goodwin, S.B.
Analysis of an EST database reveals a probable CF2 resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          janderson@purdue.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref."taxon:4565"
/clone="JA1_5B_H05_T3"
/clone_lib="Triticum aestivum Lambda Zap"
/tissue_type="leaf"
/dev_stage="9 day old seedlings"
/dev_stage="9 day old seedlings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/strain="p29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 GACGCCGCCCAGGGAATCGCCGAGGATGTCGCACAGGGCA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 GTCATGGGCGACGTGCCTGCCCTCCGCAGCATGGACGACGAGGTATTCACCTATGCC 551
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                      179 TGTGGCCGACGCCGCCAGCAACCAGACTGTGGCCGACGCCGCCCAGCAACCAGACTGTGGC
                                                                                                                          119 CCAGACTGTGGCCGACGCCAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCAGAC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 AACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAG 422
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                                                                     89 CATCGCCAACGAGGAAGCCGCCCAGGGCATCGCCGAGGACGC---CATCCAGGGCATCGC 145
                                                                                                                                                                         29 CCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACCCAGTG 88
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Oryzias latipes
Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Percomorpha; Atherinomorpha;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzianae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU176645 GO2 bp mRNA linear EST 21-MAR-1
AU176645 Sugano-Kawakami 5' end enriched colm library (OLA) from
HNI Oryzias latipes cDNA clone OLa14, O6c similar to pir|5288564|
bydroxyproline-rich glycoprotein - maize, mRNA sequence.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Sugano-Kawakami 5' end enriched cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:8090"
/clone="0Lal4.06c"
/clone="5"Sugano-Kawakami 5' end enriched cDNA library
/clone_lib="Sugano-Kawakami 5' end enriched cDNA library
(OLA) from HNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
/strain="HNI"
                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
246 c 175 g
                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="whole body"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 CGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCCAGGGAATCGCCGA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 CAACCAGACTGTGGCCGACGCCGCCAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 CGACGCCGCCAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCAGACTGTGGCCGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 CGCCAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCAGACTGTGGCCGACGCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 GGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACGGCTTCGCCAACGGGGACGC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTGTGGCCGACGCCGAGCAACCAGACTGTGGCCGACGCCGCCAGCAACCAGACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 681)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS; genome survey sequence. Tetraodon nigroviridis.
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                                                                                                                                                                                                       http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodontidae;
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                                                          74
                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="262H14"
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pufferfish
                                                                                                                                                                     .681
  15.0%;
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Score 74.8;
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DB 12;
Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernot, A.
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Matches 173; Conservative
                                   source
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                                                                                                                                                                                Genoscope
                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                        Weissenbach, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodontidae;
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112 CAACAAAAACAACRACAACRACRGCRGCAACAACAACAAAAAACAACRACAACGGCAACAA 53
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Location/Qualifiers
1. 915
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of cl-
044F19 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetracdon nigroviridis DNA sequence
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Local Similarity 54.9%;
ses 168; Conservative
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AV438522
                                                                                                                                                                                                                                                                                                                                                           Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                               The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyra yezoensis.
Porphyra yezoensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                                                                              Yana 1532–3, Kisarazu, Chiba 292–0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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1 245 c 208 g
                                                                                         /organism="Porphyra yezoensis"
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/note="Vector: pBluescriptII SK-; Sii
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                                       479 CGCCCAGGGCA 489
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Search completed: October 10, 2002, 20:28:27 Job time: 701.733 secs

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DNA encoding novel
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Human brain expres
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Human	Probe	Human	Human	Human	Probe	Human	Probe	Probe	. DNA en	Probe	Human	Human	Human	Probe	Probe		Human	Human	Human	Probe	Human	Human	Probe	Human	Probe		Human	Human	Human	Probe	Human	Probe	Human	DNA en	
foetal liver	#8606 used t	3	brain expres	1 1iv	for g	cell	#14318 for g	for	nove	#21755 used	bone marrow	brain expres	foetal liver	u u	#5050 for ge	G	3	brain expres		#10096 used		expre	•		used		bone marrow	ext	ted pr	#2635 used t		m	foetal liver	5	nove

ALIGNMENTS

AAD11123 standard; DNA; 748 BP.

Human small cell lung cancer associated gene, DKFZp434C196 #2.

Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; ds.

Homo sapiens.

19-JAN-2001; 2001WO-US02015. 21-JAN-2000; 2000US-0489101.

Stockert E, Scanlan MJ, Jager D, Old LJ, Gure AO, Chen Y;

WPI; 2001-457597/49

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is human DKFRp43dC196 DNA. This small cell lung cancer associated gene is designated as NY-SCLC-13.
                  Human small cell lung cancer associated gene, DKF2p434C196 #1
                                                                                        AAD11122;
                                                                                                                          AAD11122 standard;
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                                                      24-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is human DKFSP434C196 DNA. This small cell lung cancer associated gene is designated as NY-SCLC-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1201 BP; 255 A; 377 C; 349 G; 178 T; 42 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-457597/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES (SLOK ) SLOAN KETTERING INST CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-0489101.
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  361 CTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACG
                                                                                                      241
                                                                                                                                      241
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                                                                                                                                                                                                                                                                            121 CCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGG
                                                                                                                                                                                                                                                                                                              Local
                                      GCATCGCCAACGGGGACGCCAACGAGGCCATGGGCAACGAGGTCACCATCCACGGCATCG
                                                                    GCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCG
                                                                                                      TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGG
                                                                                                                                      TCCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGG
                                                                                                                                                                          TCGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCCATCGCCAACTGGGGACGCCG
                                                                                                                                                                                            TCGCCGCACAGGGCATCGCCAATGAGGACGCCCACCCAGGGCATCGCCAACTGGGACGCCG
                                                                                                                                                                                                                                              CCGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCCAGGGCCATCGCCAATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       500;
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Indels Length 1201;

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Gaps

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head

60 60

300 300 240 240 180 180

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Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is enco isolated nucleic acid comprising an NA Group 3 or 4 molecul
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Claim 57; Page 114-115; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                 CANCER RES.
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                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, complymentate (II) sequences. (I) is useful as hybridisation probes, complymentate chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful in gene therapy techniques (II); (II) is useful in gene therapy techniques (II); (II) is useful in gene therapy techniques (II); (II) and the polypeptide and its binding partners are useful in medical imaging of sites expressing (II); (II) and (II) are useful for treating (II) and (II) and (II) are useful 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #8481.
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                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 8481; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
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      RESULT 4
AAS72678
ID AAS7
XX AAS7
AC AAS7
XX DNA
DE DNA
XX Food
XX Food
XX Huma
KW Homo
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                                                                                                                           Drmanac RT,
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23-AUG-2000; 2000US-0649167
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                                                                 WPI; 2001-639362/73
                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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78.8%;
                                                                                                                        Tang YT;
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Sequence 1593 BP; 444 A; 429 C; 434 G; 286 T; 0 other;

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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P-PSDB; ABG08491
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993 CGAGGATGCCGCCAGGCATCGCCAACGAGGTCGCCCAGGGCATCGCCAACGAGGT 1052
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                                                                                        AAS72679
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CC Note: The sequence data for this patent did not appear in the printed consisting the sequence of the invention.

CC Note: The vipo.int/pub/published_pct_sequences.
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Best Local 9
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AAS72679;
                                                           AAS72679 standard; cDNA; 2922 BP
                                                                                                                                                                                                               2410 GCCAACGAGGACTCCGCCCACGGAATCGCCAGCGAGGACGCCGCCCACGGCATCGCCATC 2469
                                                                                                                                                                                                                                                                                                                                       2350 GGCATCGCCAAAGAGGGCGCCGCCCACGGCATCGCCAACGAGGACGCCGCCCAGGGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2050 CACGACATCGCTAACGAGGATACTGTACACGACATCGCTAACGAGGCCCGACAAGGGC 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1990 GATGCCAAGAAAGCTCCCCATGAGGACACCGTACACGACATCACTAACGAGGACGCCACA 2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3093 BP; 875 A; 904 C; 862 G; 452 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 8482; 103pp; English.
                                                                                                                                                                                                                                               441 GC---CGAGGATGTCGCCACAGGGCATCGCCAACGACGACGCCCCCAGGGCATCGCCAAC 497
                                                                                                                                                                                                                                                                                                                                                                                                   381 GGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGAATC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGTCCACCGGCTTCGCCAACGGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 ATCGCCAACGAGGAGGTTGCCCAGGGCATCGCCAATGGGGTCGCCGCACAGGGCATCGCC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 CAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC---CGAGGACGCCATCCAGGGC 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCAGGGCATCGCCAACGAGGGCGCCGCCCAGGGCATCGCCAAGGAGGACGCCGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCGCCAACGAGGACGCCCCACGGCATCGCCAGCGAGGACGCCCCCCCGCGCATCGCC 2169
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Pred. No. 7.2e-
0; Mismatches
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es 91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC polymerase chain reaction (FCR) primers, oligomers, and for chromosome CC polymerase chain reaction (FCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC contentifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or cultivating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC insorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC dispostics, forensics, gene mapping, identification of mutations in CC dispostics for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC and no produce other types of data and products dependent on DNA and CC and no produce other types of data and products dependent on DNA and CC diagnostic coding sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO or terminorial products and to the printed content the printed content the printed of the print of the products of the print of the printed content the printed of the pr
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                   1966 CACGATATCACTAACGAGGACGCTGTCCACGGCATCGCTAACGAGGCCGCCGCCCCAGGGC 2025
                                                                                                                                                                                                                                                                        1906 GATGCCAAGAAAGCTCCCCATGAGGACACCGTACACAACATCACTAACGAGGATGCCTCA 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2922 BP; 833 A; 829 C; 806 G; 454 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 8483; 103pp; English.
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23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #8483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                       24 GCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                            CAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC---CGAGGACGCCATCCAGGGC 140
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                                                                                                                                                                                                                                                                                                                                                                                                   362;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           75.48;
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 114; Indels
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Pred. No. 5.1e-31;

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                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. For this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2326 GCTAATGACACCGTACAAGGCA-CGCTAAAAGAGGACGCTGTACACGACATCGCTAATGAG 2384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2146 GACGCCGCCCAGGGCATCGCCAACGAGGACGCCGTCCAGGGCATCGCCAACGAGGACGCC 2205
                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human foetal liver single exon nucleic acid probe #15166.
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Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
                                                                                                                                                                      Claim 4; SEQ ID NO 15166; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                  WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA66861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 ACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 GACGCCGTCCTCAGCTTCGCCAACGGGGACGCCCCAGGGCCATCGCCAACGGGGACGCC 320
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                           Chen W,
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Query Match

51.5%;

Score 257.6;

DB 22;

Length 518;

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RESULT
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                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #12396 for gene expression analysis in human heart cell sample.
                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                              04-OCT-2000;
                                                                                                               03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                             WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                      congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 CGAGGACGCCGCCCACGGAATCGCCAGCGAGGACGCCGCCCAGGGCATCGCCAACGAGGT
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  Hanzel DK,
                                                                                           ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                2000GB-0024263
    Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                     05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing disease of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID No 12396; 530pp; English.
Human brain expressed single exon probe SEQ ID NO: 15288
                                                                          AAK15297;
                                                                                                           AAK15297 standard; DNA; 518 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
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                                                                                                                                                                                                                                                                       GGACACCATACAAGGCATCGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC
                                                                                                                                                                                                                                                                                                          GGACGCCGCCCAGGGAATCG----CCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC 478
                                                                                                                                                                                                                                                                                                                                                                                TAACGAGGACGCCGTCCAAGGGCATCGCTAACGAGGTGGCCGCCCAAGGGCATCGCCAACGA 421
                                                                                                                                                                                                                                                                                                                                                                                                                   CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
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                                                                                                                                                                                                                                                                                                                                             TA---ATGACACCGTACAAGGCA-CGCTAACGAGGATGCTGTACACGACATCGCTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon nucleic acid probes for analyzing gene expression in human
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75.2%;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic probes which are derived from genomic sequences expressed in the
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
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362 TRACCARGGACGCCGTCAGGCATCGCCTAACGAGGTGGCCGCCCAGGGCATCGCCCAACGA 421
383 TA---ATGACACCGTACAAGGCA-CGCTAACGAGGGATGCTGTACACGACATCGCTAATGA 438
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                                                                        CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
                                                                                                           CATCGCCAACGGGGACGCCAACGAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC
                                                                                                                                              CCATGGCATCGCCAACGAGGACGCTGCCCACGGCATTGCTAACGAGGATGCCGTGCACGG
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2000US-0236359
2000GB-0024263
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2000US-0608408.
2000US-0632366.
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Pred. No. 5.1e-
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #15758 used to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                     WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                Sequence 518 BP; 140 A; 170 C; 139 G; 69 T; 0 other;
                                                                                                                                                                                                                                                 Claim 25; SEQ ID No 15758; 654pp; English.
                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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122 CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTGCCCAAGGCATCGCCAATGGGGT 181
143 CGAGGACGCCGCCCACGGAATCGCCAGCCAGGCAGGCATCGCCCAGGGCATGGCCAACGAGGT 202
                                        83
                                                                                23 CAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGGACGCTGTCCACGGCAT 82
                                                                                           5 CTACGGCATTGCTGAGGACGCTGCCCAGGGCATCGCTAATGAGGACGCCGACCAGGGCAT 64
                                                                                                                                   Loca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCCAGGGCATCGCCAACA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTAACGAGGCCGCCGCCCAGGGCATCGCCAACGAGGACGCCGCCCCAGGGCCATCGCCAA 142
                                                            CGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC--- 121
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                        Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                  2000GB-0024263
                                                                                                                                51.5%;
75.2%;
                                                                                                                         0
                                                                                                                                 Score 257.6; DB 22; Length 518; Pred. No. 5.1e-31;
                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                         Mismatches
                                                                                                                         114;
                                                                                                                         Indels 10;
                                                                                                                      Gaps
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AAS72676
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                         biodiversity
                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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                                                                                                                                                                             P-PSDB; ABG08489
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS72676 standard; cDNA; 3345 BP
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #8480.
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                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 8480; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
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2000US-0649167
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RESULT 11
AAS73321
ID AAS73
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AAS72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gone mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at fit, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                            2436
              WO200175067-A2
                                           Homo sapiens
                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                     DNA encoding novel human diagnostic protein #8125.
                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                     AAS72321 standard; cDNA; 3522 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2376 CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2256 CGCCGCCAGGGCATCGCCAACGAGGACGCCGCCCAGGGCATCGCCAAGGAGGACGCCGC 2315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2136 CGCTAACGAGGCCGACAAAGGGCATCGCCAACGAGGACGCCCAGGGCATCGCCAA 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2076 CAACATCACTAACGAGGATGCCTCACACGACGATATCACTAACGAGGACGCTGTCCACGGCAT 2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3345 BP; 954 A; 940 C; 913 G; 538 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          422 GGACGCCGCCCAGGGAATCG----CCGAGGATGTCGCACAGGGCATCGCCAACGAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 CATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACGAGGTCACCATCCACGGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 CCACGGCTTCGCCAACGGGGACGCCGTCCTCAGCTTCGCCAACGGGGACGCCGCCCAGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 CGCCGCACAGGGCATCGCCAATGAGGACGCCACCCAGGGCATCGCCAACTGGGACGCCGT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 CGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGGAAGCCGCCCAGGGCATCGC--- 121
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                                                                                                                                                                                                                                                                                                                   CGCCCAGGGCATCGCCAACAAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                       TCTACAAGCCGTCGCTAACAAG 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGGCCGCCCAGGGCATCGCCAACGA 421
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                                                                                                                                                                                                                                                                                                                                                             GGACACCATACAAGGCATTGGTAATGAGGACGTTGTATATGACATCGCTAACAAGGACAC
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                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
          2553 CATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATGCCATATATGACATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3522 BP; 1005 A; 1006 C; 959 G; 552 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 8125; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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74.18;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The Copynucleotides are also used in diagnostics as expressed sequence tags (II). (II) is useful in gene thorapy techniques (II), (II) and its binding partners are useful in medical imaging of sites expressing (II), (II) and (II) are useful in medical imaging of sites expressing (II), (II) and (II) are useful for treating CC imaging of sites expressing (II), (II) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC anino acid sequences. AAS64197-AAS94564 represent novel human of all forms of the invention.

Note: The sequence data for this patent did not appear in the printed at the products of the printed of the products of the products of the products of the printed of the products of t

Score 250; DB 23; Pred. No. 5.6e-30; Mismatches 120; Length 3522; Indels 10; 4;

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                                                                                                                                               Matches 299;
                                                                                                                                                                                     Query Match
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2729 TCTACAAGCCGTCGCTAACAAG 2750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2613 TA---ATGACACCGTACAAGGCA-CACTAACGAGGACGCTGTACACGACATCGCTAATGA 2668
                                                                                                                                                                                                                                          Sequence 495 BP; 121 A; 174 C; 129 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2604; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157277-A2.
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                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 GGACGCCCCCCGGGAATCG----CCGAGGATGTCGCCACAGGGCATCGCCCAACGAGGACGC 478
  103 AAGCCGCCCAGGGCATCGC---CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTG 159
                                                 108 ATGAGGACCGGTACACAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGG 167
                                                                                             43 ATGAGGACGCCGACCAGGGCATCGCTAATGAGGACCACCCAGTGCATCGCCAACGAGG 102
                                                                                                                                                                     ocal
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                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                 specification,
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                                                                                                                                               Conservative
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234639
2000US-0236359
2000US-0236359
2000US-0024263
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                                                                                                                                               0; Mismatches
                                                                                                                                                                             Score 235;
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                                                                                                                                                                     Ν̈́O.
                                                                                                                                                                                           DB 22;
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                                                                                                                                                                     .3e-27
                                                                                                                                               85; Indels
                                                                                                                                                                                           Length 495;
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  RESULT 13
ABA24056
ID ABA24
XX ABA24
AC ABA24
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SED-2000; 2000US-0234687.
27-SED-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA24056 standard; DNA;
                                                                                                                                                                                                                    Claim 1; SEQ ID No 2522; 530pp; English.
                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
   Penn SG,
                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe SEQ ID NO: 2574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 AAGCCGCCCAGGGCATCGC----CGAGGACGCCATCCAGGGCATCGCCAACGAGGAGGTTG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 ATGAGGACGCCGACCAGGGCATCGCTAATGAGGACACCACCCAGTGCATCGCCAACGAGG 102
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   Hanzel DK,
                                                                                                                 7 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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Pred. No. 1
   Rank DR;
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1.3e-27;
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   04-FEB-2000; 2000US-0180312
                                                          30-JAN-2001; 2001WO-US00663
                                                                                                                        09-AUG-2001
                                                                                                                                                                                  WO200157272-A2
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                 genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                            human; placenta;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's diseases, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                               Sequence 495 BP; 121 A; 174 C; 129 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO: 2574; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in
0; Mismatches
                                 Score 235; DB 22; Length 495; Pred. No. 1.3e-27;
    85;
Indels
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108 ATGAGGACACCGTACACAACATCACTAACGAGGATGCCTCACACGATATCACTAACGAGG 167 103 AAGCCGCCCAGGGCATCGC---CGAGGACGCCATCCAGGGCCATCGCCAACGAGGAGGTTG 159 43 ATGAGGACGCCGACCAGGGCATCGCTAATGAGGACCACCCAGTGCATCGCCAACGAGG 102 CCAACGGGACGCCGCCCAGGGCATCGCCAACGGGACGCCACCAGGGGCATGGCCAACG 339 AGGTCACCATCCACGGCATCGCTAACGAGGACGCCGTCCAGGGCATCGCTAACGAGGTGG ACGCTGTCCACGGCATCGCTAACGAGGCCGCCGCCCAGGGCATCGCCAACGAGGACGCCG AGGATGCCGTGCACGGCATCGCTAATGAGGACTCCGTATACGACATCGCTAATGAGGATG 347 287

Probe #2635 used to measure gene expression in human placenta sample.

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Matches 299
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 495 BP; 121 A; 174 C; 129 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 2635; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta .
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468 CCATATATGACATCGCTAATGACACCG 494
                  400 CCGCCCAGGGCATCGCCAACGAGGACG 426
                                                             340 AGGTCACCATCCACGGCATCGCTAACGAGGGCCGTCCAGGGCCATCGCTAACGAGGTGG 399
                                                                                                                                                                                                 288 GCATCGCCAACGAGGTCGCCCCAGGGCATCGCCAACGAGGACGCCCCCCAGGGCATCG 347
                                                                                                                                                                 280 CCAACGGGGACGCCGCCCAGGGCATCGCCAACGGGGACGCCACCAAGGGCATGGGCAACG 339
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Search completed: October 10, 2002, 15:17:57 Job time: 94 secs

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	7.2	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.6	7.7	7.8	7.8
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ALIGNMENTS	US-09-050-863-2	US-09-078-294-3	US-09-078-294-4	US-08-943-731-640	US-08-943-731-215	US-08-332-766A-24	US-09-058-489-13	US-09-058-489-14	PCT-US94-04361-19	US-08-458-568A-11	US-08-332-766A-11	US-09-128-155-16	PCT-US96-00994-3	US-09-308-406-1	US-09-165-264-12	5196516-7	US-08-742-185-101	us-09-590-113-2
	Sequence 2, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 640, App	Sequence 215, App	Sequence 24, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 19, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 12, Appl	Patent No. 5196516	Sequence 101, App	Seguence 2, Appli

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COMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ITAM PC COMPATABLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/416,478A
FILING DATE: 04-APR-1995
CLASSIFICATION NUMBER: US 07/854,644
FILING DATE: 04-APR-1995
CLASSIFICATION NUMBER: US 07/854,644
FILING DATE: 08-SEP-1992
APPLICATION NUMBER: 37,971
RESISTRATION NUMBER: 37,971
RESISTRATION NUMBER: 37,971
RESISTRATION NUMBER: 37,971
RESISTRATION NUMBER: HERCEND-1A
TELECOMMUNICATION INDRAMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1871 base pairs
TYPE: nucleic acid
Grean NUMBER: SIGIL
Query Match
Best Local Similarity
   Score 500; DB 1;
Pred. No. 6.2e-111;
                           Length 1871;
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RESULT 2
US-08-474-988B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hercend, Thierry
APPLICANT: Triebel, Frederic
TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/416,478
PILIOR DATE: 04-APR-1995
CIASCIFICATION (15-APR-1995)
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 CTCACCCGGCGGCGCCCTCC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GCAGCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGCGTCACTTGGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 415 CONTY: Washington
                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ce 1, Application US/08474988B
No. 5874250
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                                                   08-SEP-1992
                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                      US 07/854,644
                                                                                                                                                                                                                           US/08/474,988B
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PATEUR NO. INFORMATION:

APPLICANT: Hercend, Thierry
APPLICANT: Hiebel, Frederic
APPLICANT: Triebel, New Proteins Produced By Human
TITLE OF INVENTION: Lymphocytes, DNA Sequences Encoding These Proteins And
TITLE OF INVENTION: Their Pharmaceutical And Biological Uses
**UNMBER OF SEQUENCES: 11
**CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
***ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                    Sequence 1, Application US/08394442B
Patent No. 5976877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1871 base pairs
TYPE: nucleic acid
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NAME/KEY:
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COUNTRY: CITY: Washington STATE: D.C.

U.S.A.

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ATTORREY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25.618
REGISTRATION NUMBER: HERC
REFERENCE/DOCKET NUMBER: HERC
TELECOMMUNICATION INFORMATION: (202) 628-5197
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/394,442B
FILING DATE: 24-FEB-1995
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                                      481 CTCACCCGGCGCGCGCCCTCC 500
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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                                                                               AGCATCAGCCAGACAGTGGCCCGCCCGCTGCCGCCCCCGGCCATCCCCTGGCCCCCGGCC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: HERC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/854,644
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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STREET: 419 Sevent
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                              Local 291;
                                                                                                                                                                                                                            270 CCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCCGGTGGTGTGG 329
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                                                                                                                                                                                               61 CCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGGG 120
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                                                                                                                                                                                                                                                                                                                             58.2%; Score 29; DB 1; Length 1164; Similarity 100.0%; Pred. No. 4.5e-61; 91; Conservative 0; Mismatches 0; Indels
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Triebel,
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Lymphocytes, DNA Sequences Encoding These Proteins And
Their Pharmaceutical And Biological Uses
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; LOCATION:
US-08-474-988B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: HERCI
TELECOMMUNICATION: TELECOMMUNICATION: 1000 158-5197

TELEPHONE: (202) 628-5197

TELEPHONE: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/474,988B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,478
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: Triebel, Frederic
TITLE OF INVENTION: NEW PROTEINS PRODUCED BY HUMAN
TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
NUMBER OF SEQUENCES: 11
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STREET: Washington
CITY: Washington
STATE: D.C.
T S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                       121
                                                                                                                                                                                                      270 CCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGG 329
                                                     330 GCCCAGGAGGGGCTCCTGCCCAGCTCCCCTGCAGCCCCACAATCCCCCTCCAGGATCTC 389
                                                                                                                                                                                     61 CCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGG 120
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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b. 5874250
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419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                      ilarity 100.0%; F
Conservative 0;
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22..1161
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linear
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                                                                                                                                                                                                                                                                                                                                       58.2%; Score 291; DB 2; 100.0%; Pred. No. 4.5e-61;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/394
FILING DATE: 24-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: BERG
REFERENCE/DOCKET NUMBER: HERG
TELECOMMUNICATION INFORMATION:
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NAME/KEY:
LOCATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Triabel, Frederic
TITLE OF INVENTION: New Prote
TITLE OF INVENTION: Lymphocyt
TITLE OF INVENTION: Their Pha
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CURRENT APPLICATION DATA:
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                                  121 GCCCAGGAGGGGCTCCTGCCCAGCTCCCCTGCACCACAATCCCCCCTCCAGGATCTC 180
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                                                                                                                                                                                                                                     61 CCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGG 120
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(202) 737-3528
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SYSTEM: PC-DOS/MS-DOS
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Lymphocytes, DNA Sequences Encoding These Proteins And
Their Pharmaceutical And Biological Uses
                                                                                                                                                                                                                                                                                                                                                                                      58.2%; Score 291; DB 2; 100.0%; Pred. No. 4.5e-61;
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US-08-474-9888-4
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: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                          Sequence 4, Application US/08474988B Patent No. 5874250
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Best Local 9
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APPLICATION NUMBER: US 07/854,644
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37.971
REFERENCE/DOCKET NUMBER: HERCEND=1A
REFERENCE/TOOK INFORMATION:
                                       GENERAL INFORMATION:
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APPLICANT: Triebel, Frederic
TITLE OF INVENTION: Lymphocytes, DNA Sequences Encoding These Proteins And
TITLE OF INVENTION: Their Pharmaceutical And Biological Uses
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CURRENT APPLICATION DATA:
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APPLICANT: Hercend, Thierry APPLICANT: Triebel, Frederic
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                                                                                                                                                                                                                                                                                                                                              768 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTGGATTCCGGCCTCTGGTCATC 827
                                                                                                                                                                                     947 TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATG 999
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                                                                                                                                                                                                                                                                    888 CACCTCCCTCTGCAGAACTTCTCCTTT-CCCCCCACCCCCCACCACTGCCCCCTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/416,478A FILING DATE: 04-APR-1995
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Similarity 99.6%;
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Pred. No. 2.3e~44; 
0; Mismatches 0; Indels
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RESULT 9
US-08-394-442B-4
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                                                                                                         Sequence 4, Application US/08394442B Patent No. 5976877 GENERAL INFORMATION:
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REGISTRATION NUMBER: HERC
REFERENCE/DOCKET NUMBER: HERC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 737-35
INFORMATION FOR SEQ ID NO:
APPLICANT: Hercend, Thierry APPLICANT: Triebel, Frederic TITLE OF INVENTION: New Prot TITLE OF INVENTION: Lymphocy TITLE OF INVENTION: Their Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,644
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION: 45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,478
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TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%; Score 221; DB 2; Length 999; 99.6%; Pred. No. 2.3e-44;
    New Proteins Produced By Human
Lymphocytes, DNA Sequences Encoding These Proteins And
Their Pharmaceutical And Biological Uses
                                                                 Frederic
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                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463 Patent No. 5670367
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FILING DATE: 24-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HERC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 737-3528 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 999 base pairs
TYPE: nucleic acid
                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Relaction DATA:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                        947 TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATG 999
                                                                                                                                                                                                                                                                                                                                                                                     181 TTTTCTGACCTCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                     768 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTGGATTCCGGCCTCTGGTCATC 827
                                                                                                    STREET: 1800 Dia
CITY: Alexandria
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TOPOLOGY: lir
                                                                   COUNTRY:
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                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAGGCTGCCTGATCTGCCCCAGCTTTCCAGCTTTTCCTCTGGATTCCGGCCTCTGGTCATC 60
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Similarity 99.6%;
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                                                                                                                     E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                     USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-232-463-14
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                                                                                                  Sequence 2, Application US/08658136 Patent No. 6071717 GENERAL INFORMATION:
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TOPOLOGY: line
IMMEDIATE SOURCE:
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LENGTH: 7218 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHAX: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Rela
 APPLICANT:
                  APPLICANT:
                                                    APPLICANT:
                                                                   APPLICANT:
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                                                                                    APPLICANT:
                                                                                                                                                                                                                                                     372 ATCCCCCTCCAGGATCTCAGCCTTCT 397
                                                                                                                                                                                                                                                                                                                   312 GAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGGCTCCTGCCAGCTCCCCTGCAGCCCCACA 371
                                                                                                                                                                                                                                                                                                                                                                                     192 CCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGATGTGGGAGGCTCAGTTCCTG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%; Score 78; DB 1; Length 7218; Lishilarity 3.1%; Pred. No. 5.3e-10; 12; Conservative 242; Mismatches 132; Indels
                                KLINGER, KATHERINE V
LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
 DACKOWSKI, WILLI
GERMINO, GREGORY
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26-AUG-1991
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                       TITLE OF INVENTION:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 ACCCCTTCCTCCACCTCCCTCTCTGCAGAACTTCTCCTTTACCCCCCCACCCCCCCACCACT 169
                                                                                                                                                                                                                                                                                                                                                                                                 170 GCCCCCTTTCCTGTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCAT 223
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TTY: FRAMINGHAM
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                                    STREET: ONE MOUNT
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ZIP: 01701
            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
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                            MASSACHUSETTS
                                                                                                                                                                  KLINGER, KATHERINE W
LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
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                                                                                                          POLYCYSTIC KIDNEY DISEASE GENE 58
                                                                                                                                                        GREGORY
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US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
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US-09-007-005-17
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TELEPAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
Type:
                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                         LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
                                                                       OTHER INFORMATION: Translation template FEATURE:
                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEI
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 GCCCCCTTTCCTTTTCTGACCTCCTTTTGGAGGGCTCAGCCCTGCCCAGACCAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 CTCTGGTCATCCCTCCCCACCCTCTCTCCAAGGCCCTCTCCTGGTCTCCCCTTCTTCTAGA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/658,136
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55.2%;
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NAME/KEY: misc_feature

; LOCATION: (1)...(289)

; OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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: Sequence 17, Application US/09244796

: Patent No. 6281344
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ 1D NOS: 33
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LENGTH: 289
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APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 28
TYPE: RNA
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                                                                                      127 YNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS
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67 YNYNYSYNYNY 57
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US-09-165-264-11/c
Job time : 65.7333 secs
                    Search completed: October 10, 2002, 19:28:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                        181 TTTTCTGACCTCC 193
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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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BG898429 HOA55-1-F
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BIG60106 II3-UP011
BIG6032 II3-UP011
AL514267 AL514267
AL547921 AL547921
AGG60752 Pan trog1
BI416660 hasp001xm
ALG66537 Drosophil
AGG081214 Pan trog1
AGG081214 Pan trog1
ALG6869 Drosophil
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53.8	53.8	•			53.8	54	54	54.2	54.2	54.2	54.4	54.6	54.8	55	55.2	55.2	55.4	55.4	55.6	55.6	55.8	55.8	55.8	56.2	56.2	56.6
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AG072464	AG136955	AG081619	CNS03PXL	вн140198	A1268505	AG160225	AG122976	BM479407	AG043735	AG032933	CNS015XQ	BI887282	CNS008MZ	AG171201	BF219496	AG119432	AG126182	BF131888	CNS016CR	BG849405	CNS01523	BI416535	CNS02RAG	AG078085	AG134650	CNS005TE
AG072464			AL255234	вн140198	AI268505 c	AG160225	AG122976	BM479407		AG032933	AL106040	BI887282	AL052079	AG171201				BF131888	AL106581	BG849405	AL104901	BI416535	AL210337	AG078085		AL060767
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ALIGNMENTS

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/Organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HOA (Human Osteoarthritic Cartilage)" /tissue_type="oartilage" /lab_host="E.coli DH10 B" /note="Vector: pSPORT 1; Site_1: Sal1; Site_2: Not1; Directional" 80 a 224 c 191 g 90 t 1 others	rel: 610-727-5598 Fax: 610-727-5598 Email: sanjay_kumar-1@gsk.com Seq primer: T7. Location/Qualifiers 1586	Contact: Sanjay Kumar UW2109 GlaxoSmithKline 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA	sequenced tags (ESTs) each from adult numan normal and osteoarthritic cartilage cDNA libraries Osteoarthritis Cartilage 9 (7), 641-653 (2001) 21482651	Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W. Identification and initial characterization of 5000 expressed	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 586) Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,		BGB98429 HOA55-1-F8.R HOA (Human Osteoarthritic Cartilage) Homo saplens cDNA

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RESULT 2
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Best Local Similarity
Matches 298; Conserv
                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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1 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTCTGGATTCCGGCCTCTGGTCATC 60
                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232;
                                                                                                                                                                                                                                                                                                                                                                                     Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries
Osteoarthritis Cartilage 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG898484 377 bp mRNA linear EST 06-NOV-200 HOAL9-1-A4 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.
BG898484
                                                                                                                                                                                                                                                                                           Tel: 610-270-7245
Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                         GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                             Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG898484.1 GI:14308733
                                                                                                                                                                                                                                                              primer:
                                               Conservative
                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                        sanjay_kumar-1@gsk.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mac, Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M.
                                                                                                                            /wau_nost="E.coli DH10 B"
/mote="Vector: psport I; Site_1: Sall; Site_2: Not1;
Directional"
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
                                                                                                                                                                                                                                               Location/Qualifiers
                                                      46.48;
                                                                                                                    163 c
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                                              0;
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                                                          Score 232;
Pred. No. 1.
                                                                                                                  71 g
                                            Mismatches
                                                                                                                    4 68
                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                     Length 377;
                                                                                                                    1 others
                                            Indels
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                                            0;
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BG900314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BG900314
                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          axoSmithKline
                                                                                                                                                                                                                                                                          51
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181 TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAG 228
                                                 274 CACCTCCCTCTGCAGAACTTCTCCTTTACCCCCCACCCCCACCACCACTGCCCCCTTTCC
                                                                                                                                                                                                                                                                             154 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTCTGGATTCCGGCCTCTGGTCATC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTCTGGATTCCGGCCTCTGGTCATC
                                                                                                                                                                                                                    61 CCTCCCCACCCTCTCCCAAGGCCCTCTCCTGGTCTCCCTTCTTCTAGAACCCCTTCCTC 120
                                                                                                                                                                                                                                                                                                          1 TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTCTGGATTCCGGCCTCTGGGTCATC 60
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                                                                                                                                                               CCTCCCACCCTCTCCAAGGCCCTCTCCTGGTCTCCTTCTTCTAGAACCCCTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                    45.4%;
al Similarity 99.6%;
227; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries
Osteoarthritis Cartilage 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 381)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG900314.1 GI:14310563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
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/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host-"E.coli DH10 B"
/note-"Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Directional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 c
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 381;
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BI060106
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AUTHORS
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                                                                                                             345 CUTGCCCAGCTCCCCTGCAGCCCCACAATCCCCCCTCCAGGATCTCAGCCTTCTGCGAAGA 404
185 CUTGCCCAGCTCCCCTCCAGCACCCCCCCCGGATCTCCACGCTTCTGCGCAGCA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                            155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bhail: asimpsoneludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=II3&t2=II3-UT0114-

160101-420-A06413-2001-01-16614-1)

Seq primer: puc 18 forward

High quality sequence stop: 661.

Location/Qualifiers
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1 (Dases I to 602)

2 (Dases I to 602)

3 (Dases I to 602)

3 (Dases I to 602)

4 (Dases I to 602)

3 (Dases I to 602)

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8 (Dases I to 602)

9 (Dases I to 602)

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 95.7
55; Conservative
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="brUf0114"
/dev_stage="Adult"
/dev_stage="Adult"
/note="0rgan: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/note="0rgan: uterus_tumor; Vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 150.8; DB 10; Length 602; Pred. No. 3.4e-19; 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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SOURCE
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AUTHORS
RESULT 6
AL514267 AL514267 S38 bp mRNA linear EST 13-FEB-2001
DEFINITION AL514267 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BB007ZD09 3
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BI060032
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ouery Match 29.8%; Score 149.2; DB 10; Length 408; Best Local Similarity 95.1%; Pred, Mo. 6.4e-19; Matches 154; Conservative 0; Mismatches 8; Indels 0;
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185 CCTGCCCAGCTCCCCTGCAGCCCCAACACCCCTCCAGGATCTCAGCCTTCTGCCAAGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 CCAGTGAAGCCTGTCCAGCCAGGGCTGAGGTCCCGGTGGTGGTGGGCCCAGGAGGGGGT 344
125 CTAGTGAAGCCTTCCAGCCAGGGGCTGAAGTCCCCGGTGGTGTGGGCCCAGGAGGGGGCT 184
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1 (bases I to 406)

1 (bases I to 406)

1 (bases I to 406)

1 (olasse, Reto, F., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. J., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Carvatho, A.F., Matsukuma, A., Baia, G. S., Simpson, D.H., Grunstein, A., deoliveita, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequence tags
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High quality
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI060032 408 bp mRNA linear EST 15-JUN-2001
IL3-UT0114-160101-419-A10 UT0114 Homo sapiens CDNA, mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL36t2=IL3-UT0114-
160101-419-A104t3=2001-01-164t4=1)
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Seq primer: puc 18 forward
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Best Local Similarity 42.7%; Prod. No. 0.0083; Matches 198; Conservative 24; Mismatches 242; Indels
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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dammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
| (bases 1 to 538)
| 1.49 B., Gruber C., Jessee J. and Polayes D.
| 1.11 length cDMA libraries and normalization
| Inpublished (2001)
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// Abartef * taxon: 9666 // Abartef * taxon: 96
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                                                                           143 ccrcggaadcccrccrggaddaccrccrerggcrgcaggaggrerccaaccrgrcagagrg 84
                                                                                                                                            365 CCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGTCACTTGGCAGCA 424
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                                                                                                                                                                                                                                                                                                               305 AGGGGCTGAGGTCCCGGTGGTGTGGGCCCCAGGAGGGGGCTCCTGCCCAGCTCCCCTGCAG 364
                                                                                                                                                                                                                                                                                                                                                                                           323 SCCCCTKSTSCCYCGGGGSCGSSSSSGSCTCGCTGCKCTGGGCGGTGTGGGGTGTGGGCK 264
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1 (bases 1 to 764)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope
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Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr.
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prime; mrNA sequence.
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174 a 170 c 238 g 23 t 159 others
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                                                                                                                                                                                                                                                                                                                                                                              192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG060752 960 bp DNA Pan troglodytes DNA, clone: PTB-048J12.F,
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Library clone:PTB-048J12.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Clone_lib="PTB Chimpanzee Male BAC Library"
24 c 670 g 38 t 135 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="PTB-048J12.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                            12.4%; 39.3%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 61.8; DB 12; Length 960; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                           296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 CAGACAGTGGCCCGCCCGCCGCCCCCGGCCCATCCCCTGGCCCCCGGCCCTCACCCGG 489
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135 CAGAACTTCTCCTTTACCCCCCACCCCCCACTGCCCCCTTTCCTTTTCTGACCTCCT 194
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                                                                                                                                                                                                                                     206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus sylvestris/Heterobasidion annosum Pinus sylvestris/Heterobasidion annosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred-Asiegbuenykopat.slu.se
Seg primer: T7 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Fred O. Asiegbu
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; mixed EST libraries.
1 (bases 1 to 1222)
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Seedling roots of scots pine were infected for 6 days with H. annosum"

/note="Vector: pr-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycella of Heterobasidon annosum (FP5)."

23 c 1007 g 4 t 79 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
/clone="hasp001xm19f"
/clone_ihasp001xm19f"
/clone_ihasp001xm19f"
/clone_ihasp001xm19f"
/clone_ihasp001xm19f"
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                                                                                                                                                                        Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be coation/Qualifiers

Location/Qualifiers
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[ (bases 1 to 987)
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR09C16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_iib="RPCI-98"
/clone="BACR09C16"
                                          /note="end : TET3"
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                     393 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 GGGGCTGAGGTCCCCGGTGGTGGGGCCCCAGGAGGGGGGCTCCTGCCCAGCTCCCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 TTCCTGGGCTTGCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCA 305
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                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Subhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045 Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-903-911, Fax:81-45-903-9170) Tel:81-45-903-911, Fax:81-45-903-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGUBIZI4 917 bp DNA linear GSS C
Pan troglodytes DNA, clone: PTB-077J19.R, genomic survey
AGD81214
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92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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Eukaryota;
                                                                                                                                                                                                                              clone tracking errors.
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Library clone:PTB-077J19.R.
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/clone="PTB-077J19.R"
                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AG110286.1 GI:16730805
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-115P11.R.
           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                        Fujiyama,A., Hattori,M.,
Totoki,Y., Watanabe,H. a
                                                                                                                                                                 Unpublished
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Totoki, Y., Watanabe, H. ar
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                              Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 35 c 666 g 46 t 102 others
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14F09 of RPCI-98 library from Drosophila melanogaster (fruit
Genoscope
                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Eukaryota; Metazoa; Endopterygota; Diptera; Brachyce
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 59 c 644 g 10 t 24 others
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/db_xref="taxon:9598"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 948)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14F09"
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DEFINITION CNS0091P

CNS0091P 925 bp DNA linear Good Portsophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit

03-JUN-1999

survey sequence

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone_lib="RPCI-98"
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                                                                                                                                                                                                                                                                    CSCCTCCCSYSYSSSTSWGSTSWGSTSGSSSSYGTSSSSDSTSTCCSCCCYMCTCCST 817
                                                                                                                                                                                                                                                                                                                                                       SSKSSASSSSVSSSGSSGSVSSNSSSASKSSSSGSVSSGSGSGSGSVS
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                                                                                                                                    - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster additional melanogaster back in the properties of the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/db_xref="taxon:7227"
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                                    03-JUN-1998;
                                                                            23-DEC-1998.
                                                                                                                     W09858059-A1
                                                                                                                                                                                                                                    Homo sapiens
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ALIGNMENTS

human; immunomodulator; Hashimoru s unjuture. A disease; type I diabetes mellitus; multiple sclerosis; Crohn's disease; rheumatoid arthritis; allograft rejection; graft-versus-host disease; Grave's ophthalmopathy; abortion; cerebral malaria; Lyme arthritis; reactive arthritis; hepatiti primary sclerosing colangitis; dermatitis; aplastic anaemia; 18-JUN-1997; Human lymphocyte activation gene 3 splice variant LAG-3V3 cDNA 26-APR-1999 (first entry) Lymphocyte activation gene 3; LAG-3; LAG-3V3; splice variant; human; immunomodulator; Hashimoto's thyroiditis; 97EP-0401404. 98WO-EP03307. Location/Qualifiers 297..1313 /*tag= hepatitis;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting mRNA encodes a truncated soluble protein which contains to 1, 22, D3 and 8 new amino acid residues. LAG-3V2 cDNA was obtained by RT-DCR amplification (see AAW06759 and AAW06762) of peripheral blood mononuclear cell RNA. The invention provides 3 splice variants (see AAW88359-61) of LAG-3 and nucleotide sequences encoding them (see AAW06754-56). The LAG-3 variants can be used in, or for the manufacture of, therapeutic compositions used to treat immune-related pathologies (claimed), in particular Thi-dependent diseases such as Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, Crohn's disease, rheumatoid arthritis, acute allograft rejection, acute graft-versus-host disease, Grave's ophthalmopathy, cerebral malaria, lyme arthritis, reactive arthritis, Crohn's disease, Scroperial according colongitis, contact dermatitis, unexplained recurrent abortion, aplastic anaemia and Helicobacter pylori-induced gastric antritis. LAG-3 variants can also be used for the manufacture of immunomodulator compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1468 BP; 231 A; 550 C; 404 G; 283 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New lymphocyte activation gene 3 (LAG-3) splice variants can be used as immunomodulators
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                      GCAGCCCCACAATCCCCCCCCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGGTCACTTGGC 420
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GCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGTCACTTGGC
                                                                       AGCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGCTCCTGCCCAGCTCCCCT
                                                                                                                                                  CTCAGTTCCTGGGCTTGCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCCTCTCC
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INST ROUSSY GUSTAVE.
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dermatitis, unexplained recurrent abortion, aplastic anaemia and

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            LAG-3V2 CDNA was obtained by RT-PCR amplification (see AAX06759 and AAX06762) of peripheral blood mononuclear cell RNA. The invention provides 3 splice variants (see AAX06754-56). The LAG-3 and nucleotide sequences encoding them (see AAX06754-56). The LAG-3 variants can be used in, or for the manufacture of, compositions used to treat immune-related pathologies (claimed), in particular Th1-dependent diseases such as Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, Crohn's disease, rheumatoid arthritis, acute allograft rejection, acute graft-versus-host disease, Grave's ophthalmopathy, cerebral malaria, Lyme arthritis, reactive arthritis, Contact
                                                                                                                                                                                                         This cDNA encodes LAG-3V2 (see AAW88360), a splice variant of human lymphocyte activation gene 3 (LAG-3) protein. LAG-3V2 lacks exon 6 due to the ligation of the donor site of intron 5 to the acceptor site of intron 6. There is no frame shift. The LAG-3V2 protein is
                                                                                                                                                                                                                                                                                       Claim 1; Page 24-25; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mastrangeli R, Romagnani S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1629 BP; 252 A; 605 C; 452 G; 320 T; 0 other;
                                                                                  mat_peptide
                                                                                                                                                                     human cytotoxic T-lymphocyte; LAG-3; HIV; CD4; AIDS; ss.
                                                                                                                                                                                                                                              AAQ12869;
                                                                                                                                                                                                                                                                      AAQ12869 standard; cDNA; 1871 BP
          25-JUL-1991
                                   WO9110682-A.
                                                                                                        sig_peptide
                                                                                                                                            Homo sapiens
                                                                                                                                                                                            Lymphocyte Activation Gene-3
                                                                                                                                                                                                                       15-OCT-1991
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Similarity 100.0%; Pred. No. 2e-105;
00; Conservative 0; Mismatches 0
                                                                                                                                                                                                                       (first entry)
                                                                   /*tag= a
315..1724
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                                                                                                                    Location/Qualifiers
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                                                          LAG-3
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FDC cDNA was isolated from a natural cytotoxic lymphocyte cDNA library constructed in lambda gt10. The LAG-3 can be expressed in insect cells (i.e. Spodoptera frugiperda SF9 cells) in membrane-bound and soluble forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphocyte membrane protein and DNA encoding it (LAG-3) - useful for antibodies and pharmaceutical products used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1871 BP; 300 A; 671 C; 524 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAQ12870-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 42-44; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-infected humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE. (INSR ) INST ROUSSY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-1990;
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                                                                                                                                                                                           1991-237986/32.
                             CTCACCCGGCGCGCCCTCC 500
                                                                                                            TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTGGATTCCGGCCTCTGGTCATC
                                                                                                                                                                 ACCCAGGGCTGAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGCTCCTGCCCAGCTCCCCT
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                                                                      AGCATCAGCCAGACAGTGGCCCGCCCGCCTGCCCCCGGCCATCCCCTGGCCCCCGGCC
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                                                                                                                                                      AGCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGCTCCTGCCCAGCTCCCCT
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Pred. No.
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AAD11121 standard;

DNA; 1872 BP

AAD11121;

24-SEP-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a DNA encoding human lymphocyte activation gene-3 (LAG-3). This small cell lung cancer associated gene is designated as NY-SCLC-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encodisolated nucleic acid comprising an NA Group 3 or 4 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; lymphocyte activation gene-3; LAG-3; synovial sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1872 BP; 300 A; 673 C; 523 G; 376 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
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                  CTCAGTTCCTGGGCTTGCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCCCTCTCCC
CTCAGTTCCTGGGCTTGCTGTTTCTGCAGCCGCTTTGGGGTGGCTCCAGTGAAGCCTCTCC
                                                                    TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATGTGGGAGG
                                                                                                                                                                                                                   CTCCCCACCTCTCCAAGGCCCTCCCGGTCTCCCTGCTTCTTCTAGAACCCCTTCCTC
                                                                                                          TTTTCTGACCTCCTTTTGGAGGGCTCAGCCCCAGACCATAGGAGAGATGTGGGAGG
                                                                                                                                             CACCTCCCTCTCTGCAGAACTTCTCCTTTACCCCCCACCCCCCCACCACTGCCCCCTTTCC 180
                                                                                                                                                                                                                                                         CCTCCCCACCCTCTCCAAGGCCCTCTCCTGGTCTCCCTTCTTCTAGAACCCCTTCCTC 120
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                                                                                                                                                                                                                                                                                                                                                                      500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Page 108-109; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 500; DB 22
100.0%; Pred. No. 2e-105;
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This CDNA encodes LAG-3V1 (see AAW88359), a splice variant of human lymphocyte activation gene 3 (LAG-3) protein. LAG-3V1 is derived from the retention of intron 4, i.e. cleavage at the donor and acceptor sites flanking intron does not occur. An in-frame stop codon located after 8 codons in the retained intron 4 leads to a 36 kDa truncated soluble LAG-3V1 cDNA was obtained by RT-PCR amphification (see AAX06757-58) of peripheral blood mononuclear cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type I diabetes mellitus; multiple sclerosis; Crohn's disease; rheumatoid arthritis; allograft rejection; graft-versus-host disease; Grave's ophthalmopathy; abortion; cerebral malaria; Lyme arthritis; reactive arthritis; hepatitis; primary sclerosing colangitis; dermatitis; aplastic anaemia;
                                                                                                                                                                                                                                                                                                       (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV. (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (INSR ) INST ROUSSY GUSTAVE.
                                                                                                                                                Claim 1; Page 21-22; 49pp; English.
                                                                                                                                                                                                                               P-PSDB; AAW88359.
                                                                                                                                                                                                                                                                             Mastrangeli R,
                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
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                                                                                                                                                                                 lymphocyte activation gene 3 (LAG-3) splice variants be used as immunomodulators
                                                                                                                                                                                                                                               1999-080953/07.
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                                                                                                                                                                                                                                                                             Romagnani S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 297..1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
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RESULT 6
AAQ12871
ID AAQ1
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                                                                                                                                                                                                                                                                                             Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA. The invention provides 3 splice variants (see AAW88359-61) of LAG-3 and nucleotide sequences encoding them (see AAX06754-56). The CLAG-3 variants can be used in, or for the manufacture of, pharmaceutical or therapeutic compositions which are used to treat immune-related pathologies (claimed), in particular Thi-dependent diseases such as Hashimoto's thyroiditis, type I diabetes mellitus, multiple scierosis, Crohn's disease, rheumatoid arthritis, acute allograft rejection, acute graft-versus-bost disease, Grave's ophthalmopathy, cerebral malaria, Lyme arthritis, reactive arthritis, dermatitis, unexplained recurrent abortion, aplastic anaemia and the Helicobacter pylori-induced gastric antritis. LAG-3 variants can also be used for the manufacture of immunomodulator compounds (claimed), which can mimic or alter the biological function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                AAQ12871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                          human cytotoxic T-lymphocyte; LAG-3S; HIV; CD4; AIDS;
                                                                     Polyhedrin-soluble LAG-3 fusion construct.
                                                                                                    15-OCT-1991
                                                                                                                                                             AAQ12871 standard; DNA; 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCCCCACCCTCTCCAAGGCCCTCTCCTGGTCTCCTTCTTCTAGAACCCCTTCCTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCTCCCTCTCTGCAGAACTTCTCCTTTACCCCCCCACCCCCCCACCACTGCCCCCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGGCTGCCTGATCTGCCCCAGCTTTCCCAGCTTTCCTCTGGATTCCGGCCTCTGGTCATC
                                                                                                                                                                                                                                    CTCACCCGGCGCGCCCCTCC
                                                                                                                                                                                                                                                                 CTCACCCGGCGCGCCCCTCC 500
                                                                                                                                                                                                                                                                                             AGCATCAGCCAGACAGTGGCCCGCCCGCCGCCGCCGCCCGGCCATCCCCTGGCCCCGGCC
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                                                                                                  (first entry)
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Pred. No. 2.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 498 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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RESULT 7
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ID AAQ1
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AC AAQ1
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Best Local S
Matches 291
                                                                                                                                                                                                                                                                                                                     FDC cDNA was isolated from a natural cytotoxic lymphocyte cDNA library constructed in lambda gt10. It encodes LAG-3, a membrane-bound protein. A soluble form (LAG-35) of the protein can be produced in insect cells (i.e. Spodoptera frugiperda SF9 cells) by removing the transmembrane region-coding sequence. This construct encodes the first 3 extracellular Ig-like domains of LAG-3 (V domain and two C2 domains) fused to a 17 amino acid fragment of the insect protein polyhedrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
sig_peptide
                                                                                                                                                                                                                                                                                      Sequence 1164 BP; 182 A; 426 C; 340 G; 216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-infected humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphocyte membrane protein and DNA encoding it (LAG-3) useful for antibodies and pharmaceutical products used to tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hercend T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page 49-50; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INRM ) INSERM INST NAT SANTE
(INSR ) INST ROUSSY G.
                        450
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GCCGCCCCGGCCATCCCCTGGCCCCCGGCCCTCACCCGGCGGCGCCCCTCC
                                              GCTGCCCAGACCATAGGAGAGATGTGGGAGGCTCAGTTCCTGGGCTTGCTGTTTCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1991-237986/32.
                                                                                                          GCCCAGGAGGGGGCTCCTGCCCAGGCTCCCCTGCACAATCCCCCCTCCAGGATCTC
                                                                                                                                                                                           GCTGCCCAGACCATAGGAGAGGTGGGGAGGCTCAGTTCCTGGGCTTGCTGTTTCTGCAG
                                                                                               GCCCAGGAGGGGGCTCCTGCCAGCTCCCCTGCAGCCCCACAATCCCCCTCCAGGATCTC
                                                                                                                                                                                                                                                                                                              AAQ12869-70.
                                                                                                                                                                                                                                       58.2%; Score 291; DB 12; ilarity 100.0%; Pred. No. 1.4e-57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triebel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90FR-0000126
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106..1161
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                                                                                                                                                                                                                                                                Length 1164;
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   291
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0,

AAQ12870; 15-OCT-1991

(first entry)

AAQ12870 standard;

DNA;

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RESULT 8
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Best Local :
                                                    Domain D1; lymphocyte activating gene 3; LAG-3; reduced affinity; class II molecule; immunomodulator; treatment; autoimmune disease;
                                                                                                                                                    AAV07462 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a suitable promoter for expression of LAG-3. It is also claimed as a DNA sequence which encodes a polypeptide fragment of LAG-3 although no corresponding amino acid sequence is given. See also AAQ12869 and AAQ12871.
  WO9823741-A1
                     Homo sapiens.
                                           graft rejection; anticancer immunotherapy; ss.
                                                                                      DNA encoding the first domain, D1, of the LAG-3 protein.
                                                                                                            01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 999 BP; 214 A; 278 C; 302 G; 205 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Page 48; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lymphocyte membrane protein and DNA encoding it (LAG-3) - useful for antibodies and pharmaceutical products used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-infected humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter sequence for LAG-3 expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSR ) INST ROUSSY
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                                                                                                                                                                                                            CTCCCCACCCTCTCCCAAGGCCCTCTCCTGTCTTCTTCTTAGAACCCCTTCCTC
                                                                                                                                                                                                                                                                                                                     CCTCCCCACCCTCTCCAAGGCCCTCTCCTGGTCTCCCTTCTTCTAGAACCCCTTCCTC 120
                                                                                                                                                                                                                                 TTTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAGATG 233
                                                                                                                                                                                                                                                       CACCTCCCTCTGCAGAACTTCTCCTTT-CCCCCCACCCCCCACCACTGCCCCCTTTCC
                                                                                                                                                                                                                                                                                                                                            TCAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTGGATTCCGGCCTCTGGTCATC 827
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 221; DB 12;
Pred. No. 1.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
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Query Match
                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antiantemalc; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulators for treating autoimmune disease, for controlling graft rejection and in anticancer immunotherapy (e.g. of leukaemia and melanoma), and also to produce antagonists or agonists of the interaction between LAG-3 and Class II major histocompatibility molecules. Cells in which the mutants are exposed at the surface are useful in binding/adhesion assays to study binding to particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein encoded by lymphocyte activating gene 3 (LAG-3). The sequence is used to create mutants AAW62901-02. The mutants have reduced, or no, affinity for Class II molecules. These mutants are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mutants of lymphocyte activating gene-3 protein - comprise extracellular domains, having reduced interaction with Class II molecules, useful as immuno-modulator for treating, e.g. auto-immune
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                        Human immune system associated gene SEQ ID NO: 1126.
                                                                                                                                                                                                                                                                             ABL33153 standard; DNA; 5689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 447 BP; 49 A; 188 C; 152 G; 58 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes the first extracellular domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 62pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSR ) INST ROUSSY GUSTAVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-322721/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 CTCCAGCCAGGGGCTGAGGTCCCGGTGGTGGGCCCAGGAGGGGGGCTCCTGCCCAGCTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 40.8%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGGCTCCTGCCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                        GGCCCTCACCCGGCGCGCGCCCTCC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCAGCATCAGCCAGACAGTGGCCCGCCCGCTGCCCCCCGGCCATCCCCTGGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCCTCACCCGGCGCGCCCCTCC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCAGCATCAGCCAGACAGTGGCCCGCCCGCCCGGCCCCCGGCCATCCCCTGGCCCCC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGGTCACT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGGTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mastrangeli R, Triebel F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204; DB 19; Length 447; pred. No. 9.9e-38;
                                                                                                                                                                                                                                                                             BP.
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ABL34551/c
ABL34551/c
ID ABL345
XX ABL345
AC ABL345
XX DT 26-MAR
XX DE Human
XX
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Best Local S
Matches 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
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                Human metastasis associated gene SEQ
                                              26-MAR-2002
                                                                                                         ABL34551 standard;
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2000DE-1043826
                                             (first entry)
                                                                                                         DNA;
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81.2%;
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Pred. No. 1.5e
0; Mismatches
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L.5e-37;
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bowel disease;
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Best Local S
Matches 237
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation,
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Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                          26-MAR-2002
                                                                                                                                                   ABL33152 standard; DNA; 5689
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                                                           Human immune system associated
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237; Conserv
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                          (first entry)
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81.2%;
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ds.
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Pred. No. 1.5e-37;
0; Mismatches 55; Indels 0
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                                                           gene SEQ ID NO:
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                                                                                                                                                                                                                                                                                   5240
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis, psoriasis and inflammatory/ulcerativ diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1125; 32pp + Sequence Listing; German.
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             (first entry)
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Human; chromosome mapping; gene mapping; gene therapy;

forensic;

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07-APR-2000;
30-JUN-2000;
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also for
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                                                                                                                    AAS85793 standard;
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                                                                              AAS85793;
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2000DE-1032529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000DE-1019058
                                        (first entry)
human diagnostic protein #21597.
                                                                                                                    CDNA; 3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 106.4; DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5e-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5689;
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AAS86048
ID AASE
XX
AC AASE
XX
DT 13-E
XX
DE DNA
                                                                                                                                                                                                                                                                                                                CC polypertide (II) sequences. (I) is useful as hybridisation probes, CC polypertide (II) sequences. (I) is useful as hybridisation probes, CC polypurase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC quantifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or GC quantifiating a polypeptide in tissue, as molecular weight markers and as CC afood supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at the first of the invention of the printed contains and contains of the invention.
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                                                                                                    RESULT 14
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                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 21597; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food supplement;
                                                                                                                                                                                         2250 CCGCCCAGTGGCCCGCTCACCCC 2191
                                                                                                                                        2190 GCGGCGCCCTCC 2179
                                                                                                                                                                                                                                                                                           Sequence 3267 BP; 572 A; 914 C; 970 G; 811 T; 0
DNA encoding novel human diagnostic protein #21852
                         13-FEB-2002
                                                  AAS86048;
                                                                          AAS86048 standard; cDNA; 5912 BP
                                                                                                                                                                 489
                                                                                                                                                                                                                  429 CCAGACAGTGGCCCGCCCGCCCGCCCCGGCCCATCCCCTGGCCCCCGGCCCTCACCCG 488
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DB; ABG21606.
                                                                                                                                                                 GCGGCGCCCTCC 500
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                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0540217.
2000US-0649167.
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                        13.4%; 95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TY
                                                                                                                                                                                                                                          Score 67.2; D
Pred. No. 3e-0
0; Mismatches
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                        3e-06;
                                                                                                                                                                                                                                                                     DB 23; Length 3267;
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                                                                                                                                                                                                                                                                                                other;
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The invention relates to isolated polynucleotide (I) and collective (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical collingual colling
                                                                                                                                                                                        RESULT 15
AAZ17263
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Best Local
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess became the contract of the co
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1018 CCGCCCAGTGGCCCGCCGCCTGCCGCCCGGCCATCCCCTGGCCCCCGGCCCTCACCCG 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 21852; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG21861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
AAZ17263;
                                                                                                                                       AAZ17263 standard; cDNA; 1337 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 GCGGCGCCCTCC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGCGCCCTCC 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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12-OCT-1999

(first entry)

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                                                                                                                                                                                                                                                                          The present invention describes a library of human polynucleotides CC comprising the sequences given in AAZI2532 to AAZI779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell course of the 5248 polynucleotide sequences given in AAZI2532 to AAZI779. The CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, cmapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to detection of an CC arrays for diagnostics (which may be used to detection of an CC identify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC diagnosis, prognosis and management of colorectal cancer, breast cancer, cand lung cancer. The polynucleotides can also be used to screen for nentify and antarophets
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2250-2251; 2479pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1998;
28-JAN-1998;
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                                                                                                                                                                                                                           Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
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31-MAR-1998;
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                                                                                                                                                                                                                                                                  peptide analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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62
                                                                                                                                                                    Local Similarity
                                                                                                             2 CAGGCTGCCTGATCTGCCCAGCTTTCCAGCTTTCCTCTGGATTCCGGCCTCTGGTCATCC 61
                    CTCCCCACCCTCTCCCAAGGCCCTCTCCTGGTCTCCCTTCTTCTAGAACCCCTTCCTCC 121
                                                                                                                                                    Conservative
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98US-0080114.
98US-0080515.
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                                                                                                                                                                                                                                                                  and antagonists.
                                                                                                                                                                    10.0%;
26.5%;
                                                                                                                                                  0;
                                                                                                                                                                Score 49.8; DB
                                                                                                                                                    Mismatches
                                                                                                                                                                                      DB 20; Length 1337;
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1072 CNNCNCNCNNCCNNCCNNC 1090
                         482 TCACCCGGCGCGCCCCTCC
                                                                                                                                                                                                                                                                                                                                   362 CAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGTCACTTGGCA 421
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                                                   GCATCAGCCAGACAGTGGCCCGCCCGCCTGCCGCCCCGGCCATCCCCTGGCCCCCGGCCC 481
                                                                                                                                                               GCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCCAGGAGGGGGGCTCCTGCCCAGCTCCCCTG
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Search completed: October 10, 2002, 15:17:48
Job time: 102 secs

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Result
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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US-09-130-114-1
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US-07-885-971-15
US-07-885-971-15
US-08-087-783A-15
US-08-194-088-15
US-08-194-088-15
US-09-165-264-8
US-09-165-264-8
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	5244792-1	us-09-263-023-1	PCT-US93-03993-1	US-08-458-240-1	US-08-146-930-1	US-08-318-837-1	US-09-058-260-7	US-08-694-078-7	US-08-781-802-7	US-09-103-840A-1	US-09-103-840A-2	US-07-945-283-1	US-09-103-840A-2	US-09-028-934-28	US-09-165-264-12	US-09-165-264-14	US-08-458-745-1	

ALIGNMENTS

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; sequence 2, Application US/09050863; Patent No. 6114111
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                                                                                                                                                      ; MOLECULE TYPE: US-09-050-863-2
  밁
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: S11VA, Robin M.
REGISTRATION NUMBER: 38,304
REPERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 949-8711
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF SEQUENCES: 5
                                                                                                                                                                               LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLEDITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0.
CURRENT APPLICATION LOMBER: US/09/050,88
FILING DATE: 30-MAR-1998
131 GCCCAGATAGACGCCCCGGCCCCGGCTCCTGGAGTCCCGCCGCCTGCTGCCCGGCCG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                              12.0%;
Similarity 50.6%;
                                                                              Conservative
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                                                                                              Score 60; DB 3; Length 2580; Pred. No. 0.00034;
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US-09-359-081-2
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Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCRET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 781-1989
TELEPRONE: (415) 781-1989
TELEPAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
           Matches 170;
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: U5/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
APPLICATION NUMBER: 09/050,863
APPLICATION NUMBER: 09/050,863
APPLICATION TOMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 CCTCCTGCTCCTGCCCCTCCTCCTGCTCCTGCCCCT 686
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                                            Match 12.0%;
Local Similarity 50.6%;
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                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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           Conservative
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Hao, Ying
Hiang, Betty
Payan, Don
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                                       Score 60; DB 4; Length 2580; Pred. No. 0.00034;
Mismatches 165; Indels
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APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/LD903US1
CURRENT FILING DATE: 1998-08-06
RUMBER OF SEQ ID NOS: 36
SOFTWARE: FILING DATE: 1998-08-06
SOFTWARE: FSSTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 5452
TYPET: NOM-
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Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                               ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                                                                                                                           CGCCATGCTGC-ACTGCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT 369
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Pred. No. 0.00035
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US-08-910-647-1/c
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Patent No. 6251433
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (510) DO TELEFAX: (510) TO SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 1-ENGTH: 9600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: FUJICA, Sharon M.
REGISTRATION NUMBER: 38.459
REFERENCE/DOCKET NUMBER: 1218.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                         370
                                                                                                                       887
                                                                                                                                                  311 CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCCGCCGCCATACCCTGCCTTCT 369
                                                                                                                                                                                  947
                                                                                                                                                                                                           191 AGGACCCCACCCCGCCTGCCGCCGGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250
                                                                                                                                                                                                                                                                                                                                   767 CCTCCTGCTCCTGCCCCCCTCCTGCCCCCCT 732
                           430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                          94608-2916
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4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 0.00036;
0; Mismatches 165; Indels
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RESULT 5

US-07-885-971-15/c

RESULT 6

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US-07-884-811-15/c; Sequence 15, Application US/07884811; Patent No. 5316921
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LEMGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 755
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: UFILING DATE: 19920518 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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2301 CCTCCTGCTCCTGCCCCCTCCTGCTCCTGCCCCCT 2266
                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                               191 AGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250
                                  430 ACACCAGCTATGCCCCGCGGGCCACCGCCTCCAGCT 465
                                                                                                          311 CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT 369
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CITY: South San Francisco
STATE: California
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Similarity 50.6%;
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US-08-087-783A-15/c; Sequence 15, Appl
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS NUMBER OF SEQUENCES: 21
                                                                                   2301 CCTCCTGCTCCTGCCCCCTCCTGCTCCTGCCCCT 2266
                                                                                                                                                    TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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MEDIUM TYPE: 5.25 in
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                                                                                                                   430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: 19920518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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   Application US/08087783A
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/884811

FILING DATE: 18-MAY-92

PRIOR APPLICATION UNMBER: 07/885971

APPLICATION UNMBER: 07/885971

FILING DATE: 18-MAY-92

APPLICATION INFORMATION:
MANGE: MAISCHARD, DIADO L.

REGISTRATION UNMBER: 55,600

REFERENCE/DOCKET WUMBER: P075

TELECOMMUNICATION INFORMATION:
TELECHHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                               2481
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LENGTH: 10596 base pairs
TYPE: Nucleic Acid
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NUMBER OF SEQUENCES: 22
2301 CCTCCTGCTCCTGCCCCTCCTGCTCCTGCCCCT 2266
                                                                CURRENT APPLICATION DATA:
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                             430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                              311 CGCCATGCTGC - ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTTGCCTTCT 369
                                                                                                                                                                                                                                                                                            191 AGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250
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CITY: South San Francisco
STATE: California
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RESULT 8

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RESULT 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 170;
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APPLICANT: GODOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18 MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: nucleic acid
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TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
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                                             2301 CCTCCTGCTCCTGCCCCCTCCTGCTCCTGCCCCT 2266
                                                                                                        430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                                                                                                                                                                                            251 CCCGCAGCATGAACCCCCGCCGGCGGCCGGCGGCCCTGCAGAG 310
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TELEX: 910/371-7168
TELEX: 910/371-7168
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T: 460 Point San Bruno Blvd
South San Francisco
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US-08-194-087-15/c

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; TOPOLOGY: US-08-194-087-15
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Patent No. 5879910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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2301 CCTCCTGCTCCTGCCCCCCTCCTGCCCCCT 2266
                                                                             430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                                                                                                                             311 CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCCTGCCTTCT 369
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CITY: S
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 77
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                                                                                                   CCCGCAGCATGAACCCCCGCCGGCGGGCAGCCTCCTGTACAGCCCGCCGCCCCTGCAGAG 310
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RESULT 11
US-09-128-155-16
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Best Local Similarity 50.0
Matches 170; Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/88
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                     2301 CCTCCTGCTCCTGCCCCTCCTGCTCCTGCCCCT 2266
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                 191 AGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250
                                                                                                       430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                                                                                                                                                                                                                                                           251 CCCGCAGCATGAACCCCCGCCGGCGGCGGCAGCCTCCTGTACAGCCCGCCGCCCCCTGCAGAG 310
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CITY: South San Francisco
STATE: Callifornia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER
                                                                                                                                              CGCCATGCTGC-ACTGCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT 369
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Pred. No. 0.00037;
0; Mismatches 165; Indels
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US-09-165-264-8/c
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOW DESS THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FRASTSEQ for Windows Version 3.0
                                                                                                     Sequence 8, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
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Patent No. 6117654
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              FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
                                                    APPLICANT: Vinayagamoorthy, Thuradayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                             470 ACC 472
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                                                                                                                                                                                                                                                                                                                                                  410 CGGCAGCCAGCCCTGCCCAGACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCTTGCC
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Gaps

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US-09-165-264-13/c
; Sequence 13, Application US/09165264
; Patent No. 6197510
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                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8
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                                                                                                                                                         Query Match 10.0%;
Best Local Similarity 47.5%;
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                           SOFTWARE: |
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                       LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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CGCCGGCGGGCAGCCTCCTGTACAGCCCGCCGCCCCTGCAGAGCGCCCATGCTGCACTGCC 327
                                                  GCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTACCCCGCAGCATGAACCCC
                                                                                                    CCGCCTCCTTCCTCGGCAGCCAGCCTGCCCAGACACCAGCTATGCCCCCGTGGCCACCG 456
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                                                                                                                                                           Mismatches
                                                                                                                                                                      DB 4; Length 320;
0.029;
                                                                                                                                                        165; Indels
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US-08-718-388-5/c
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                                                                                                                                                                                                                                              Query Match
Best Local S
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3661 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                             114 CCACCACGAGCGAGAAGCCCAGATAGACGCCCCGGGCGCCCCGGGTCCTGGAGTCCCGC 173
234 GCCATGGACAGGGATTACCCGCAGCATGAACCCCCGGCGGGGGGGCAGCCTCCTGTACAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448
                                                                                                                                                                                           54 CCGCGGGCTCCGCCCCGGCCGGACCCGGGCCCGAGATCATGATGCTGCCGCCACCGCCG 113
                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: PO BOX 747 CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22040-0747
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                                                            CGCCTGCTGCCCGGCCGAGGACCCCCACCCCGCCTGCCGCCGATGCTTGCAGTGGGGCCC
                                                                                              TGCGCGGGCGCACAAGGCCGTGGCAGGGCGCCAGCGGGCCGTCGCTGGCGAGATCACC 2686
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                                                                                                                                                                                                                             tch 9.8%; al Similarity 45.9%; 168; Conservative
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PO BOX 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 205-8000
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                                                                                                                                             Query Match 9.8%;
Best Local Similarity 45.9%;
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MORIKAWA, MINORU APPLICANT: HARADA, NAOKI TIPLE OF INVENTION: GENE ENCITIVE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2565 CCGCCCACCGCCTTCAGGTCGTCTGCGGGGTCCTGGTTGTAGTTCCCGCATAAGCCACAG
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
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ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                         NUMBER OF SEQUENCES:
6880 TGCGCGGCGCACAAGGCCGTGGCAGGGCCGCCAGCGGGCCGTCGGTGGCGGAGATCACG 6821
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                       114 CCACCACGGAGCGAGAAAGCCCAGATAGACGCCCCGGGGCCCCGGGGTCCTGGAGTCCCGC 173
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                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                       CCGCCCACCGCCTTCAGGTCGTCTGCGGGGTCCTGGTTGTAGTTCCCGCATAAGCCACAG
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AGCGAG 6575
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Search completed: October 10, 2002, 19:27:34 Job time: 104.733 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AG084012 Pan trog1
AL099352 Drosophil
AL543262 AL543262
BI149078 602910755
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BE409724 601301584
BB664186 BB664186
BE952238 UI M-CD0-
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AG030581 Pan trog1
BI416695 hasp001xo
AL220271 Tetraodon
                                                                                   AA948370 oq46f04.s
BI416657 hasp001xn
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AL579455 AL579455
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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AL053013 Drosophil	CNS0091P	12	925		•	45	a
£5	AL581447	ø	925			44	
SH.	AQ742453	12	880	•		43	C
Pal	AG060559	12	864		•	42	C
AG132157 Pan trogl	AG132157	12	863		68.2	41	C
SP_	A2185303	12	836			40	
Pai	AG126228	12	670			39	O
Pai	AG043036	12	613		•	38	O
SP_	AZ183795	12	827			37	C
Pai	AG123077	12	643		68.6	36	C
Dro	CNS006B4	12	908		69	35	
BG441241 GA_Ea001	BG441241	10	925	13.8	69.2	34	
AI357868 qv13b02.x	AI357868	9	641			33	
BM477735 AGENCOURT	BM477735	10	1128			32	C
	AQ893474	12	821	13.9	69.4	31	C
	AQ893056	12	1080			30	C
	B1952198	10	831			29	O
	BG809582	10	782			28	O
	BG809598	10	816			27	Q
AL104949 Drosophil	CNS0153F	12	1101		70	26	
	AG128304	12	1023		70	25	C
AL053013 Drosophil	CNS0091P	12	925	•	70	24	
	AG137991	12	1139		70.2	23	C
BG786316 SEAUMC006	BG786316	10	927		•	22	C
	BG786264	10	576		70.6	21	a
SP_1	A2194927	12	741		~	20	C
AG060267 Pan trogl	AG060267	12	810	14.3	71.6	19	C
AL066742 Drosophil	CNS0072Q	12	932	14.5	72.4	18	C

ALIGNMENTS

DEFINITION source Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 483)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project (2001) BM148224

483 bp mRNA linear EST 30-NOV-20
TCAAP1Q9825 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP9825, mRNA Homo sapiens Email: clones@txccc.org EST BM148224.1 GI:17168744 primer: M13 primer /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_orapesps"
/clone="ToAAP9855"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA" /tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="UH10B"
/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored /sex="male" Location/Qualifiers Sequencing Center EST 30-NOV-2001

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DEFINITION
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 402)

Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny, Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
Unpublished (2000)

Contact: Dr. Judith F. Margolin
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402 bp mRNA linear EST 03-OCT-2001
TCAAP1E0685 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0685, mRNA
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Children's Cancer Center and Human Genome Sequencing Center
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Double-stranded cDNA was then digested with BamHl and XhoI and directionally cloned into the BamHl and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., 71 a 208 c 137 g 67 t
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98.8%;
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Pred. No. 2.6e-67;
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                                                           TCATGAGCTCCGCCTCCTTCCTCGGCAGCCAGCCCTGCCCA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at Baylor College of
1102 Bates, MC3-3320
Tel: 832-824-4536
Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double-stranded cDNA was then digested with BamH1 and Xho and directionally cloned into the BamH1 and Sali sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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/dev_stage="pediatric 6 years"
/lab_host="pH10B"
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M1) Baylor-HGSC project=TCAA"
/sex="male"
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/db_xref="taxon:9606"
/clone="TCAAP0685"
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/cell_type="myeloid cell"
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TITLE
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                            BB664186 1XEN full-length enriched, 0 day neonate lung Mus musculus cDNA clone E030029A20 5', mRNA sequence.
BB664186 BB664186.1 GI:16497940
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Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone=lib="NAGE:3636141"
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/clone=lib="NIH_MGC_21"
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/lab_host="BHID8 (phage-resistant)"
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/lab_host="gran: placenta; Vector: pOTB7; Site_1: XhoI;
/lab_host="gran: placenta; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRJ (cDM andde by oligo-dT priming:
Directionally cloned into EcoRIXhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1 RBb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."

1.0 a 235 c 240 g 127 t
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Pred. No. 1.6e-20;
0; Mismatches 20; Indels
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramate; M. and Havasaki, T., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muramatsu, M. and Hayashizaki, Y.
MIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y.
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pBluescript KS(+) after bulk excision from Lambda FLC I."
                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="0 day neonate"
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/clone="E030029A20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type-"lung"
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UI-M-CDO-ayk-d-03-0-UI.Sl NIH BMAP_Ret2 Mus musculus cDNA clone
UI-M-CDO-ayk-d-03-0-UI 3', mRNA sequence.
Email: mEST@mail.nih.gov Oligo-dT track not found, Not I site shown in beginning of sequence Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares
                                                                                                                                     National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 695)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                          Contact: Chin, H
                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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442 CCCCCGTGGCCACCGCCTCCAGCTTGCCACCAAAGACCTGCGACTTTGCTCAGGACTCC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 CCTCCACTTGCCTGATGCTGGCAGTGGAACCCATCGATGGGGACTTCCCTCCACATG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 ACTGTCCTTGGTGGGGCAGTTTCTCACCGTCTTTGTACCCCACCTTCTCCAGTGAAAACC 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCTCCAGCGACAGCC 381
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Texas Children's Cancer Center and Human Genome at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536 Fax: 832-825-4038
                                                                                                                                                        Unpublished (2000)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 131) Wei, F. Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEZ42275

131 bp mRNA linear EST 03-OCT-2001
TCAAP1E1545 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1545, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seq primer: M13 Forward
                                                                                                                                                                                                                     Pediatric Leukemia cDNA Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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TAG_SEQ-None found"

134 c 173 g 143 t
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/db_xref="taxon:10090"
/clone="UI-M-CD0-ayk-d-03-0-UI"
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/dev_stage="1 day"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.28;
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Pred. No. 2.
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                                                                                                                        Sequencing Center
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clones@txccc.org

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                                                                                                                                              JOURNAL
                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seq primer: M.3 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       BC019206 2658 bp mRNA linear HTC 11-DEC-
Mus musculus, Similar to KIAA0963 protein, clone IMAGE:5052084.
                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                         Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Genter Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                            Mus musculus
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                  BC019206.1
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/first strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGACGACTGGACGGCCGCAGGAGGAG(T)VN
3'; V-A,C,G; N-A,C,G,T] and then dG tailed. Second strand
was primed with a BamHI-dC primer
[5'ARAGACTCGAGTCCGCGCGCAATAATAATAATAATC)
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI ard SalI sites of
lambda pSB vector. Library went through one round of
normalization. Library was constructed by Mei Yu at RIKEN
of Japan (Carninci P, Mestover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagacka S, SasakiN, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)*

19 a 47 c 49 g 15 t lothers
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/clone_llb="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 9.3e-10;
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Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
                                                                                 AG084012.1 GI:16635814 (SS; GSC (genome survey sequence). GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-081K02.R.
                                                                                                                                                                                                    Pan troglodytes DNA, clone: AG084012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone has the following problem: incomplete processing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg, Maryland,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                          Pan troglodytes
                                                                                                                                                                                                                                                               AG084012
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
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761 c 696 g 601 t
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                                                                                                                                                                                                                              635 bp DNA linear GSS (
ne: PTB-081K02.R, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109;
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Subhiro-chou, Tsutumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170) Tel:81-45-503-911, Fax:81-45-503-9170) Tel:81-45-603-9110, Fax:81-45-503-9170) Tel:81-45-503-9170) Tel:81-45-503-9170 Fax:81-45-503-9170 Fax:81-45-50
                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                          Genoscope
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hazapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 776)
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male BAC Library"
236 c 189 g 105 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 951)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreffegenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/clone_lib="DrosBAC"
/clone="BACN04P24"
/note="end: SP6"
a 439 c 135 g
   /organism="Homo sapiens"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
/clone="csb01001yc22"
/clone=1ib="fy7_nF1066_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; lst strand cDNA
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/plasmid="pBeloBAC11"
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Pred. No. 0.00038
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BI149078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184;
                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                           http://image.llnl.gov
Plate: LLAM11141 row: m column: 13
                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI149078 612 bp mRNA linear EST 05-JUL-2001
High quality sequence start: 14 High quality sequence stop: 581.
                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://fulllength.invitrogen.com
492 c 154 g 118 t 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 AACAGTTCGTTGGGTTCCACCCCATTCCTTGGTGGCCAGTCTTGCCCTGAAACCAGCTAC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTTGCCTTCTCCAGCGACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 AGCTCCCACCCCTGGAGGTGGCATCCAG------CTACAGAACCGACTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 AACCCCCGCCGGCGGCAGCCTCCTGTACAGCCCGCCGCCCTGCAGAGCGCCATGCTGC 321
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                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 274)
                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                          TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                High quality sequence stop:
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/clone="IMAGS:5052084"
/clone="IMAGS:5052084"
/clone="IMAGS:5052084"
/clone="IMAGS:5052084"
/clone="IMAGS:5052084"
/lab_bost="0H10B (T1 phage=resistant)"
/lab_bost="0H10B (T1 phage=resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 199 c 165 g 126 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                       Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus sylvestris/Heterobasidion annosum pinus sylvestris/Heterobasidion annosum Eukaryota; mixed EST libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B141657 834 bp mRNA linear EST 15-AUG-2001 hasp001xm12f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp001xm12f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Swedish University of Agriculture,
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                                                                                               /Clone="lh="Heterobasidion annosum - Scots pine infection /clone=lib="Heterobasidion annosum - Scots pine infection /clone_lib="Heterobasidion annosum - Scots pine infection /clone="seedling roots of scots pine were infected for 6 days with H. annosum" lecors : EcoR; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of pine roots infected for 6-days with mycelia of
                                                                                   Heterobasidon annu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "a 45 c 100 g 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
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15.0%;
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Score 74.8; DB 10;
Pred. No. 0.0021;
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Pred. No. 0.0018;
                                                                                          annosum (FP5).
50 g 27 t
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Pan troglodytes DNA, clone: PTB-003A05.F, genomic survey sequence.
AG030581
AG030581.1 GI:16557454
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-003A05.F.
                                                                                                                                                                                                                                                                                                                                                                                                     (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
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Tel:81-45-503-9170
Tel:81-45-503-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Subhiro-chou, Tsurumi-ku, Yokobama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                      tracking errors.
/organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGCTCCGCCTCCTCCGCCAGCCAGCCCTGCCCAGACACCAGCTATGCCCCCGTG 449
                                Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbuenykopat.slu.se
Seq primer: T7 primer.
                                                                                                                                                   Contact: Fred O. Aslegbu
Dept. of Forest Mycology & Pathology
                                                                                                                                                                                                      Eukaryota; mixed EST libraries.

1 (bases 1 to 798)

Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.

Expressed sequence tags of randomly selected CDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
                                                                                                                                                                                                                                                                                                                          Pinus sylvestris/Heterobasidion annosum Pinus sylvestris/Heterobasidion annosum
                                                                                                                                                                                                                                                                                                                                                                                                                   B1416695 798 bp mRNA linear EST 15-AUG-2001 hasp001xo20f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp001xo20f, mRNA sequence.
                                                                                                                 Sweden
                                                                                                                              Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                       Unpublished (2001)
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/sex="male"
            Location/Qualifiers
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Search completed: October 10, Job time: 701.733 secs

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/clone_lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
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EST clone BH41. H
Human secreted pro
Human musculoskele
Human colon cancer
Nucleotide sequenc
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                                                     Stockert E, Scanlan MJ, Jager D,
                                                                                     (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                              Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; meianoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; ds.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Scoring table: Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 1.0

1736436 segs, 858457221 residues

Searched:

Run on:

OM nucleic - nucleic search, using sw model

Result

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SUMMARIES

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4877 4924 343 114 1553 1000 799 1218 1925

AAD11120 AAC75998 AAV87103 AAC15646 AAL37392

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08-FEB-2001 (first entry)
                                                                    AAC75998;
                                                                                                                                 AAC75998 standard; cDNA; 4924 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide, used to treat or prognose a disorder obaracterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
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Human ORFX ORF1553 polynucleotide sequence SEQ ID NO:3105

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A AAC74446 to AAC75606 encode the proteins given in AAB40237 to AAB43397.

CC which represent the human ORRX open reading frames 1 to 3161. The ORRX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary: CC antiparchic; antiparkinsonian; nontropic; neuroprotective; costeopathic; anticorvulsant; antiarthritic; immunosuppressant; costeopathic; anticorvulsant; antiarthritic; immunosuppressant; cantiduction; vanibacterial; antiviral; antifungal; antirhordic; antiproid; and antianemic. The sequences can be used for determining the prosence of or predisposition to, or preventing or treating conditions associated with an OREX-associated disorder. The presence of or predisposition to, or preventing or treat concers, pathological conditions associated with an OREX-associated disorder. The concisis acids can be used to express OREX proceins in gene therapy concisis acids can be used to express OREX proceins in gene therapy are proteins and nucleic acids may be used to treat concers, proliferative disorders, neurodegenerative disorders, osteoarthritis, concisis and the proteins and nucleic acids may be used to treat concers, proliferative disorders, neurodegenerative disorders, osteoarthritis, concisis and proteins and nucleic acids may be used to treat concers, proliferative disorders, osteoarthritis, concerns and proteins and nucleic acids may be used to treat concerns, concisis and proteins and associated disorders, asthma, concerns and properly and associated antipage, antimal, antinflammatory disease; to enhance constitute, and as a contraceptive.
                                Matches
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriaric; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999; 99US-0127607.

02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728.

30-MAR-2000; 2000US-0540763.
                                                                                                                                                 Sequence 4924 BP; 892 A; 1694 C; 1572 G; 765 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 2323-2326; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621.
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Locar
500;
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DB; AAB41789.
                                                    Similarity
                                Conservative
                                                100.0%;
                        0;
                                                    Score 500;
Pred. No.
                            Mismatches
                                                        4e-89;
                                                                                    DB 21;
                        0;
                        Indels
                                                                                    Length 4924;
                        0;
                    Gaps
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    밁
This sequence represents an expressed sequence tag () polynucleotide of the invention. The polynucleotides
                                                         New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                             Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV87103 standard; cDNA; 343 BP
                                    Claim 1; Page 453-454; 633pp; English
                                                                                                                                                                                                                                          15-OCT-1998.
                                                                                                                                                                                                                                                                  W09845435-A2
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAV87103;
                                                                                                           WPI; 1999-070076/06.
                                                                                                                                              Agostino MJ,
                                                                                                                                                                                            10-APR-1997;
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                                                                                                                                   Racie
                                                                                                                                                                     (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGCCCAGACACCAGCTATGCCCCCGTGGCCACCACCACCTCCAGCTTGCCACCAAGAACCT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCTTCTCCAGCGACAGCCGCCCGTTCATSAGCTCCGCCTTCCTTCCTCGGCAGCCAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGCAGAGCGCCATGCTGCACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGGGATTACCCGCAGCATGAACCCCCGCCGGCGGCAGCCTCCTGTACAGCCCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGACTTTGCTCAGGACTCC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTGCAGAGCGCCATGCTGCACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCCGGCCGAGGACCCCACCCCGCCTGCCGGCCGATGCTTGCAGTGGGGCCCGCCATGG
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    Jacobs Κ,
Spaulding V,

                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                            97US-0835913.
                                                                                                                                                                                                                   98WO-US06954.
                                                                                                                                  Treacy M;
                                                                                                                                             Lavallie ER, McCoy JM,
                                                                                                                                              Merberg
  (EST), and (EST)
             and is
  invention are
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RESULT 4
AAC15646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemostaticychemokinetic activity, haemostatic activin/inhibin activity, chemokractic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 343 BP; 58 A; 143 C; 69 G; 73 T; 0 other;
                                                                                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 19721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC15646 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                              26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCCACCGCCTCCAGCTTGCCACCAAAGACCTGCGACTTTGCTCAGGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATGAGCTCCGCCTCCTTCCTCGGCAGCCAGCCCTGCCCAGACACCAGCTATGCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                            99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.6%;
                                                                                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 173; DB 20;
Pred. No. 2.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; cDNA isolation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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The present sequence is one of a large number of 5' ESTs derived from mRNAS encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA

Claim 1; SEQ ID 19721; 71pp + CD-ROM; English.

diagnostic, forensic, gene therapy and chromosome mapping procedures New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo

2000-500381/45.

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RESULT 5
AAL37392/c
ID AAL37392 standard; DNA; 1553 BP.
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Best Local
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    11-JUL-2000
11-JUL-2000
14-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
                                                                                                                                                                                                              28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                       31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibetrail; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200155367-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL37392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human musculoskeletal system related polynucleotide SEQ ID NO 3757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 114 BP; 24 A; 42 C; 38 G; 7 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Sir
hes 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 AGGCTCGGAGAAACAGGCGCCGCGGGGCTCCGCGCCCGGGCCGGACCCGGGGCCCGAGATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 22.2%;
Similarity 97.3%;
09; Conservative
    2000US-0179065
2000US-0184664
2000US-0184663
2000US-019874
2000US-0199076
2000US-0199123
2000US-0299467
2000US-0299467
2000US-021513
2000US-0216647
2000US-0216647
2000US-0217496
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US01338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 110.8; DB 2
Pred. No. 3.5e-13;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 114;
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        11-SEP 2000
21-SEP 2000
25-SEP 2000
25-SEP 2000
26-SEP 2000
27-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
20-CCT 2000
02-CCT 2000
03-CCT 2000
03-CCT 2000
04-CCT 2000
05-CCT 2000
06-NOV 2000
07-CCT 2000
08-NOV 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SE
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14 - NUG - 2000

14 - AUG - 2000

18 - AUG - 2000

22 - AUG - 2000

23 - AUG - 2000

23 - AUG - 2000

23 - AUG - 2000
2000US-0241826.

2000US-0246474.

2000US-0246475.

2000US-0246476.

2000US-0246476.

2000US-0246477.

2000US-0246477.

2000US-0246477.

2000US-0246523.

2000US-0246523.

2000US-0246524.

2000US-0246526.
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2000US-0225270.
2000US-0225447.
2000US-0225757.
2000US-0225758.
2000US-0225758.
2000US-0225759.
2000US-0225279.
2000US-0225279.
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2000US-0237039.
2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0229343
2000US-0229344
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2000US-022950
2000US-022950
2000US-0230438
2000US-0231242
2000US-0231242
2000US-0231244
2000US-0231414
2000US-0231411
2000US-0231411
2000US-0231414
2000US-0231414
2000US-0231414
2000US-0232080
2000US-0232401
2000US-0233063
2000US-0233063
2000US-0233063
2000US-02334274
2000US-02334274
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2000US-0236369.
2000US-0236370.
2000US-0236802.
2000US-0237037.
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2000US-0227182.
2000US-0227009.
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (AAB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, other cancers e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Croh's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Croh's disease, (c) cardiovascular disorders such as myocardial isohaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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08-DEC-
08-DEC-
                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 3757; 781pp + Sequence Listing; English.
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-2000;
                       parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-451937/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOV-2000;
            at
                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
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2000US-0249245.
2000US-0249264.
2000US-0249265.
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2000US-0249212.
2000US-0249213.
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2000US-0249209.
2000US-0249210.
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2000US-0246610.
2000US-0246611.
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2000US-0249216.
2000US-0249217.
2000US-0249218.
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2000US-0249300
          ftp.wipo.int/pub/published_pct_sequences
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AAA02484/c
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Best Local
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                                                                                                                                                                                                                                                          Williams LT, Escor.
Reinhard C, Glese K, Ri
Lamson G, Drmanac R, C
Lamson G, D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA02484 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; osetrogen receptor-positive breast cancer; therap oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                 Claim 1; Page 994; 1097pp; English.
                                                                                                                                                                                                           Polynucleotide library used to determine
                                                                                                                                                                                                                                        WPI; 2000-126369/11.
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                                                                                                                                                                                                                                                                                                                                             HYSEQ
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                                                                                                                                                                                                                                                                                                                                             INC.
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98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
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                                                                                                                                                                                                                                                                                 J, Innis MA, Randazzo F, Ke Crkvenjakov R,
                                                                                                                                                                                                                                                                       Garcia V,
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Pred. No. 5.1
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                                                                                                                                                                                                                                                                     Kennedy GC, Pot D, Ka
R, Dickson M, Drmanac
Jones LW, Stache-Crain
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                                                                                                                                                                                                              cancerous states
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RESULT 7
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Best Local :
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                                                                                                                            Fusion protein, stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; infilammation; nitro drug; IkappaB regulator protein; infilammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease;
                                                                                  Epstein-barr virus.
                                                                                                                   cancer; pathological condition;
                                                                                                                                                                                                                   Nucleotide sequence of the stabilising sequence-encoding insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, cestrogen receptor-positive breast cancer, cestrogen receptor-
                                                                                                                                                                                                                                                               18-NOV-1998
                                                                                                                                                                                                                                                                                                                                AAV55831 standard; DNA; 799 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                     480 NCNCCCNNCGNC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                       489 GCTCAGGACTCC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                             (first entry)
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Pred. No.
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PF 17-NOV-1997; 97WO-IB01508.

EXX 25-JUN-1997; 97US-0048945.

PR 25-JUN-1997; 97US-0048945.

PR 15-NOV-1996; 96US-0030986.

EXX (MASU/) MASUCCI M G.

EXX (MASU/) MASUCCI M G.

EXX (MASU/) MASUCCI M G.

EXX Masucci MG;

EXX WPI; 1998-312463/27.

EXX Wew fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats

EXX Disclosure; Fig 4B; 120pp; English.

Exx Disclosure; Fig 4B; 1
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δÃ 밁 VQ 밁 Š Дb Ş B QΥ Qy DЬ Matches Query Match 430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465 131 GCCCAGATAGACGCCCCGGCCGCCCGGGTCCTGGAGTCCCGCCGCCTGCTGCCCGGCCG 190 Local CGCCATGCTGC - ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT CCCGCAGCATGAACCCCCGGCGGCGGGCAGCCTCCTGTACAGCCCGCCGCCCCCTGCAGAG AGGACCCCACCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250 170; Similarity Conservative 12.0%; 0; Score 60; Pred. No. Pred. Mismatches 0.0029 DB 19; Length 799; 165; Indels 1; Gaps 97 1;

RESULT 8
AAAO2488/c
ID AAAO2488 standard; cDNA; 1218 BP.
XX
AC AAAO2488;

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96 CCTCCTGCTCCTGCCCCTCCTGCTCCTGCCCCCT 61

19-MAY-2000

(first entry)

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CA AAA00010 to AAA02716 represent polynucleotides isolated from cDNA CC libraries constructed from human colon cancer cell lines. The present CC invention also describes a method of detecting differentially expressed CC genes correlated with a cancerous state of a mammalian cell, comprising CC detecting at least one differentially expressed gene product in a test CC sample derived from a cell suspected of being cancerous, where detection CC concerous state of the cell from which the test sample was derived. CC cancerous state of the cell from which the test sample was derived. CC differentially expressed genes correlated with a cancerous state of a CC cancerous of the cell from which the test sample was derived. CC detecting and mapping related genes correlated with a cancerous state of a CC cancerous of diseases and disorders (e.g. identification of corresponsiveness of cancer to therapy). This is particularly for breast CC cancer, coestrogen receptor-positive breast cancer, coestrogen receptor-positive breast cancer.
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Matches 123
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Reinhard C, Glese K, Re
Lamson G, Drmanac R, C
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 995-996; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide library used to determine cells -
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                                                                                                                                                                                                                                     Sequence 1218
 852
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CGCGGGCTCCGCCCGGCCGGACCCCGGGCCCGAGATCATGATGCTGCCGCCACCGCCGC 114
                                                        CACCACGGAGCGAGAAGCCCAGATAGACGCCCCGGGCGCCCCGGGTCCTGGAGTCCCGCC 174
                             GCCTGCTGCCCGGCCGAGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCG 234
                                                                                                                                                                            al Similarity
123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIRON CORP. HYSEQ INC.
                                                                                                                                                                         12.0%;
nilarity 27.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer cell line polynucleotide sequence SEQ ID NO:2479
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98US-0085537.
98US-0085696.
                                                                                                                                                                                                                                     BP; 9 A; 31 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105234
98US-0105877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Randazzo F, K
Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Innis MA,
                                                                                                                                                                            0;
                                                                                                                                                                              Score 60; DB 21; Length 1218; Pred. No. 0.0029; O; Mismatches 323; Indels
                                                                                                                                                                                                                                        494 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R, Dickson M, Drmanac S,
Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Garcia PD, Sudduth-Klinger J;
Kennedy GC, Pot D, Kassam A;
R, Dickson M, Drmanac S, Labat
                                                                                                                                                                                                                                        37 T; 647 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancerous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orip; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene thera multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell immortalisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1998;
06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732
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                                                                                                                                                                                                                                                                                                                                                 Damaj BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 NCCCCNNNANCNNCGNNGNNCCCCCC 527
The present sequence is a DNA encoding Epstein Barr Virus Nuclear Antigen 1 (EBNA 1), which is obtained from commercially available
                                                                                               Claim 24; Fig 2; 86pp; English.
                                                                                                                                                      New method for expressing genes useful for gene therapy
                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                            (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAGCCCTGCCCAGACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCTTGCCACCAA 474
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                                                                                                                                                                                                                                                        AAY28843.
                                                                                                                                                                                                                                                                                                                                                    Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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98US-0130114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US03307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a // Product= "EBNA 1" (product= "EBNA 1" (pros:799..800, aa:Gly) // trans1_except= (pos:799..800, aa:Gly) // The sequence is described throughout the specification as being 1926 nucleotides long, but sequence of only 1925 bp has been given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1925
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                                                                                                                                                                                                    from recombinant eukaryotic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
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Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid pCMVEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orip) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for one amplification. Cell immortalization.
            P-PSDB; AAY95856
                           WPI; 2000-515062/46.
                                                                                                                                                                                                WO200047778-A1
                                                                                                                                                                                                                          Epstein-barr virus
                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                    EBV; nuclear antigen 1; EBNA1; episome; transfection; selection;
                                                                                                                                                                                                                                                                                               Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA
                                                                                                                                                                                                                                                                                                                            07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   AAA50254 standard; DNA; 1926 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1925 BP;
                                                       Horlick RA, Chelsky D;
                                                                                 (PHAR-) PHARMACOPEIA INC
                                                                                                              11-FEB-1999;
                                                                                                                                         11-FEB-2000; 2000WO-US03547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 CCCGCAGCATGAACCCCCGCCGGCGGGCAGCCTCCTGTACAGCCCGCCGCCCCTGCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCATGCTGC - ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amplification, cell immortalisation, etc.
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                                                                                                              99US-0249585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 A; 352 C; 872 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 1925;
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Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;

Score 60;

DB 21; Length 1926;

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protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as a tag for the cells. The method is applicable to cell culture or intact organisms, for gene therapy. It allows the rapid establishment of eukaryotic cells that stably and reliably express a gene of interest, using a novel method of selection, and maintenance of that selection without the need for exogenous
                                                                                                                                                                                                                                                                            and the selective pressure specified by the marker is maintained. Under these conditions, only cells containing both episomes live. Preferably, EBNA1 is expressed from 1 of the episomes, and the protein of interest from the other episome. Either or both epitopes may further comprise a nucleic acid sequence encoding a protein desired to be expressed in the cell (e.g. a therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising an BBV orip and a gene encoding a second protein, where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce doubly transfected cells which also express an antigen that promotes retention of the episomes by the cells. The doubly transfected cells are maintained under conditions in which the first and second proteins and the selectable marker are expressed, first and second proteins and the selectable marker are expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of DNA encoding the Epstein-Barr virus (EBV) nuclear antigen protein 1 (EBNA1, see AAY95856). EBNA1 is utilised in a novel method for obtaining a eukaryotic cell that is stably transfected with at least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising an EBV origin of replication (oriP, see AAA50253), a gene encoding a first protein whose expression results in cell death and a selectable marker for antermore action.
                                                    selection factors, such as antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for eukaryotic cells; and (2) a second episome
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Matches
338
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                                                                                                                                  311 CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT
                                                                                                                                                                                                                131 GCCCAGATAGACGCCCCGGCCGCCCGGGTCCTGGAGTCCCGCCGCCTGCTGCCCGGCCG 190
                                                                                                                                                                                     Local Similarity
                                                                                                      CCTCCTGCTCCTGCCCCTCCTGCTCCTGCCCCT
                                                    AGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                     12.0%;
                                                                                                                                                                                                                                                                                                                          0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                        0.003;
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AAF82902/c ID AAF82902 standard; DNA; 1926 BP
 29-JUN-2001
                                AAF82902;
(first entry)
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430 ACACCAGCTATGCCCCCGTGGCCACCGCCTCCAGCT 465

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Best Local S
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a composition comprising nucleic acid, histone HI protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host call. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Epstein-barr virus (EEV) tethering protein ENNAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robertson ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBV; latency-associated nuclear antigen; LANA; EBNA1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBV tethering protein EBNA1 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 9C; 60pp; English.
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                                                                                                                                                                                                                                                                          191 AGGACCCCACCCCGCCTGCCGCCCGATGCTTGCAGTGGGGCCCGCCATGGACAGGGATTA 250
                                                                                                                                                                                                                                                                                                          131 GCCCAGATAGACGCCCCGGCGCCCCGGGTCCTGGAGTCCCGGCCGCCTGCTGCCCGGCCG 190
251 CCCGCAGCATGAACCCCCCGCCGGCGGGCAGCCTCCTGTACAGCCCCGCCGCCCCTGCAGAG 310
                                  CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCTGCCGCCATACCCTGCCTTCT 369
                                                                                                                                      2001-281736/29.
                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                             12.0%; Score 60; DB 22
50.6%; Pred. No. 0.003;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 1926;
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                                                                                                                                                                                                                                                                                                                                             1; Gaps
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the Epstein Barr nuclear antigen. It is used to produce bait vectors of the invention. The specification describes a compositions and methods for a genetic system of detecting protein-protein interactions in a mammalian host cell. The system comprises bait and test, both containing selection genes, and viral origin of replications which require bound viral replication proteins to effect replication. The compositions is useful for detecting an interaction between a bait protein and a test protein. It is useful in a mammalian two-hybrid system for detecting protein-protein interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for detecting protein-protein interactions in a mammalian two hybrid system comprises bait and test vector which consist of selection gene, vector viral origin of replication and fusion gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Origin of replication; protein-protein interaction; replication; two-hybrid system; nuclear antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA75454;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2580 BP; 632 A; 512 C; 1054 G; 382 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a mammalian host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 17-20; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-593546/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6114111-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the Epstein Barr nuclear antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 CCTCCTGCTCCTGCCCCTCCTCCTCCTCCCTCCT 303
311 CGCCATGCTGC-ACTGCCCCTACTGGAACACCTTCTCGCCTGCCGGCCATACCCTTCT 369
                                                                                                                                    191 AGGACCCCACCCCGCCTGCCGCCGATGCTTGCAGTGGGCCCCGCCATGGACAGGGATTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 GCCCAGATAGACGCCCCGGCGGCCCCGGGTCCTGGAGTCCCGCCGCCGCCTGCCCGGCCG 190
                                                                                                                                                                                                        251 CCCGCAGCATGAACCCCCGCCGGCGGCAGCCTCCTGTACAGCCCGCCGCCCCTGCAGAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Payan D, Huang B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9805-0050863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 165; Indels
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                                                       The present sequence is an anti-sense strand of commercially available plasmid pcMyEBNA from which Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) encoding DNA is obtained. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orip) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, can be used to transfect cell immortalisation, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-1998;
06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-sense strand; plasmid pcMVEBNA; BBNA ]; episome; transfection; Epstein Barr Virus Nuclear Antigen 1; origin of replication; EBV orip; eucaryotic host cell; recombinant cell line; ion channel; multiple gene expression; receptor; transporter protein; gene theral transcription factor; adhasion molecule; antisense therapy; gene amplification; cell immortalisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-610610/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New method for expressing genes from recombinant eukaryotic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-sense strand of pCMVEBNA plasmid.
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/product= "EBNA 1 protein"
/note= "Epstein Barr Virus Nuclear Antigen 1"
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Sequence 5452 BP; 1108 A; 1736 C; 1246 G; 1362 T; 0 other;

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This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the invention.
                                                                                                                                                    Production of antisense libraries, used for identifying antisense agents and for identifying target sites for antisense-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1964
                                                                                                                Claim 16; Page 43-50; 63pp; English.
                                                                                                                                                                                              WPI; 1999-610866/52.
                                                                                                                                                                                                                     Ruffner DE, Pierce ML,
                                                                                                                                                                                                                                              (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                         28-MAR-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                              28-MAR-1999;
                                                                                                                                                                                                                                                                                                                                         07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; DNA library; identification; multiple cloning site; MCS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector pShuttle DNA
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                                                                                                                                          of a selected gene
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Pred. No. 0.003
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  WO9806437-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; vaccine; polycationic agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide delivery; plasmid pCMVKmITR-EPI; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector plasmid pCMVKmITR-EPI.
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                                                                                                                                                            promoter
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                                                                                             terminator
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4928..5104
                                                                                           6818..7050
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/note= "AAV inverted terminal repeat"
                                                                                                             /*tag= e
/note= "CMV immediate-early enhancer/promoter"
                                                                                                                                                                                'rpt_type= INVERTED
'note= "AAV inverted
                                                                                                                                                                                                                                                                                                                                                                                                                                          'product= "EBV nuclear antigen A"
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                                            "bovine growth hormone polyA sequence"
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Pred. No. 0.003;
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Search completed: October 10, 2002, 15:17:31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pCMYKMITR-EPI, which contains an Epstein-Barr virus (EBV) origin of replication from plasmid pCEP4, a coding region for EBV nuclear antigen A from pCEP4, a pair of inverted terminal repeats from adeno-associated virus, a cytomegalovirus enhancer/promoter, a bovine growth hormone polyA sequence, and a kanamycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense and protect it against serum degradation, particularly for use i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9600 BP; 2326 A; 2376 C; 2817 G; 2081 T; 0 other;
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Page 12

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2 US-08-343-443B-106

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2 US-08-313-443B-106

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2 US-08-313-32A-8

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RESULT 1 US-08 -287-442-3 Sequence 3, Application US/08287442 Patent No. 5670350 GENERAL INFORMATION: APPLICANT: Lam, Stephen T. APPLICANT: Ligon, James M. APPLICANT: Ligon, James M. APPLICANT: Hill, Dwight S. APPLICANT: Hill, Dwight S. APPLICANT: Hill, Dwight S. APPLICANT: Howell, Charles R. APPLICANT: Becker, J. Ole TITLE OF INVENTION: Gene Activa ORRESSOED: CIBA-GERIGY COrpora STREET: 7 SKyline Drive CITTY: Hawthorne STATE: New York COUNTRY: USA ZIP: 10532 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER PATENTION ONTA: APPLICATION NUMBER: US-005/MS-D SOFTWARE: PATENTIA Release #1 CORENT APPLICATION ONTA: APPLICATION NUMBER: US-008/287 FILLING DATE: 01-191 APPLICATION UNMBER: US-008/08/7 FILLING DATE: 01-191 APPLICATION UNMBER: US-07/908 FILLING DATE: 02-701-192 APPLICATION UNMBER: US-07/908 FILLING DATE: 03-701-193 APPLICATION UNMBER: US-07/908 FILLING DATE: 08-AUG-199 ATTORNEY/AGENT INFORMATION: NAME: Elmer, James Scott NAME: Elmer, Jame	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
ication US/08287442 150 1510 1510 1510 1510 1510 1510 1510	B 3705 5 PCT-US96-03940-7 B 5648 5 PCT-US96-03940-7 B 38 4 US-09-07-097-1 7 838 5 PCT-US94-10457-1 7 946 2 US-08-816-6059-1 7 1415 1 US-08-236-918A-7 7 1425 4 US-08-236-918A-7 7 1623 4 US-08-9-5158-1 7 6232 4 US-08-456-2008-51 7 7175 1 US-08-456-2008-51 7 7175 2 US-08-456-2008-11 7 7175 2 US-08-123-0750-88 7 7175 2 US-08-13-0790-8 7 7175 3 US-08-149-3970-8 7 7175 3 US-08-450-306-8 7 7175 3 US-08-450-306-8 7 7175 3 US-08-149-3970-8 7 7175 3 US-08-450-262-8	
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Rest Local Similarity 50...
78; Conservative
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APPLICANT:
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                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clas-GEIGY Corporation
STREET: 7 Skyline Drive
COMPUTER READABLE FORM:
                                                                                                                                               APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
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OTHER INFORMATION: /note= "ORF 3, transcribed right to OTHER INFORMATION: left"
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OTHER INFORMATION: /not OTHER INFORMATION: rigl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1906..3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction INDIVIDUAL ISOLATE: fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            INFORMATION:
                  10532
                                              Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pCIB137
                                                                                                                                                                                                     Gaffney, Thomas D.
Lam, Stephen T.
Ligon, James M.
Hill, Dwight S.
Stein, Jeffrey I.
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CGA267356
                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3633
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left"
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right"
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right"
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TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5559 base pairs
TYPE: nucleic acid
                                                                                                                                                       Query Match
                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linea
MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/287,442
PILING DATE: 08-AUG-1994
FILING DATE: 08-AUG-1994
FILING DATE: US 08/087,636
                                        1198 GGTTCCTGCGCTATGTCGCGGGGGAAATCACCCGCAACCTGCTGATCCTGATCCAGCCCG 1257
                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 4616..4691
OTHER INFORMATION: /not
OTHER INFORMATION: left
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 08-AUG-1990
AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 01 FILING DATE: 01-JUL-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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169 TGCTGAGGATGGCCTGGTCTGCCACCCTCGTGGTAGCATTTTGCATGTGTAACAGGGT 228
                                                                        109 GATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCCTGCTGCAGGCTG 168
                                                                                                                                                                                                      NAME, KEY: misc_feature LOCATION: 4731.5318
OTHER INFORMATION: /note= "ORF 3, transcribed right to OTHER INFORMATION: left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 210..1688
OTHER INFORMATION: /note-OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 1906..3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/908,284
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCIB137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M: Pseudomonas fluorescens
CGA267356
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 07/570,184
08-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                50.3%;
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left"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                   0;
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                                                                                                                                   Score 31.8; DB 1; Length 5559; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ORF 1, transcribed left to
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                                                                                                                   Mismatches
                                                                                                              77;
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US-08-460-298-3
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APPLICANT: Gatiney
APPLICANT: Lam, St
APPLICANT: Ligon,
APPLICANT: Hill, D
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                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic single
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/8/460,298
APPLICATION NUMBER: US 08/08/460,298
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/287,442
APPLICATION NUMBER: US 08/287,442
APPLICATION NUMBER: US 08/087,636
EILING DATE: 01-701-1994
APPLICATION NUMBER: US 07/908,284
EILING DATE: 02-701-1992
PRIOR APPLICATION NUMBER: US 07/908,284
EILING DATE: 02-701-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/570,184
EILING DATE: 08-ANG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elmer James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
                   INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: PCIB137
                                                                                                                                                                                        STRANDEDIALE.
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1318 CCGCCGCCGCGTGCGCATCGAGCGGGAAAAGAAGC 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stein, Jeffrey I.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 CTCCCCTCTGGGGCACAACAACAAGAGAAGTTGC 263
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CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                      ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                         SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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Lam, Stephen T.
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                                                                                                                                                                                                               DNA (genomic)
                                                              fragment
                                                                                    5.6 kb EcoRI-HindIII restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                 CGC 1506/CIP4
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; OTHER INFORMATION: /note= "ORF 3, transcribed right to ; OTHER INFORMATION: left"
US-08-460-298-3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Stein, Jeffrey I.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,442
FILING DATE: 08-AUG-1994
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1318 CCGCCGCCGGGTGCGCATCGAGCGGGAAAAGAAGC 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1258 AGCTGCGCCTTGAACTGCGCACCACGCTGTTCCAGGTGCAACAGTCCGGTGTTGCGGTGA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1198 GGTTCCTGCGCTATGTCGCGGGGGGAAATCACCCGCAACCTGCTGACCCTGATCCAGCCCG 1257
                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCCTTATCCTGCTGCAGGCTG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 CTCCCCTCTGGGGCACAACAACAAGAGAAGTTGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 210..1688
OTHER INFORMATION: /not OTHER INFORMATION: rigi
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GETGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 4731..5318
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                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 10532
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                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%;
11 Similarity 50.3%;
78; Conservation
                                                                                                                                                                                                                                                                                                                          USA
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Lam, Stephen T.
                                                                                                                          UMBER: US/08/459,174
02-JUN-1995
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left"
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right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.8; D
Pred. No. 1.3;
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RESULT 5
PCT-US93-0630DA-3
; Sequence 3, Application PC/TUS9306300A
; GENERAL INFORMATION:
; APPLICANT: CIBA-GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 4731..5318
; OTHER INFORMATION: /note= "ORF 3, transcribed right to
OTHER INFORMATION: left"
US-08-459-174-3
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           1318 CCGCCGCGGGTGCGCATCGAGCGGGAAAAGAAGC 1352
                                                                                                                                                                                                                                      1258 AGCTGCGCCTTGAACTGCGCACCACGCTGTTCCAGGTGCAACAGTCCGGTGTTGCGGTGA 1317
                                                                                                                                                                                                                                                                                                              1198 GGTTCCTGCGCTATGTCGCGGGGGAAATCACCCGCAACCTGCTGACCCTGATCCAGCCCG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/REY: misc_feature
LOCATION: 210..1688
OTHER INFORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: /note= "ORF 2, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356
INDIVIDUAL ISCUATE: 5.6 kb ECORI-H
INDIVIDUAL ISCUATE: fragment
IMMEDIATE SOURCE:
CLONE: PCIB137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: 4616_.4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 02-JUL-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
US 07/908,284
                                                                                                                                                                                                                                                                        169 TGCTGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAACAGGGT 228
                                                                                                                                                                                                                                                                                                                                                109 GATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCCTGCTGCAGGCTG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                             229 CTCCCCTCTGGGGCACAACAACAAGAGAAGTTGC 263
                                                                                                                                                                                                                                                                                                                                                                         Local 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5559 base pairs
TYPE: nucleic acid
STRANGEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                      50.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                                                                                                                                       Score 31.8; DB 1; Length 5559; Pred. No. 1.3; 0; Mismatches 77; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGC 1506/CIP4
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CLASSIFICATION
CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION UMBER: US 07/908,284
APPLICATION NUMBER: US 07/908,284
ETLING DATE: 02-UT-1992
ATTORNEY/AGENT INFORMATION:
NAME: SPEUILL, W. MUTICAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18210/A/
TELECOMMUNICATION INFORMATION:
TELEPAN: (919)541-8615
TELEPAN: (919)541-8615
TELEPAN: (919)541-8619
INFORMATION FOR SEQ ID NO: 3:
SEQUIENCE CHARACTERISTICS:
LENGTH: 5559 base pairs
myde: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                             IMMEDIATE SOURCE
                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                          STRAIN: CGA267356
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER FILING DATE: 02-J
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                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hawthorne
                      pCIB137
                                                                                                 M: Pseudomonas fluorescens
CGA267356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligon, James M.
120 Marquette Dr
Cary, NC 27513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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125 Tradescant Road
Chapel Hill, NC 27514
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4002 Basle
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Raleigh, NC 27613
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                                                                                                                                                                                                                  linear
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725 Surry Trail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ecker, J. Ole
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xyan, TX 77802
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                                                          fragment
                                                                                 5.6 kb EcoRI-HindIII restriction
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US-08-761-258-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198 GGTTCCTGCGCTATGTCGCGGGGGAAATCACCCGCAACCTGCTGACCCTGATCCAGCCCG 1257
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: Ciba-Geig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1318 CCGCCGCCGGTGCGCATCGAGCGGAAAAGAAGC 1352
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NAME/KEY: misc_feature
LOCATION: 210..1688
OTHER INFORMATION: /note- "ORF 1, transcribed left to
OTHER INFORMATION: right"
             ATTORNEY/AGENT INFORMATION:
NAME: Me149, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Genetically Fourth Activity
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 TGCTGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTTGCATGTGTAACAGGGT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 CTCCCCTCTGGGGCACAACAACAAGAGAAGTTGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCCTGCTGCAGGCTG 168
                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note-
OTHER INFORMATION: left"
                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               ZIP: 10591
                                                                                                                                                                                                                                                                                            STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "ORF 3, transcribed right to OTHER INFORMATION: left"
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LOCATION: 4731..5318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 1906..3633
                                                                                        CLASSIFICATION: 424
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TELEPHONE:
                                                                                                          FILING DATE:
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 4616..4691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Application US/08761258 5756087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligon, James M.
Hill, Dwight S.
Lam, Stephen T.
Gaffney, Thomas D.
                                                                                                                                                                                                                                                                                                                             E: Ciba-Geigy Corporation
520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                  Torkewitz, Nancy
VENTION: Genetically Modified Pseudomonas Strains
(919) 541-8587
                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 31.8; D: 50.3%; Pred. No. 1.3; tive 0; Mismatches
                                                                                                                                                                Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "ORF 2, transcribed left to
                                                                                                                              us/08/761,258
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: MISC_feature LOCATION: 210..1688
OTHER INFORMATION: /prod OTHER INFORMATION: /note OTHER INFORMATION: respe
                                                                                                                                                                                                                                                        FEATURE:

NAME/FOR: miso_feature
LOCAFION: complement (
OTHER INFORMATION: /fu
OTHER INFORMATION: /gr
OTHER INFORMATION: /pr
OTHER INFORMATION: /no
OTHER INFORMATION: uvr
OTHER INFORMATION: res;
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NAME/KEY:
LOCATION:
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1258 AGCTGCGCCTTGAACTGCGCACCACGCTGTTCCAGGTGCAACAGTCCGGTGTTGCGGTGA 1317
                                                                              1198 GGTTCCTGCGCTATGTCGCGGGGGAAATCACCCGCAACCTGCTGACCCTGATCCAGCCCG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
    NAME/KEY: misc_feature
    LOCATION: complement (5574..7397)
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                   169 TGCTGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAACAGGGT 228
                                                                                                                      109 GATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCCTTATCCTGCTGCAGGCTG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: Si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: complement (4616..4691)
OTHER INFORMATION: /product= "tena"
OTHER INFORMATION: /note= "(complementary DNA strand) Homology to glyW from E
OTHER INFORMATION: Coll."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /product= "sensor kinase" or kinase has homology to OTHER INFORMATION: /note= "Coding sequence for sensor kinase has homology to OTHER INFORMATION: rcsC, firE, and bvgS genes of E. coll, M. Xanthus, and OTHER INFORMATION: Borditella pertussis, respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
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STRAIN:
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OTHER INFORMATION:
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                                                                                                                                                                               Local
                                                                                                                                                              78;
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                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t: Pseudomonas fluorescens CGA267356 (aka MOCG134 and aka BL915)
                                                                                                                                                              Conservative
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                                                                                                                                                                               50.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- "methyltransferase"
/note- "Coding sequence for methyltransferase has homology
the cheR and frzF genes from E. coli and Myxococcus xanthu
respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atidyltrans."

note= "Coding sequence for
CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltran
se has homology to pgsA."
                                                                                                                                                                                                                                                        regulator/transcription activator"
/product= "gacA (aka gafA)"
/note= "Coding sequence for gacA (aka gafA) has homology t
uvry and gacA genes of E. coli and Ps. fluorescens,
respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "UVR exonuclease subunit C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CDP-diacylglycerol-glycerol-3-phosphate-3-phosph
                                                                                                                                                                                                                                                                                                                                                            /function= "response
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
                                                                                                                                                              0
                                                                                                                                                                               Score 31.8; DB 1; Length 10753; Pred. No. 1.9;
                                                                                                                                                              Mismatches
                                                                                                                                                            77; Indels
                                                                                                                                                              0;
                                                                                                                                                              Gaps
                                                                                                                                                              0;
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RESULT 7
US-08-977-306-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (91) 541-805/
INFONMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                FEATURE:

NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: /prod
OTHER INFORMATION: /notee
OTHER INFORMATION: rcsc,
OTHER INFORMATION: BORdi
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL; N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCE.

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 595534@artis Corporation

STREET: 3054 Cornwallis Road

TTTV. Research Triangle Park
                                                       FEATURE:
                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 210.1688
OTHER INFORMATION: /prod
OTHER INFORMATION: /note
OTHER INFORMATION: respe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Torkewitz, Nancy
APPLICANT: Stafford, Jill M.
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Genetically Modified Pseudomonas Strains TITLE OF INVENTION: with Enhanced Biocontrol Activity NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1318
                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 CTCCCCTCTGGGGCACAACAACAAGAGAAGTTGC 263
LOCATION: complement (4616..4691)
OTHER INFORMATION: /product= "trna"
                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCCGCCGGGTGCGCATCGAGCGGGAAAAGAAGC 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I, Application US/08977306
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                                                                                                                                                                                                                                                                                                         Plasmid pEll
                                                                                                                                                                                                                                                                                                                                      : Pseudomonas fluorescens
CGA257356 (aka MOCG134 and aka BL915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                   misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                           NO
                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                     /product= "methyltransferase"
/note= "Coding sequence for methyltransferase has homology to
the chek and frzF genes from E. coli and Myxococcus xanthus,
respectively."
                                                                /product= "sensor kinase"

/note= "Coding sequence for sensor kinase has homology to the rcsC, frzE, and bygS genes of E. coli, M. Xanthus, and Borditella pertussis, respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us/08/977,306
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US-08-343-443B-106/c
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Best Local S
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NAME/KEY:
LOCATION:
                                                                                                                NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
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OTHER INFORMATION:
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OTHER INFORMATION:
               COUNTRY: U
                                                                                STREET:
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                                                   STATE:
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                                                                                                ADDRESSEE:
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Similarity 50.3%;
78; Conservative
                                                               Philadelphia
                                             PA
                                                                              E: Weiser & Associates
230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                       Auring Delattre, Original Chantal
                                 USA
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Thomas, Gilles
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Peter, Martine
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LOCATION: complement (7400..8041)

OTHER INFORMATION: /function= "response

CITER INFORMATION: /function= "response"

OTHER INFORMATION: /product= "gacA (aka gafA)"

OTHER INFORMATION: /note= "Coding sequence for gacA (aka gafA) has homology t

OTHER INFORMATION: uvry and gacA genes of E. coli and Ps. fluorescens,

OTHER INFORMATION: respectively."
APPLICANT: ZUCMAN, JESSÍCA
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECUGRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUDORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1318 CCGCCGCGGGTGCGCATCGAGCGGGAAAAGAAGC 1352
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OTHER INFORMATION:
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"CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltrans."

Anote= "Coding sequence for CDP-diacylglycerol-glycerol-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phosphate-3-phospha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "UV\hat{R} exonuclease subunit C"
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MEDIUM TYPE: COMPUTER: IE

E: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-08-343-443B-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/FF
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA: FR 92,
FILING DATE: FR 92,
FILING DATE: 20-MAY-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                 APPLICANT: Thomas, Gilles
APPLICANT: Zucman, Jessica
APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TRANSLATIONS
TITLE OF INVENTION: TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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SOCTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 GGCCGTGAAAGCCAGCCAACTGCCGCAAAATCACCCAGCCGATTGGGGGGTTTCCCATC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 GG 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GG 93
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Local Similarity 67.7%;
es 42; Conservative
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LOCATION: 1..!
                                                                                                            ADDRESSEE: Weiser & Associates STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                        COUNTRY:
                                                                                          CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, Application US/08343443B
5. 5968734
                                      19102
                                                                       PA
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Desmaze, Chantal
                                                        USA
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Peter, Martine
Ploougastel, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                Aurias, Alain
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20-MAY-1992
Floppy disk
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    Mismatches

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Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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; LENGTH: 500
; TYPE: PRT
; ORGANISM: Human
US-09-141-000-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09141000; Patent No. 6054295; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-141-000-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-343-443B-1
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                             Query Match 5.9%; Score 29.6; DB 3; Length 500; Best Local Similarity 8.4%; Pred. No. 1.9; Matches 38; Conservative 132; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR TITLE OF INVENTION: RECEPTOR PROTEINS FILE REFERENCE: 19999Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8394
TELEPAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2371 base pair
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
EILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
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456 TYD..S.B....YW...SHTYTWTMT..K....MDK.BMC..MBSR.D.BTMTTA.Y... 397
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                                           44 TTATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTTA 103
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illarity 67.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              989.6121P
                                                                                         0;
                                                                                    Gaps
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0;

104 AATTAGATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCCTGCTGCA 163

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RESULT 12
US-08-050-132A-8/c
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; Sequence 8, Application US/08050132A
                                                                                                             Db 514554 GCGTGCCGAAAGTC 514541
                                                                                                                                                                                                 Db 514674 GTTGACGCCTATGCTGGCGCTTGGTGCAATGGCCAGTGCGGTGTTGGGTTCGCCGGTGGA 514615
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US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TOBERCULOSIS
TILE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DATE: 24366-24007.00
CURRENT PELICATION NUMBER: US/09/103,840A
CURRENT PELILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTMARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                   435 TGCTGCCCAAAATC 448
                                                                                                                                                                                                                                          315 GCTTACTCCAATGGCTGAGAGAGGTGCTATGGCCAGTCCTCCCAGAGCTCTGCAGCTGCA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 GGTTTCCCATCGGCGCACCCTGCCCGGAGCCAAG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 TGCGTGATAACGGCCGTGAAAGCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 .GSMYYYMA..G.NAT.GSR..NC..AYM..TMGT.GSTBCRDRCST.HCGB.G.YM..T 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 BM.MMRYYB....TYR....CT.YSD..HK.RH.TRB.MHHR..SYRB.C....KWTS. 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 TGGCCAGTCCTCCCAGAGCTCTGCAGCTGCACTTGGGGGTTGGACAGTCTCGTGCTTGTCC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 .RSB.MA..MMT..S...S.R.SS.SH.YYMRM.YCCYBYH.YBC.M.KCBM.GMK.YGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 GGAAATGCATCTCCCATTGGAACAGCCCTGGGCTTACTCCAATGGCTGAGAGAGGTGCTA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 ..SK.HC.S.SS.C..DMTWC..BB..YHT.HG.AA.TM.HC..KC...KTR.MH..TB. 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AGGGTCTCCCCTCTGGGGCACAACAACAAAGAAGTTGCTAAGGACAAGAAGCAGGTGC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 GGCTGTGCTGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAAC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 .A...MCAYW...DY.S..RH..T.D..H..M.BT..H..RKSHSNT.T.TM.AB...M. 337
                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 S.SDDS.TH.CSS.SS..AM..SCGSSC.DYHHS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 N.KR.GM.TSH.K.CSTGH.RSMYG.ACC.CTCT.K..SH.CNTDAC.T.C.CCSTHSSC 37
                                                                                                                                                                                                                                                                                                                                                                         h 5.9%;
Similarity 52.2%;
70; Conservative (
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                         Score 29.6; DB 4; Length 4403765; Pred. No. 54; 0; Mismatches 64; Indels 0;
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                                                                                                                                                                                                                                                                                                            ; LOCATION: US-08-050-132A-8
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 470 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DN.
HYPOTHETICAL: NO
FRAGMENT TYPE: C --
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION UNMBER: 32,245
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOZNEY, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME: UNITS: bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UKGANISM: Homo sapiens
CELL LINE: W138 (genom.
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
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452 CAGCC 456
                                        287 GCGTGTTTCGTCGGCGTCACATCGTCAGCCAAGGGGAAGAAGCAGCCGCCCTTACACTCG 228
                                                                                 347 ACACAGCAGCCTTGCCCACCTTTGTGGGGAACTTGAGATGCACCAGGGTCTGCACGATA 288
                                                                                                                                                                          332 AGAGAGGTGCTATGGCCAGTCCTCCCAGAGCTCTGCAGCTGCACTTGGGGGGTGGACAGTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: human genomic library CLONE: lambda 111-1
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                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                5.8%; Score 29; DB 1; Length 470; 52.0%; Pred. No. 2.9; ative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/050,132A
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227 TAGGC 223

Query Match 5.8%; Score 29; DB 3; Length 470; Best Local Similarity 52.0%; Pred. NO 2.9; Matches 65; Conservative 0; Mismatches 60; Indels

0; Gaps

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; LOCATION:
US-08-750-222A-8
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APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNI
HYPOTHETICAL: NO
FRAGMENT TYPE: C:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE,DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 875-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                FEATURE:
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                POSITION IN GENOME:
                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/750,222A FILING DATE: 04-DEC-1996 CLASSIFICATION: 435
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CITY: Cambridge
                                                                                                                                                                                                                                                                                      CELL LINE: W130 ,
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                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                              NAME/KEY:
                                                                                 NAME/KEY:
                                                                                                                LOCATION:
                                                                                                                                 NAME/KEY:
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                                                               LOCATION:
                                                                                                                                                                LOCATION:
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lambda 111-1
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Legal Affairs - 87 CambridgePark Drive
             mRNA
1..470
                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                             mat_peptide
124..453
                                                                                                                1..456
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                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                             W138 (genomic DNA)
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                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                 double
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RESULT 14
US-08-815-652B-8/c
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                                                                    CELL LINE: W138 (genomic DNA)
IMMEDIATE SOURCE:
LIBRARY: human genomic library
CLONE: lambda 111-1
POSITION IN GENOME:
UNITS: bp
FEATURE:
                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 470 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
OLECTOR OF TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WOZNEY, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KAPINOS, Ellen J.
REGISTRATION NUMBER: 32,245
REGERRECE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kapinos, Ellen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                               MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AGAGAGGTGCTATGGCCAGTCCTCCCAGAGCTGCAGTTGGGGGTGGACAGTC 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                                NAME/KEY: exon
LOCATION: 1..470
                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                C-terminal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAPINOS, ELLen J.
REGISTRATION UNMEER: 32.245
REGISTRATION INFORMATION:
TREEPRINCE/DOCKET NUMBER: G1 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPAX: (617) 876-5951
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 base pairs
TYPE: nucleic acid
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US-08-254-353A-8/c
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APPLICANT: ROSEN, Vicki A.
APPLICANT: ROSEN, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
ADDRESSEE: Genetics Institute, Inc.
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FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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347 ACACAGCAGGCCTTGCCCCACCTTTGTGGGGAACTTTGAGATGCACCAGGGTCTGCACGATA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 TAGGC 223
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                                                                                                                        LENGTH: 470 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    CELL LINE:
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STATE: MA
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Legal Affairs - 87 CambridgePark Drive
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W138 (genomic DNA)
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FEATURE:
NAME/KEY:
LOCATION:
US-08-254-353A-8
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Search completed: October 10, 2002, 19:26:08 Job time: 2506.73 secs
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Best Local S
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POSITION IN GENOME:
UNITS: bp
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LIBRARY: human
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LOCATION:
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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Perfect score:
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score greater
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A2939272
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A0587521 CITBI E1-
AZ34779 1M0079E03
AZ128097 OSJNBADO8
B1528538 602924971
A164581 603006E12
AQ99128 RfC00047
B1889964 ZF637-1-0
BE774740 MR4 UM002
BM411416 EST585743
AZ39272 ZM0195112
BM412789 EST58715
AL034994 k8710245
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AL034994 K87102398 CE31959
AE653538 UI-M-AP1-
A1227158 UJ03a09.9
AL365067 AL365067
AL1117764 k9224a43
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AUTHORS
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VERSION
KEYWORDS
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AQ587521
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                          Map Building
Unpublished (1997)
Other_GSSS: CITBI-E1-2643G14.TR
Other_GSSS: CITBIP-E1-2643G14.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Re
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 675)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ587521 675 bp DNA linear GSS 07-JUN-1999 CITBI-E1-2643G14.TF CITBI-E1 Homo sapiens genomic clone 2643G14,
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence.
AQ587521
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/note~"Vector: pBeloBACll; Site_1: EcoRI; Site_2: EcoRI;
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/db_xref="taxon:9606"
/clone="2643G14"
/clone_lib="CITBI-E1"
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9 AI875988
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BI303148
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BF721846 maa32e03.
BF721846 mab2c02.
A1119356 uf03c04.y
A1314561 uf48d10.y
BF012479 ux56h01.y
BF9385764 602045265
BF385764 602045265
BF385764 602056470
BT221810 602937071
BF722677 mab34d02.
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BG148031 i492e10.y
AQ312808 CIT*HSP-2
A1225883 ui22f11.y
AW012295 u004d06.y
AI785097 ui73f10.y
BF143525 602910604
BG922396 602817123
BF344234 602045476
BG922396 602817427
BF344234 602045476
BG93248 u160d04.y
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AI875988 uj53e11.y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAACAGGGTCTCCCCTCTGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCACAAC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 AAGCTTGGTGCCATCTATTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTTAAATTAGATTGGTGTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGCTTGGTGCCATCTATTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTC 60
                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0079 row: E column: 03
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                      Onpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 723)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Resilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                      High quality sequence stop: 723.
                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC344779 723 bp DNA linear GSS 29-SEP-20 1M0079E03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0079E03 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                             plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                        USA
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CalTech Human BAC Library D"
a 134 c 162 g 206 t
                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0079E03"
                                                                                                                                                                                                 Location/Qualifiers
                                                               /sex="Male"
                                                                               /clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.8%;
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VERSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 GGCAGGGCTACAATATCATCAAGCACCATTTAGATTGGTGTAA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGCTTGGTGCCATCTATTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSJNBb0086H01r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone OSJNBb0086H01r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                             Seq primer: GGAAACAGCTATGACCATGClass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ128097.1 GI:8204877
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                                                                                                                                                                                                                                                                                                                      quality sequence start: 19 quality sequence stop: 615.
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(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114 |gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically competent E. coil XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
                                                                                                                                                           /cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                /clone_lib="CUGI Rice BAC Library (ECORI)"
/tissue_type="Leaf"
/lab_host="E coli DH10B"
                                                                                                                                     /clone~"OSJNBb0086H01r"
                                                                                                                                                                                                                  ∕strain="Japonica"
                                                                                                                                                                                                                                          /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%;
63.1%;
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Pred. No. 0.055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 TTTCTTTTTCTATACTTGTTCTAGAGATTCTAGAGAAAATGAGACATAGTGAAGCCAGAG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 AATGGCAAACTCTACGCCTTTTATTTTAAATTAGATTGGTGTGATTTGATGCTGACG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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High quality sequence start: 27
High quality sequence stop: 295.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate::LLAM11155 row: n column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1 (base 1 to 606)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI526538 606 bp mRNA linear EST 29-AUG-2001 60502924971F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5057489 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI526538.1 GI:15351330
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Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1931). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies in order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Orya sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatively 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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/db_xref="taxon:10090"
/clone="IMAGE:5057489"
/clone_lib="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                 /organism="Mus musculus"
/strain="CZECH II"
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RESULT 4 BI526538

KEYWORDS

FEATURES

Query Match Best Local Similarity

7.2%; 53.1%;

Score 35.8; DB 9; Length 669; Pred. No. 5.4;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 TCCGCCTCCAGCCCGCAGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 GGCGCACCCTGCCCGGAGC 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 GGCCGTGAAAGCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGGTTTCCCATC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 CCGCGTGCTGTGCGGCTGTAGCTAGTGGTTGGCTTCTTCCTGTTCGGCCGGGACCCG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIG49581 669 bp mRNA linear EST 30-APR-1999 603006F12.x1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.

AIG49581 AIG49581
                                                                                                                                                                                                                               Email: walbot@stanford.edu
Plate: 603006 row: F col
                                                                                                                                                                                                                                                             855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                             Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 669)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
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Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                       Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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   140 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="salt stress"
/lab_host="E. col1 XL Gold"
/note="Organ: root; Vector: pBluescriptII SK(+) XR;
Seedling stressed root cDNA library from Wang/Bohnert lab"
a 225 c 179 g 125 t
                                                                           Value_110="50"3 - Stressed root cDNA library from Wang/Bohnert lab"

/tissue_type="seedling"
/dev <tao.~"--"
                                                                                                                                                       /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                       /db_xref="taxon:4577"
/clone_lib="603 - str
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RESULT 6
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                  197 TGGCGCCATTATATTTAACCAATCCCGTCCATACTGTATAAGATCCTTTTTCATATTGTA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 AACCACATCCTTGTGATGTGA 355
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                                                                                                                                                                                                                                  Local
                                                                                                                                                         6 TGGTGCCATCTATTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTCAGGCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCCGAGCCAGCTGCCGAAATGGAACTACGACGGCTCCAGCACCGGGCAAGCTCCCGGA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Dabborn, P.J., Bowen, D. and Blattner, F.R. Bellen, P. Bowen, D. and Blattner, F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Photorhabdus luminescens.
Photorhabdus luminescens
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REG00847 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone FLG00847, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: ffrench-Constant
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                                                                                                                                                                                                                                                                                                                   /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M1 Janus."
kb) 135 c 101 g 228 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:29488"
/clone="PLG00847"
                                                                                                                                                                                                                                                                                                                                                                                                           library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Photorhabdus luminescens strain Wl4 M13
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Pred. No. 5.4;
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BE774740
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ORGANISM
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                                                                                                                                                                                                                                                                                                 398 TTGTCCTGCGTGATAACGGCCGTGAAAGCCAGC 430
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laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr. 63-73, D-1419 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
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ZF637-1-000206 Zebrafish shield stage whole embryo CDNA library
MPMGp637 Danio rerio cDNA clone MPMGp637_6E15;MPMGp637E156 5', mRNA
Homo sapiens
                                                                                                             BE774740 339 bp mRNA linear EST 20-SEP-200 MR4-UM0021-300600-008-e09 UM0021 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H. EST sequencing of a zebrafish shield stage cDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
                                                                   BE774740.1
                                                                                             BE774740
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iibrary MPMGp637"

/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XLI blue MRF"
/lab_host="E.coli, XLI blue MRF"
/note="Vector: pSportl; Site_1: NotI; Site_2: SalI;
oligo-d"-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
a 210 c 159 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7955"
/clone="MPMGp637_6E15;kBMGp637E156"
/clone_lib="Zebrafish shield stage whole embryo cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
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                                                                      GI:10228395
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Pred. No. 7.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                           74 AGATCTCCACTTAGCCAAAGGGCTGCGAGAGGTGAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 CATCAAATAGTGCATGAGGTGGTGACAGAACCAGTGCGGGATTCCATCACCAGTCGGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=MR4-UM0021-300
600-008-e09&t3=2000-06-30&t4=1)
See primer: puc 18 forward
Unit Control of the primer of the pure seen in the FAPESP/LICR Human Cancer Genome
See primer: puc 18 forward
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Roldman, G., H., Carvalho, A., F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                        BM4111416 B85 bp mRNA linear EST 22-JAN-20 EST558743 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG56F7 5' end, mRWA sequence.
                                                     Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
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Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai
                                                                                                                                                                                                                BM411416.1 GI:18263046
                                             Lycopersicon
                                                                                                                                                                     coma to
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/db_xref="taxon:9606"
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  plasmid inserts
Unpublished (2000)
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477 CGTTAGCAGGGGACTCATTAGGACTTGAAAGCATGGATATGATGCTCAAAATTATA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 TGCTGCAGGCTGTGCTGAGGATGGCCTGGTCTGCCACCCTCC-TCGAGTAGCATTTTGCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 TATCATAAAATGCATTGGTACATTTCTGTGTTCACTACATTTCTTGTGACCGTCTTACAC 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 TATTTTAAATTAGATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 TACAGCTTTATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
                            1 (bases 1 to 781)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ939272 781 bp DNA linear GSS 26-APR-200
2M0198J12F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0198J12 F, DNA sequence.
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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This clone is available through the Clemson University Genomics
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100 Jordan Hall, Clemson, SC 29634, USA
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                             AZ939272.1 GI:13799778
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/tissue_type="Pericarp"
/dev_stage="breaker"
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/clone="cLEG56P7"
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/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 CACGGGGAACGCAGTTATCTGATTTCCAGCCAAGAAACTGGACATCAAGCCACGCTCTC 323
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                                                                                                                                                            BM412789
EST587116 tomato breaker fruit
cLEG61K23 5' end, mRNA sequenc
  Lycopersicon esculentum Eukaryota; Embryophyta; Tracheophyta; Epharyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Class: plasmid ends
High quality sequence stop: 781.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                רטזוושנט
                                                                                                                             BM412789.1 GI:18264419
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Insert Length: 10000 Std Erro
Plate: 0198 row: J column: 1
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.lax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA42 (gil4732114|gbhAF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M019BJ12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC2M library"
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                                                                                                                                                                       end, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
                                                                                                                                                                                                                         790 bp
                                                                                                                                                                                                   Lycopersicon esculentum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 781;
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                                                                                                                                                                                                                                                                                                                                                 AL034894
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                                                                                                                                                                                                                            VERSION
     TITLE
                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                477 CGTTAGCAGGGGACTCATTAGGACTTGAAAGCATGGATATGATGCTCAAAATTATA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 AACGACTGACCCTTTTCTTGAATTCATCCCTTTTTTTCCCTCCATTCCTTAGCAGCTTCCA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 TGTGTAACAGGGTCTCCCCTCTGGGGCACAACAACAAGAGAAGTTGCTAAGGACAAGA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 TGCTGCAGGCTGTGCTGAGGATGGCCTGGTCTGCCACCCTCC-TCGAGTAGCATTTTTGCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 TACACTTTGTAGCAATGACATCCCAGCCAAAAGAACGATGATAAGCCATTTTATCAGCTT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 TATCATAAAATGCATTGGTACATTTCTGTGTTCACTACATTTCTTGTGACCGTCTTACAC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 TACAGCTTTATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118;
                                                                                                                                                                                                                                       AL034894 J/O DP MINING MUS musculus k8710A45 Beddington mouse dissected endoderm Mus musculus clone 528_9H17 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        il (bases 1 to 790)

Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tso, J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
                           Harrison, S.M., Dunwoodie, S.L., Arkell, R.M., Lehrach, H. and Beddington, R.S.
                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Isolation of novel tissue-specific genes from cDNA libraries
                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                   EST
                                                                                                                                                                                                                            AL034894.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0%;
Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asteridae;
                                                                        (bases 1 to 376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhOI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of 1ycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
/clone="cLEG61K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/cultivar="TA496"
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                                                                                                                                                                                                                            GI:6646520
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    Mismatches

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                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE
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Best Local (
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                                                                                                 MEDLINE
                                                                                                                      JOURNAL
                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 GCTGCCCACCCTGCACGCCCGAGCGTCTGGCCGCCTTGCGGGCCCCCACCCGACGCGCCCT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TGCTGCTGCTCTTGGGCGCGGGCGGCTGCGGCCCCGGGGTGCGCCGAGGTGCTGCTTCC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GCGCCGAGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 GCCCGGAGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 GCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGGTTTCCCCATCGGCGCACCCT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 TGCAGCTGCACTTGGGGGTGGACAGTCTCGTGCTTGTCCTGCGTGATAACGGCCGTGAAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           госат
                                                                                                                                                                                                                                                                                                                                                                                                                                             AL023086 389 bp r
t8219b39 Beddington mouse dissected
clone 528-4C13 5', mRNA sequence.
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Dissected endoderm 7.5 days.
Average insert size: 1.2 kb (range: 0.2 - 2.kb).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: pavner@pasteur.fr clone available from Ressourcenzentrum, Heubnerweg 6, D-14059 Berlin, Germany. Web site http://www.rzpd.de Seq primer: CCGGTCCGGAATTCCCCGGGT;
                                                                                                                                                                                                           Harrison, S.M., Dunwoodle, S.L., Arkell, R.M., Lehrach, H. and Beddington, R.S.
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence only submitted.
Vector: pSportl; site_1: NotI; site_2: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEC Mouse Transcript Mapping Consortium Genoscope – CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Development 121 (8), 2479-2489 (1995) 95401865
                     EEC Mouse Transcript Mapping Consortium Genoscope - CNS
                                                                 Contact: Wiles, M., Lehrach, H.
                                                                                                 95401865
                                                                                                                                                              Isolation of novel tissue-specific genes from cDNA libraries representing the individual tissue constituents of the gastrulating
                                                                                                                                                                                                                                                                                                                                                                                                      AL023086.1 GI:6645659
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                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%;
Similarity 54.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rue Gaston Cremieux, 91000 Evry, France
rue Gaston Cremieux, 91000 Evry, France
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                                                                                                              opment 121 (8), 2479-2489 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally.~ High quality sequence only submitted.~ Average insert size: 1.2 kb (range: 0.2 ~ 2.kb)"

151 c 125 g 61 t 1 others
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//db_xref="taxon:10090"
/clone="528_9H17"
/clone=1ib="Beddington mouse dissected endoderm"
/tissue_type="dissected endoderm"
/dev_stage="7.5 dpc"
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Pred. No. 10;
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                                                                    and Avner, P.
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d endoderm Mus musculus
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 GCGCCGAGC 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGCTGCTCTTGGGCGCGGGCGGCTGCGGCCCCGGGGTGCCGAGGTGCTGTTCC 194
CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BNAP CDNA clones from RESEARCH GENERICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BNAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 101-139, >(CAG)n#Simple_repeat 143-177
                                                                                                                                                                                                                                                              Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone available from Ressourcenzentrum, Heubnerweg 6, D-14059
Berlin, Germany. Web site http://www.rzpd.de
Seq primer: CCGGTCCGGAATTCCCGGGT:
                                                                                                                                                                                                                                                                                                                                         97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 391) Bonaldo, M.F., Lennor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE653538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UI-M-AP1-agk-h-04-0-UI.rl NIH_BMAP_MST_N Mus musculus cDNA clone
UI-M-AP1-agk-h-04-0-UI 5', mRNA sequence.
                                                                                                                                                                                           Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dissected endoderm 7.5 days.
Average insert size: 1.2 kb (range: 0.2 - 2.kb).
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                                                                                                                                                                                                                                              20892-9643,
                                                                                                                                                                                                                                                                                                                                                                                      discovery
                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE653538.1 GI:9979444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                     mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                              Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: pSport1; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. - High quality sequence only submitted. - Average insert size: 12 & t (range: 0.2 - 2.kb)"

154 c 132 g 65 t
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/db_xref="taxon:10090"
/clone="528-4C13"
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/clone_lib="Beddington mouse dissected endoderm"
/clssue_type="dissected endoderm"
/tissue_type="dissected endoderm"
/dev_stage="7.5 dpc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Lennon, G. and Soares, M. B
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Pred. No. 1
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RESULT 15
AI227158
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GCTGCCCACCCTGCACGCCCGAGCGTCTGGCCGCTTGCGGGCCCCCCACCCGACGCGCCCT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 GCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGGTTTCCCATCGGCGCACCCT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 TGCAGCTGCACTTGGGGGTGGACAGTCTCGTGCTTGTCCTGCGTGATAACGGCCGTGAAA 424
                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                    Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIZZ/158 399 bp mRNA linear EST 29-
uj03a09.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1890808 5' similar to gb:X81580 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
AIZZ7158
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Seq primer: M13 Reverse.
                                                                                                                                             Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                     Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI227158.1 GI:3810211
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Location/Qualifiers
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/note-"Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_MST_N library is a normalized library constructed
from mouse striatum. The tag is a string of 5 pucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories."
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/clone="UI-M-AP1-agk-h-NST_N"
/clone_11b="NHH BMAP_MST_N"
/dev_stage="27-32 days"
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54.3%;
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Pred. No. 10;
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Search completed: October 10, 2002, 20:28:09 Job time: 701.733 secs
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                                                       226 GCGCCGAGC 234
                                                                                 485 GCCCGGAGC 493
                                                                                                         166 GCTGCCCACCCTGCACGCCCGAGCGTCTGGCCGCCTTGCGGGCCCCCACCCGACGCGCCCT 225
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primer CGACCTGCAGCTCGAGCACA."
a 156 c 132 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1890808"
/clone_lib="Sugano mouse liver mlia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                              54.38;
                                                                                                                                                                                                                  Score 34.6; DB 9;
Pred. No. 10;
0; Mismatches 59;
                                                                                                                                                                                                                   59; Indels
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Result
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           Score
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33.6
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1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1981.DAT:*
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                                                                                                                                                  Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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AAD11119
AAD20201
AAF84712
AAZ1537B
AAQ04551
AAH08825
AAH15237
AAF16216
                                                                                                                                                                            SUMMARIES
          Nucleotide sequenc
Human gene express
Rat BRL-3A binding
Human cDNA clome (
Human cDNA sequenc
Human prostate can
                                                                                                                                   Description
                                                                                           Human small cell l
Corynebacterium gl
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AAD11119
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ALIGNMENTS

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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; SOXZ1; ds.
(LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human small cell lung cancer associated gene, SOX21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD11119;
                                                                                                  21-JAN-2000; 2000US-0489101.
                                                                                                                                                 19-JAN-2001; 2001WO-US02015.
                                                                                                                                                                                                  26-JUL-2001.
                                                                                                                                                                                                                                              WO200153349-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1167..1997
/*tag=_a
                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Human SOX21 protein"
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AAD20201/c
                                                                  RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCIC-10, encoding human SOX21 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by isolated nucleic acid comprising an NA Group 3 or 4 molecule
                           AAD20201 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8372 BP; 1996 A; 2143 C; 2104 G; 2124 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 57; Page 100-105; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGCCCGGAGCCAAGAAG 500
                                                                                                                                                                                                             GAAAGCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGTTTCCCATCGGCGCA
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                                                                                                                                                                                                                                                    GAAAGCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGGTTTCCCATCGGCGCA 480
                                                                                                                                                                                                                                                                                             GCTCTGCAGCTGCACTTGGGGGGTGGACAGTCTCGTGCTTGTCCTGCGTGATAACGGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACAACAACAAGAGAAGTTGCTAAGGACAAGAAGCAGGTGCGGAAATGCATCTCCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 500; DB 22; 100.0%; Pred. No. 1.1e-152;
                             2811 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jager D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gure AO, Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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AAF84712/c
ID AAF84712 standard; DNA; 2811
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for preparing L-amino acids by formenting coryneform bacteria, comprising fermenting the L-amino acid producing bacteria in which at least the glucose 6-phosphate dehydrogenase (zwf) gene is amplified, and concentrating and isolating the L-amino acid produced. The L-amino acids produced are used in animal nutrition, human medicine, foodstuffs industry and the pharmaceuticals industry. The present sequence is Corynebacterium glutamicum strain ASO19 glucose 6-phosphate isomerase (pgi) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-amino acid; fermentation; coryneform bacteria; animal nutrition; glucose 6-phosphate dehydrogenase; zwf; human medicine; foodstuff industry; glucose 6-phosphate isomerase; pgi;
                                                                                                                                                                                                                                                                         2804 GCCCGCTCTAGAAGTACTCTCGAGAAGCTTTTTGAATTCTTTGGATCACCTACCATCTGC 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2811 BP; 592 A; 744 C; 764 G; 711 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing L-amino acids by fermenting coryneform bacteria transformed with the glucose 6-phosphate dehydrogenase gene is particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burke K, Sahm H,
Stapelton C, Moe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170995-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum glucose 6-phosphate isomerase (pgi) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD20201;
                                                                                                             2684 CCCACACCAACCGAAGACTTCCACAGGAAGAAGAAACCTTCGACGGC 2637
                                                                                                                                                                                         2744 GGCATAAAACCCATGAGGATATACGTCGCAAACGAAGTAAACCCCAAACATCAACCCGAGC 2685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 49-52; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to produce L-lysine and L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2000; 2000US-0531269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2000; 2000WO-EP06303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEGS ) DEGUSSA AG.
(KERJ ) FORSCHUNGSZENTRUM
(UYNA-) UNIV NAT IRELAND.
                                                                                                                                                                                                                                                                                               180 GCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAACAGGGTCTCCCCTCTGG 239
                                                                                                                                                                                                                                    240
                                                                                                                                                  TTGGAACAGCCCTGGGCTTACTCCAATGGCTGAGAGAGGTGCTATGGC 347
                                                                                                                                                                                                                               GGCACAACAACAAGAGAAGTTGCTAAGGACAAGAAGCAGGTGCGGAAATGCATCTCCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639130/73.
DB; AAE12461.
                                                                                                                                                                                                                                                                                                                                                           84;
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FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Glucose 6~phosphate isomerase (pgi)"
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kel B, Thierbach G;
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BP
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Pred. No. 3.
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Best Local :
                                                                                                                                                                                                                            The present sequence encodes a coryneform bacterial glucose-6-phosphate isomerase (gpi). After attenuation of the gpi gene, coryneform bacteria exhibit an improved metabolic flux through the pentose phosphate cycle and produce nucleotides, vitamins, and in particular L-amino acids, particularly L-lysine and L-tryptophan, in an improved manner. Attenuation may be achieved by reducing or switching off either the expression of the gpi gene or the catalytic properties of the enzyme protein. Microorganisms, in particular Corynebscutum glutamicum in which the gpi gene is attenuated or switched off, optionally in which the gpi gene is attenuated or switched off, optionally in combination with amplification of further genes, are useful for producing nucleotides witched of further genes, are useful for
                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleotide sequence from coryneform bacteria encoding glucose-6-phosphate isomerase, attenuation of which increases metabolic flux through pentose phosphate cycle in the bacteria, producing L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacteria; glucose-6-phosphate isomerase; gpi; metabolic flux; pentose phosphate cycle; L-amino acid; nucleotide production; vitamin production; L-amino acid production; ss.
                                                                                               2804 GGCCGCTCTAGAAGTACTCTCGAGAAGCTTTTTGAATTCTTTGGATCACCCTACCATCTGC 2745
                                                                                                                                                                                             Sequence 2811 BP; 592 A; 744 C; 764 G; 711 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 13-16; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2000; 2000EP-0118052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a bacterial glucose-6-phosphate isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF84712;
 2684 CCCACACCAACCGAAGACTTCCACAGGAAGAGAGAAACCTTCGACGGC 2637
                                                                                                                                                                                                                     producing nucleotides, vitamins or L-amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunican LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNA-) UNIV NAT IRELAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DEGS ) DEGUSSA-HUELS AG
                                                                                                                     180 GCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCATGTGTAACAGGGTCTCCCCTCTGG 239
                                                                       240 GGCACAACAACAAGAGAAGTTGCTAAGGACAAGAAGCAGGTGCGGAAATGCATCTCCCA 299
                                                                                                                                                          госат
                       TTGGAACAGCCCTGGGCTTACTCCAATGGCTGAGAGAGGTGCTATGGC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-267593/28
)B; AAB68033.
                                               GGCATAAAACCCATGAGGATATACGTCGCAAACGAAGTAAACCCAAACATCAACCCGAGC 2685
                                                                                                                                              84;
                                                                                                                                                        6.7%;
Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moeckel B;
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccormback A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-0396478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 373..2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "glucose-6-phosphate isomerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapelton C,
                                                                                                                                               0; Mismatches
                                                                                                                                                         Score 33.6;
Pred. No. 3.
                                                                                                                                                         3.3;
                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burke K,
                                                                                                                                               84; Indels
                                                                                                                                                                     Length 2811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Donohue M;
                                                                                                                                              0;
                                                                                                                                              Gaps
                                                                                                                                               0
                                              Matches
                     Query Match
                                               Sequence 774 BP; 233 A; 119 C; 123 G; 251 T; 48 other;
            Local
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Similarity

6.78;

DB 20;

Conservative

33 TGCATACAGCTTTATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGC 92

0; Mismatches Score 33.4; Pred. No. 1.

106;

Indels Length

0; Gaps

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CC comprising the sequences given in AAZI232 to AAZI7779. Also described is CC comprising the sequences given in AAZI232 to AAZI7779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell CC suspected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotide sequences given in AAZI2532 to AAZI779. The CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polynuclpotisms. Polypoptides encoded by the polynucleotides CC can be used for raising antibodies for experimental, diagnostic and CC detection of pulproprisms. Polypoptides encoded by the polynucleotides CC carrays for diagnostics (which may be used to determine function of an CC encoded protein); and to detect differences in expression levels between CC diagnosis, prognosis and management or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC cancer. The polynucleotides can also be used to screen for CC peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ15378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crkvenjakov R, Dickson M, Drmanac R, Drmanac S
Escobedo J, Garcia PD, Garcia V, Giese K, Inn
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ15378 standard; cDNA; 774 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1377; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09938972-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0072910.
98US-0075954.
98US-0080114.
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Labat I;
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RESULT 5
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                                                                            Matches
                                                                                                                 Sequence 1214 BP; 254 A; 363 C; 375 G; 222 T; 0 other;
                                                                                                                                    of the binding protein. See also AAQ04550,Q04552 and AAQ04553
                                                                                                                                                               Disclosure; ; pp; English.
                                                                                                                                                                               Insulin-like growth factor binding protein - comprising amino acid sequence of defined sequence, useful for blocking effects of excessive growth factor.
                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                           The fragment is derived from rat BRL-3A cells.
                                                                                                                                                                                                                      WPI; 1990-158010/21.
P-PSDB; AAR04909.
                                                                                                                                                                                                                                                                                      11-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04551 standard; DNA; 1214 BP
                                                                                                                                                                                                                                                 Blinkert C,
                                                                                                                                                                                                                                                                  (SANO ) SANDOZ AG.
                                                                                                                                                                                                                                                                                                         08-NOV-1989;
                                                                                                                                                                                                                                                                                                                                              EP369943-A.
                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor-binding protein; growth factor; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat BRL-3A binding protein precursor-encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ04551;
                                                                                                                                                                                                                                                                                                                            23-MAY-1990.
   106 GCTGCCCACCCTGCACGCCCGAGCGTCTGGGCCGCCTGCGGACCCCCACCCGACGCGCCCCT
                    425 GCCAGCCAACTGCTGCCCAAAATCACCCAGCCGATTGGGGGGTTTCCCATCGGCGCACCCT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
                                                       365 TGCAGCTGCACTTGGGGGTGGACAGTCTCGTGCTTGTCCTGCGTGATAACGGCCGTGAAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 AATAGGCTTTAACTGATTTTGTGATTATTGATATTAGAAATGTTTAAAATTAAGATATTA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 TGCCTTCAGAATTATGGCGACCTCTGCGATGGAAGAATGGGATCAGAGAAGGATACAC 278
                                      46 TGCTGCTGTTGGGCGGGCGGTTGCGGTCCTGGGGTGCGCCGAGGTGCTGTTCC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                    ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATGTGTAACAGGGTCTCCCCT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTTTATTTTAAATTAGATTGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTTCATGAAGCTGAGTGGTGAGCACACCAGTGTTATATTCTCTCTATATAACTTTGT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCTGCTGCAGGCTGTGCTGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTT 212
                                                                            69;
                                                                           Conservative
                                                                                                                                                                                                                                                 Heinrich GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                      88GB-0026451
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93..904
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 6..92
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                                                                                    6.6%; Score 33; 53.5%; Pred. No.
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                                                                                                                                                                                                                                                 Schwander J;
                                                                           0;
                                                                           Mismatches
                                                                                             DB 11; Length 1214;
                                                                           60;
                                                                                                                                           It encodes the precursor
                                                                           Indels
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   165
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ID AAH088
                             В
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                           Sequence 573 BP; 169 A; 124 C; 107 G; 167 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                               Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH08825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 GCGCCGAGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 GCCCGGAGC 493
                                                                                                                                                                                                                                                                                                                                                               Isogai T,
 50.0%;
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary ctrand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises a teast 15 nucleotides; or (b) a combination CC complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the CC polynucleotide which comprises a 3'-end sequence, where the CC pligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence, and sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primer sets can be used in antisense therapy and CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers are also useful to AAH13628 and AAH13633 to AAH18742 represent human cDNAs sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; AAB92446 to AAH13632 to AAH13632 and AAH13639 to AAH13638. All of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID 5660; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
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Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K, Y
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Score 32.8; DB 22; Pred. No. 2.5;

Length 573;

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ARCSULT 7
AAMH15237
ID AAHH1
ACC AAHH1
ACC AAHH1
ACC AAHH1
ACC ACHH1
ACC ACH
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-OF primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1east 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers are useful for synthesising polynucleotides of the specification. The primers are useful for synthesising polynucleotides and the comprises at 1east 15 nucleotides and the combination of CC carticularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers also useful for the full-length cDNAs. The primers also worth the full-length cDNAs. The primers also worth to AAH13628 and CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH15237 standard; cDNA; 1952 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 13352; 2537pp + CD ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tull-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 TTAGGATGATCCTTGAAAGCCCTTTAGAAGGGTGCCATGTTGGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 TGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 TGGAGTTGCATCATACTCAGGGGTTAGCTTCCAAGGTCAGTACATAGGTAAAATGGGCTA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTTAAATTAGAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGTGATTTGATGCTGACGGGAGTGAGAGTAATGGCCTTATCCTGCTGCAGGCTGTGC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T, Hayashi K, (
1 T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
AAF16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY
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                                                                                                                                                                                                                                 Claim 1; Page 1091-1092; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000WO-US05988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF16216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TocaT
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1 Similarity 50.0%;
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                AAB57013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
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Pred. No. 5;
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AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1798 TTAGGATGATCCTTGAAAGCCCTTTAGAAGGGTGCCATGTTGGA 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1678 AAATTATACTGACAATATTATGGCATTTTTAAGATCATGGCATTTTAATTTACATTAGAG 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1952 BP; 547 A; 421 C; 385 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer antigen nucleotide sequence SEQ ID NO:651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1738 TGGAGTTGCATCATACTCAGGGGTTAGCTTCCAAGGTCAGTACATAGGTAAAATGGGCTA 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 TGAGGATGGCCTGGTCTGCCACCCTCCTCGAGTAGCATTTTGCA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTTAAATTAGAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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Best Local
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     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
12-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antioiflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antiscking; antianaemic; antiarthritic; cancer; anticheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidabetic; antiulcer; anticorvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nervous system related polynucleotide SEQ ID NO 12743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA20412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA20412 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1366 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
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     2000US-0179065
2000US-0184664
2000US-0186350
2000US-0198676
2000US-0199076
2000US-0199123
2000US-0209467
2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216887
2000US-0217487
2000US-0225214
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                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US01334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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Pred. No. 4.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; 327 G; 386 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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     14 - NUG - 2000
14 - NUG - 2000
14 - NUG - 2000
14 - AUG - 2000
14 - AUG - 2000
14 - AUG - 2000
22 - AUG - 2000
22 - AUG - 2000
23 - AUG - 2000
01 - SEP - 2000
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07 - CCT - 2000
08 - SEP - 2000
09 - SEP - 2000
00 - 20 - CCT - 2000
01 - SEP 
 2000US-0233063
2000US-0233064
2000US-0233064
2000US-0234274
2000US-0234274
2000US-0234284
2000US-0234894
2000US-0235836
2000US-02363637
2000US-02363636
2000US-02363636
2000US-02363703
2000US-02363703
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2000US-0237039
2000US-0237039
2000US-0241785
2000US-0241785
2000US-0241785
2000US-0241787
2000US-0241787
2000US-0246476
2000US-0246626
2000US-0246626
2000US-0246626
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2000US-0246526
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2000US-0225777
2000US-0225757
2000US-0225759
2000US-02256861
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2000US-02256861
2000US-0229344
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2000US-0229344
2000US-0239363
2000US-0239363
2000US-0231243
2000US-0231243
2000US-0231413
2000US-0231400
2000US-0231400
2000US-0231400
2000US-0232399
2000US-0232390
2000US-0232390
2000US-02323400
2000US-0232400
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein and issues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) Lumune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's chiese, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal cand parasitic infections, but was obtained in electronic format directly crom WIPO at ftp.wipo.int/pub/published_pct_sequences.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                              Sequence 32248 BP; 10625 A; 6481 C; 6425 G; 8717 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 12743; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-541565/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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-NOV-2000;
-NOV-2000;
-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-024929
2000US-0249300
2000US-0250391
2000US-0251039
2000US-0251030
2000US-0251030
2000US-0256719
2000US-0251479
2000US-0251868
2000US-0251869
2000US-0251869
2000US-0251990
2000US-0251990
2000US-0251997
2000US-0251997
2000US-0251997
2000US-0251997
 6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM;
 Score 32.6;
 DB 22;
 Length 32248;
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AAL37122/c ID AAL37122 standard; DNA; 32248 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AAATTAGATTGGTGTGATT 121
| | | | | | | | | | |
25852 CAATCTGCCTTTTGTCAGT 25870
                                                                                                                                                                                                                                                                                                                 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; mootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antifilammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US01338.
                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                             WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human musculoskeletal system related polynucleotide SEQ ID NO 3487
                                                                                                                                                                                                                                                                           2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-01846350.
2000US-0189874.
2000US-019872.
2000US-0198123.
                                                                                                                                          2000US-0220964.
2000US-0224518.
2000US-0224519.
2000US-0225213.
                                                                                                                                                                                               2000US-0214886.
2000US-0215135
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217487
                                                                                                                       2000US-0225266.
                                              2000US-0226279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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2000US-0237040
2000US-023935
2000US-023935
2000US-0229935
2000US-0240960
2000US-0241785
2000US-0241809
2000US-0241809
2000US-0241809
2000US-0246477
2000US-0246477
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2000US-0246477
2000US-0246477
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2000US-0246477
2000US-0246477
2000US-0246477
2000US-0246527
2000US-0246528
2000US-0246539
2000US-0246611
                                                     Дb
                                                                                    QΥ
                                                                                                                                                                                                  Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB030087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human trissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Cronh's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
10-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                     6457 TCTAAAGGCTCCTGTGTCATGAAAAAGTATGATTAGATCAATTTGTATGCCTTTTCTTCT 6398
                                                                                                                                                                                                  Sequence 32248 BP; 8717 A; 6425 C; 6481 G; 10625 T; 0 other;
                                                                                                                                                                                                                         parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 3487; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-451937/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen
103 AAATTAGATTGGTGTGATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                      43 TITATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA,
                                                                                                                             50;
                                                                                                                                          6.5%;
Similarity 63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
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2000US-024921

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2000US-024921

2000US-024921

2000US-024921

2000US-024921

2000US-024924

2000US-024924

2000US-024924

2000US-024926

2000US-024926

2000US-024926

2000US-024929

2000US-0250160

2000US-0250160

2000US-0250160

2000US-0251030

2000US-0251030

2000US-0251186

2000US-0251868

2000US-02511868

2000US-02511869

2000US-02511869

2000US-02511869

2000US-02511869

2000US-02511869

2000US-02511869

2000US-02511869

2000US-02511869
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                          0; Mismatches 29;
                                                                                                                                            Score 32.6;
Pred. No. 2
                                                                                                                                                           DB 22;
                                                                                                                          Indels
                                                                                                                                                         Length 32248;
                                                                                                                          0;
                                                                                                                          Gaps
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0,

01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
15-SEP-2000
15-SEP-2000
16-SEP-2000
16-SEP-2000
16-SEP-2000
17-SEP-2000
18-NOV-2000
18-NOV-2000
18-NOV-2000
18-NOV-2000
18-NOV-2000
18-NOV-2000
19-NOV-2000
19-NOV-2000
10-NOV-2000
11-NOV-2000

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RESULT 11

ARASZÓ

ID ARASZÓ

XX ARASZÓ

XX ARASZÓ

XX Human

XX Human

XX Human

XX Cereb

XX Cereb

XX Cereb

XX Color

XX II-JA

PR 31-JA

PR 31-JA

PR 14-AI

PR 1
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14 - AUG - 2000

15 - AUG - 2000

16 - AUG - 2000

17 - AUG - 2000

18 - AUG - 2000

19 - AUG - 2000

10 - AUG - 2000

22 - AUG - 2000

23 - AUG - 2000

20 - AUG - 2000

21 - AUG - 2000

21 - AUG - 2000

22 - AUG - 2000

23 - AUG - 2000

24 - AUG - 2000

25 - AUG - 2000

27 - AUG - 2000

28 - AUG - 2000

29 - AUG - 2000

20 - AUG - 2000

20 - AUG - 2000

20 - AUG - 2000

21 - AUG - 2000

22 - AUG - 2000

23 - AUG - 2000

24 - AUG - 2000

25 - AUG - 2000

26 - AUG - 2000

27 - AUG - 2000

28 - AUG - 2000

29 - AUG - 2000

20 - SEP - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungloide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; cerebral ischaemia; anglogenesis; occilar disorder; cerebral ischaemia; entitorior; ocular disorder; cerebral infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS26795 standard; DNA; 32248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunosuppressive; antiarthritic; ds; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genomic DNA encoding partial novel secreted protein, Seq ID 1769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS26795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155322-A2
                                                                                                         2000US-022526

2000US-022527

2000US-022547

2000US-022547

2000US-022575

2000US-022575

2000US-022687

2000US-022686

2000US-022686

2000US-022686

2000US-0227182

2000US-0227182

2000US-0227182

2000US-0228924

2000US-0228924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0179065
2000US-0184664
2000US-0184664
2000US-0186350
2000US-0198123
2000US-0198123
2000US-0205515
2000US-0205515
2000US-0215135
2000US-021684
2000US-021684
2000US-021684
2000US-021684
2000US-021689
2000US-0229344.
2000US-0229345.
2000US-0229509.
2000US-0229513.
                                                                                           2000US-0229343.
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     08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
13-CCT-2000

13-CCT-2000

20-CCT-2000

20-NOV-2000

20-CCT-2000

20-NOV-2000

20-NOV-2000

20-CCT-2000

20-NOV-2000

20-NO
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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2000US-023341413

2000US-023341413

2000US-023341413

2000US-0232081

2000US-023298

2000US-0233963

2000US-0233963

2000US-0233963

2000US-0233963

2000US-0233963

2000US-0233998

2000US-0233998

2000US-0233998

2000US-0234623

2000US-0234634

2000US-0236363

2000US-0236370

2000US-0236370

2000US-024674

2000US-024674

2000US-024677

2000US-0249211

2000US-0249211

2000US-0249211
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2000US-0230438.
2000US-0231242.
2000US-0231243.
2000US-0231244.
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Db
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                                                                                                                                                                                                               The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to CP prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility comes and so the proteins can also be used in alleviating symptoms associated with the disorders and in clud autoimmune diseases e.g. radioimmunoassays or enzyme linked conclude autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other colsorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to parallation, for supporting cell culture of primary tissues, to cregenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to regenerate tissues and in chemotaxis. The polypeptides can also be used cas a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present content of the invention.
                                                                                                                                                                    Query Match
Best Local :
25852 CAATCTGCCTTTTGTCAGT 25870
                                                                     25792 TCTAAAGGCTCCTGTGTCATGAAAAAGTATGATTAGATCAATTTGTATGCCTTTTCTTCT 25851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 DEC
01 DEC
05 DEC
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06 DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488783/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                  103 AAATTAGATTGGTGTGATT 121
                                                                                                   43 TTTATGGGAACATTTGTCAGGCAAAAGTATAATAATGGCAAACTCTACGCCTTTTATTTT 102
                                                                                                                                                                 Local
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0251989.
2000US-0251990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249218.
                                                                                                                                                             6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                              0;
                                                                                                                                                           Score 32.6;
Pred. No. 27;
                                                                                                                                              Mismatches
                                                                                                                                                                                   DB 22;
                                                                                                                                              29;
                                                                                                                                                                              Length 32248;
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0;

0;

Query Match Best Local Matches

60;

Conservative

0;

46;

Indels

0; Gaps

0;

Similarity

56.5%;

Score 32.4; DE Pred. No. 6.2; 0; Mismatches

DB 21; Length 1671;

Sequence 1671 BP; 481 A; 294 C; 325 G; 571 T; 0 other;

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RESULT 12
AAC79977/c
cc antiarthritts, antifreemmatic, antiproliferative, cytostatic, cardiant, corresponding, cerebroprotective, nootropic, neuroprotective, antibacterial, corvividae, fungicide, ophthalmological and vulnerary activity and can be used for gene therapy. (I) and (II) are used to prevent, treat or committee a medical condition in e.g. humans, mice, rabbits, goats, corresponding a pathological condition or succeptibility to a pathological condition. The antibodies to (II) and also be used in alleviating committees and in diagnostic immunoassays corresponding a pathological condition or succeptibility to a pathological condition. The antibodies to (II) can also be used in alleviating committees and in diagnostic immunoassays.

Cc e.g. radiolmmunoassays or enzyme linked immunosorbent assays (ELISA). Clisorders which are diagnosed or treated include autoimmune diseases committees and indiagnostic immunoassays.

Cc Disorders which are diagnosed or treated include autoimmune diseases.

Cc of the breast or liver, cardiovascular disorders e.g. cardiac arrest, correbrovascular disorders e.g. cardiovascular disorders e.g. cardiovascular ischemia, angiogenesis, nervous constitution, to supporting call culture of primary tissues, corresponding and continuous, to maintain organs before transplantation, for supporting cell culture of primary tissues, corresponding and continuous, to maintain organs before transplantation, for supporting cell culture of primary tissues, the organization and and titue or preservative to increase or decrease strong contents and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; treatment; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; ocular disorder; hyperproliferative disorder; nervous system disorder; neuron; skin aging; wound healing; epithelial cell proliferation; transplantation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )977/c
AAC79977 standard; cDNA; 1671 BP
                                                  capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel isolated nucleic acid molecules (I) encoding a human secreted proteins (II) which have immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim la; Page 357; 418pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted proteins, preventing, treating or ameliorating a disorder, e.g. Alparkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999; 99US-012650b
07-JAN-2000; 2000US-0174852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000WO-US07723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein encoding cDNA for gene 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC79977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
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DB; AAB45054.
                                                                            as a food additive or preservative to increase or decrease storage
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PR 01-SEP-2000; 2000US-0229344. PR 01-SEP-2000; 2000US-0229345.	PR 01-SEP-2000; 2000US-0229387. PR 01-SEP-2000; 2000US-0229343.	23-AUG-2000 30-AUG-2000	22-AUG-2000	22-AUG-2000	18-AUG-2000	14 - AUG - 2000 14 - AUG - 2000	14-AUG-2000	14-AUG-2000	14 - AUG - 2000	14 - AUG - 2000	14-AUG-2000	14-AUG-2000	14 - AUG - 2000	14-AUG-2000	26-JUL-2000	26-JUL-2000	14 - JUL - 2000	11-JUL-2000	07-JUL-2000	07-JUL-2000	28-JUN-2000	07-JUN-2000	19-MAY-2000	18~APR-2000	16-MAR-2000;	02-MAR-2000;	24-FEB-2000;	PR 31-JAN-2000; 2000US-0179065; PR 04-FRB-2000: 2000US-0180628.		PF 17-JAN-2001; 2001WO-US01240.	PD 02-AUG-2001.		PN W0200155302-A2.	OS Homo sapiens.	1	KW sigmoid disease; antibacterial; antiviral; antiinflammatory; KW cytostatic ds	intestinal inflammatory disorder; malabsorption syndrome; c	KW inflammatory bowel disease: IBD: neoplastic disorder: gene therapy:		DE Genomic sequence #306 encoding human colon associated polypeptide.	DT 17-DEC-2001 (first entry)		AC AAS39887;	ID AAS39887 standard; DNA; 5003 BP.	87/c	RESULT 13		Db 1138 ACAGGAGACAGTACTCCTTATAACTGGCTTTGGTTTTGAGTGATCT 1093	GCCTTTTATTTTAAATTAGATTGGT	Db 1198 ATGTTAGACTATTCACTAGGTACTGTAATATTCTTGTAGTTCTGAGGTGAAGGTAAACCA 1139	1/ ATTTGGACTATGCCTTGCATACAGCTTATGGGAACATTTGTCAGGCAAAAGTATAATA	
	PR 17-NOV-2000; 2000US-0249212. PR 17-NOV-2000; 2000US-0249213.	17-NOV-2000;	17-NOV-2000;	PR 17-NOV-2000; 2000US-0249207.	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	PR 08-NOV-2000; 2000US-0246525.	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	01-NOV-2000;	20-OCT-2000;	20-OCT-2000;	20-OCT-2000;	20-OCT-2000;	٠.	20-OCT-2000;	20-OCT-2000;	13-OCT-2000;	02-OCT-2000;	02-OCT-2000;	02-0CT-2000;	02-OCT-2000;	29-SEP-2000;	PR 29-SEP-2000; 2000US-0236368.	29-SEP-2000;	29-SEP-2000;	27-SEP-2000;	26-SEP-2000;	25-SEP-2000;	21-SEP-2000;	21-SEP-2000;	14-SEP-2000;	14-SEP-2000;	PR 14-SEP-2000; 2000US-0232400.	14-SEP-2000;	14-SEP-2000;	12-SEP-2000;	08-SEP-2000;	PR 08-SEP-2000; 2000US-0231414.	08-SEP-2000;	•• ••	08-SEP-2000;	R 06-SEP-2000;	R 05-SEP-2000;	05 - 255 - 3000

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Matches
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Best Local :
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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         AAS39888;
                                           AAS39888 standard; DNA; 5003 BP
                                                                                                                                            4856 TTGGGAGCTTTATTGAAATTGTATTAAATT 4827
                                                                                                                                                                                                                     Sequence 5003 BP; 1809 A; 870 C; 1047 G; 1277 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon including colon cancers and also testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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                                                                                                                                                                            78 TGGCAAACTCTACGCCTTTTATTTTAAATT 107
                                                                                                                                                                                                                                         TTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTCAGGCAAAAGTATAATAA 77
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2000US-0251030.
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2000US-0256719
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2000US-0250160
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2000US-0249217
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60.0%; Pred. No. 11;
ative 0; Mismatches
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2000US-02118290

2000US-0218290

2000US-022963

2000US-0224518

2000US-0224518

2000US-0225213

2000US-0225214

2000US-0225214

2000US-0225214

2000US-0225266

2000US-0225266

2000US-0225266

2000US-0225276

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2000US-0225275

2000US-0225757

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2000US-0233063
2000US-0233065
2000US-0233065
2000US-0234274
2000US-0234274
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2000US-0235488
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2000US-0240960.
2000US-0241221.
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2000US-0249244
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                  Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colit digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                                                                                                                                                                                4916
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                               WO200155314-A2
                                                                                                                                          Human digestive system antigen genomic sequence SEQ ID NO: 3834.
                                                                                                                                                                       05-NOV-2001 (first entry)
                                                                                                                                                                                                     AAK90258;
                                                                                                                                                                                                                                   AAK90258 standard; DNA; 5003 BP
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                                                       Homo sapiens.
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Similarity 60.0%;
54; Conservative
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0; Mismatches Score 32.4; Pred. No. 11;

Indels Length 5003;

0;

Gaps

0

colitis;

DB 22; 36;

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The present invention relates to the isolation of novel human colon cc associated polypeptides (AAU22701), and the cDNA and genomic sequences encoding for them. The sequences of the invention are useful cc in the diagnosis, treatment, prevention and/or prognosis of disorders cof the colon including colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities (e. g. atresia and stenosis), bacterial and viral infections, colitis, cc (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, cc (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, cc (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, cc (e.g. polyps and adenomas, intestinal obstruction and signoid diseases. Cc (e.g. lactose intolerance), intestinal obstruction and signoid diseases. Cc (e.g. lactose intolerance), intestinal obstruction and signoid diseases. The polynucleotides sequences of the invention can also be used in gene cc harapy. AAS39582-AAS40060 represent DNA sequences encoding for the covel human colon associated polypeptides of the invention. On the printed specification, but was obtained in electronic format directly from WIPO cat first part of the printed specification, but was obtained in electronic format directly from WIPO cat first part of the printed specification, but was obtained pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5003 BP; 1810 A; 870 C; 1046 G; 1277 T; 0 other;
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2000US-0251876.
2000US-0251868.
2000US-0251868.
2000US-0251869.
2000US-0251989.
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2000US-0251997.
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220000			26-JUL-2000; 2000US-022963. 14-AUG-2000; 2000US-022964. 14-AUG-2000; 2000US-0224518. 14-AUG-2000; 2000US-0224519. 14-AUG-2000; 2000US-0225213. 14-AUG-2000; 2000US-0225266. 14-AUG-2000; 2000US-0225266. 14-AUG-2000; 2000US-0225267. 14-AUG-2000; 2000US-0225268. 14-AUG-2000; 2000US-0225268. 14-AUG-2000; 2000US-0225269. 14-AUG-2000; 2000US-022577. 14-AUG-2000; 2000US-0225759.	
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(HUMA-) HUMAN GENOME SCI INC. ROSEN CA, Barash SC, Ruben SM; WPI; 2001-502630/55.			8 - NOV - 2000; 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2	1000; 2000US-0236369 2000; 2000US-0236370 2000; 2000US-0236802 2000; 2000US-0237037 2000; 2000US-0237039 2000; 2000US-0237039 2000; 2000US-0239036 2000; 2000US-0241937 2000; 2000US-0241785 2000; 2000US-0241785 2000; 2000US-0241785 2000; 2000US-0241785 2000; 2000US-024184617 2000US-0244617

Disclosure; SEQ ID NO 3834; 986pp; English. Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - $\,$

The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.

Sequence 5003 BP; 1809 A; 870 C; 1047 G; 1277 T; 0 other;

Matches Query Match Best Local S tch 6.5%; al Similarity 60.0%; 54; Conservative (Mismatches Score 32.4; DB 22; Pred. No. 11; 36; Indels Length 5003; Gaps

0;

δÔ 18 TTTTGGACTATGCCTTGCATACAGCTTTATGGGAACATTTGTCAGGCAAAAGTATAATAA 77

DЪ

Ş Db 4856 TTGGGAGCTTTATTGAAATTGTATTAAATT 4827 78 TGGCAAACTCTACGCCTTTTATTTTAAATT 107

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Sequence 11, Appl
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Sequence 17, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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US-08-379-580-3
US-08-379-580-3
US-08-276-852-156
US-08-299-575-170
US-08-899-575-170
US-09-103-840A-2
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                                                                                                                                                                                            Sequence 20, Appli
Sequence 20, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 170, App
            Sequence 3, Appli
Sequence 7, Appli
Sequence 156, App
Sequence 155, App
Sequence 155, App
Sequence 170, App
Sequence 170, App
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Sequence 171, Appli
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US-09-043-937A-3
IS-quence 3, Application US/09043937A
PATENT NO. 6211432
PATENT INFORMATION:
APPLICANT: BOUDET, ALAIN-MICHEL
PICHON, MAGALLE
PICHON, MAGALLE
APPLICANT, JAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 0 0 0 0 0 0 0 0
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                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                   COMPOUTER: IMP PC COMPACIBLE
COMPETER: IMP PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-UL1-1998
CLASSIFICATION NUMBER: WO PCT/FR96/01544
FILING DATE: O3-OCT-1995
APPLICATION NUMBER: FR 95.11623
FILING DATE: O3-OCT-1995
APPLICATION NUMBER: 36.663
REFERENCE/DOCKET NUMBER: 1487-20
TELEPHONE: 703-816-4000
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ABLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMAS, PASCAL
BRIAT, JEAN-FRANCOIS
BRIAT, JEAN-FRANCOIS
TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-COA
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRIMA-PETTENATI, JACQUELINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BECKERT,
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US-08-437-607A-1
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US-08-437-607A-2
US-08-437-607A-2
US-08-457-179-109
US-09-18-10-88-3
US-09-816-98-3
US-08-455-35A-14
US-08-455-35A-14
US-08-655-227-17
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US-08-655-21-17
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US-09-144-759-19
US-09-144-759-19
US-09-144-759-19
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NAME/KEY: CDS
LCCATION: 195..1310
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-043-937A-3
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                                                                                            NAME: FUGIT, Donna R.

REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-847-7166
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2
Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: You, Oimin M.
APPLICANT: You, Oimin TITLE OF INVENTION: Identification of a DNA Region
TITLE OF INVENTION: Potentially Useful for the Detection of Mycobacterium
TITLE OF INVENTION: Ransasii
NUMBER OF SEQUENCES: 20
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 GCGCGTGCAGGGCTGCCAGGGGGTCTTCCACACCGCCTCCCCCGTCACCGACGACCGGG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 AAACCAGGAACTGGTACTGCT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 AGCCCGCGGGTTCCTGCTGAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658 AGCGCGGGCCCGACGTCGTGGTCGACGACGTCCTGCGAGCCTCGAGTTCTGCGAGA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 AGCTAGAGCCCAGGCAGACTGTGAATGCGACCTGTTCGAGAGAACTCATCAGGTGCGAGA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 CCGGCACGGTGCGGCGGGTGTTTCACGTCGTCCATCGGCGCCGTGACCATGGACCCCA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 GTTGCGAGGGGCGGACCAAGCCCCAACCCCGGGGAATCCGAGCAGGTATATAAGGGGCCC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 AGCAAATGGTGGAGCCGGCGGTGCGCGGCGCGCGGCGAGG 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                        TOPOLOGY:
                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07417-6800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
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                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
                                     linear
               DNA (genomic)
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V: 435
                                                            double
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RESULT 3
US-09-336-039-20/c
US-09-336-039-20/c
Sequence 20, Application US/09336039
Patent No. 6391176
Patent INFORMATION:
GENERAL INFORMATION:
You, Qimin
You, Qimin
Ž
                  Query Match
Best Local Similarity
Conserva
                                                                                                                                 ORGANISM: Mycobacterium gastri; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-336-039-20
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US-08-937-580-20
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                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 311 base pairs
203 CCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGGGCGTGGGGTGAACGAAAGGGCT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 CCGTAGGCATTTCGACCGCGGGATGGCGATCAGGAGCAGCCTTGGGACCAGCCGACGCGTT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 CCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGGGCGTGGGGGTGAACGAAAGGGCT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 CATCAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 CCCGAACTTTTTTTTTTCCAGCCAGGCCGAACGGGGCTCGGTAATGATTGGCCAGGGCG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CATCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 ACCCGAGTTCGTCGCCGCCACCGACGCCGACCCGTCGATGGCTGACGCATGGCTGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/937,580
FILING DATE: 25-5EP-1997
ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 9-3690/5510-13
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-847-7166
TELEPAX: 201-848-9228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/336,039
FILING DATE: 18-Jun-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOU, Qimin
TITLE OF INVENTION: Identification of a DNA Region
Potentially Useful for the Detection of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
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Similarity 53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                            Conservative
                                         6.3%; Score 31.6; DB 4; Length 311; 53.2%; Pred. No. 0.36; ative 0; Mismatches 59; Indels
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-847-7166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-848-9228 INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of a DNA Region
TITLE OF INVENTION: Potentially Useful for the Detection of Mycobacterium
TITLE OF INVENTION: kansasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harris, James M. APPLICANT: You, Qimin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                 148 CCGTAGGCATTTCGAYCGMGSKATGGCGRTCARGAGCAGCCWGGGACCAGMRSMCGCGTT 89
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                                                                                                                                                                                                         203 CCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGGGCGTGGGGGTGAACGAAAGGGCT 262
                                       323 CATCAC 328
                                                                                                                     263 CCCGAACTTTTTTTTTCCAGCCAGGCCGAACGGGGGCTCGGTAATGATTGGCCAGGGCG 322
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/937,580 FILING DATE: 25-SEP-1997 CLASSIFICATION: 435
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28 CATCGC 23
                                                                                   88 ACCCGAGTTCGTCGCCGCCACCGACGCGACCCGTCGATGGCYGACGCATGGCTGGGCCG 29
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium gastri and Mycobacterium ORGANISM: kansasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                   Match 6.0%;
Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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E: DNA (genomic)
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RESULT 5
US-09-19/c
US-09-356-039-19/c
; Sequence 19, Application US/09336039
; Patent No. 6291176
; GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-336-039-19
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
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                                                             RESULT 6
US-09-103-840A-1
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Best Local S
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NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 93690/5510-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-847-716
TELEPHONE: 201-849-928
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            323 CATCAC 328
                                                                                                                                                                                                                                                                                                                              148 CCGTAGGCATTTCGAYCGMGSKATGGCGRTCARGAGCAGCCWGGGACCAGMRSMCGCGTT 89
                                                                                                                                                                                                                                                                                                                                                                       203 CCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGGGCGTGGGGGTGAACGAAAGGGCT 262
                                                                                                                                                                                                                                                                                263 CCCGAACTTTTTTTTTTCCAGCCAGGCCGAACGGGGGCTCGGTAATGATTGGCCAGGGCG 32
                                                                                                                                                   28 CATCGC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.0%;
Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/336,039
FILING DATE: 18-Jun-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07417-6800
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
CORDENCESE: Becton Dickinson and Company
STREET: 1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YOU, Qimin
TITLE OF INVENTION: Identification of a DNA Region
Potentially Useful for the Detection of Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/937,580 FILING DATE: 25-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium gastri and Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 311; Pred. No. 1.2;
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OY 316 CAGGGCGCACCACTGCGAACCTGCTCAATCACGGGCTCCGCGGTTGCGAAGGGCGGACCA 375
Db 2151568 CAGGACGCAGCCCGGTAATCGTCTCAATCACTGCCGCCTCGGGCAGCCGTGGTTGTATGC 2151627
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LENGTH: 4411529
TYPE: DNA
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE OF INVENTION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00772
FILING DATE: 28-JUL-1993
PRIOR APPLICATION UNBER: FR 92/09433
PRIOR APPLICATION UNBER: FR 92/09433
FILING DATE: 03-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith Julie K. 619
REGISTRATION NUMBER: ST92049-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2151688 CAGGGA 2151693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tocque, Bruno
TITLE OF INVENTION: Peptides Inhibiting Ras Protein
TITLE OF INVENTION: Activity, Preparation and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Duchesne, Marc
APPLICANT: Schweighoffer, Fabien
APPLICANT: Tocque, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AGCCCCAACCCCGGGGAATCCGAGCAGGTATATAAGGGGGCCCAGCTAGAGCCCAGGCAGA 435
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                                                                                                                                                                                                                                                                                 FILING DATE:
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52.4%;
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US-08-190-687B-7
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Best Local
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  APPLICATION NUMBER: 07/74,644
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-198
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
PRICETORY NUMBER: 07/210,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Clair,
APPLICANT: Clair,
APPLICANT: GAP Genc.
TITLE OF INVENTION: GAP Genc.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun GTREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (610)454-3839
TELEPAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                     REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
07/774,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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CANT: Wong, Gail L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; 1 Similarity 70.9%; 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
1.,1548
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linear
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)N: 435
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                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-276-852-156
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                                                                                                                                                                                                                                                                                                           PILING DAVID. 514
CHASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
PILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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                                      Query Match
      Matches
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                                                                                                                   TELEFAX: 619-554-6312
INFORMATION FOR SED ID NO: 156:
SEDUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
TODRICORY. columnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                            NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla CITY: La Jolla CITY: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 92037
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les 39; Conservative
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Match 5.9%;
Local Similarity 50.3%;
ses 72; Conservative
                                                                                                           TOPOLOGY:
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119..3259
                                                                                                           circular
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0; Mismatches
  Score 29.4; DI
Pred. No. 11;
0; Mismatches
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                                    DB 1;
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      71; Indels
                                    Length 13254;
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      0;
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RESULT 10
US-08-276-852-170
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Patent No. 5652138

GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Berner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                       Matches
                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
4287 GGGCAGGCATGACCTCAGCATTTGTTCCTGTAATCTTGACCCCAGCATACAAGCAGGCGC 4346
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8908 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCCACACCACACAGTAAT 8849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8848 ACGGACCTTGGGGCCCAGGAAAG 8826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA COUNTBY.
                                                                                                                                                                                                 MOLECULE TYPE:
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                       116 GGGGGGTCACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCT 175
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                            5.9%;
Similarity 50.3%;
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                                                                                       Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                 DNA (genomic)
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                                                                                     Score 29.4; Di
Pred. No. 11;
0; Mismatches
                                                                                                                                 DB 1; Length 13254;
                                                                                          71;
                                                                                          Indels
                                                                                          0;
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176 CTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAA 235

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                                                                                                                                                                         Query Match
Best Local Similarity
Matches 72; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                              TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: quable
    8908 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCACACCACCACAGTAAT 8849
                                                                                    8968 GGGCAGGCATGACCTCAGCATTTGTTCCTGTAATCTTGACCCCAGCATACAAGCAGGCGC 8909
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FITTING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: PLOY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NAME: US 08/276,852
FILING DATE: 18-UIL-1994
APPLICATION NUMBER: US 08/178,302
REPRINCE NUMBER: US 08/178,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4407 ACGGACCTTGGGGCCCAGGAAAG 4429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                        116 GGGGGGTCACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCT 175
                                           176 CTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 GAGGGGCGTGGGGTGAACGAAAG 258
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                    circular
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N: 435
                                                                                                                                                                                       5.9%;
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                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                          Score 29.4;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCR1452P
                                                                                                                                                                                                           DB 1; Length 13254;
                                                                                                                                                               71; Indels
                                                                                                                                                                  0; Gaps
                                                              Db
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                                                                                                                                              Db
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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUU-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA: US 07/954,148
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
                                                                                                                                              4287 GGGCAGGCATGACCTCAGCATTTGTTCCTGTAATCTTGACCCCAGCATACAAGCAGGCGC 4346
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APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                            4347 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCACACCACACAAGTAAT 4406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8848 ACGGACCTTGGGGCCCAGGAAAG 8826
                                                                                                                                                                    116 GGGGGTCACCTCCTCAGGTTTCGTTCCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCT 175
236 GAGGGGCGTGGGGTGAACGAAAG 258
                                                                                                     176 CTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GAGGGGCGTGGGGTGAACGAAAG 258
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fitting, Thom REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 24-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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                                                                                                                                                                                                                              Local Similarity es 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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CA
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E: Patent Counsel
10666 No. 5770440th Torrey Pines Road, Suite 220,
                                                                                                                                                                                                                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas
                                                                                                                                                                                                                                               5.9%; Score 29.4; DB 1; Length 13254; 50.3%; Pred. No. 11;
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                                                                                                                                                                                                                            0; Mismatches 71; Indels
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4407 ACGGACCTTGGGGCCCAGGAAAG 4429

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                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-011.
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 156, Application US/08899575 Patent No. 5804440
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
                                                                            8908 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCACACCACCAGTAAT 8849
                                                                                                                                                        8968 GGGCAGGCATGACCTCAGCATTTGTTCCTGTAATCTTGACCCCAGCATACAAGCAGGCGC 8909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-SEP-1992 ATTORNEY/AGENT INFORMATION:
8848 ACGGACCTTGGGGCCCAGGAAAG 8826
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                               176 CTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAA 235
                                                                                                                                                                                116 GGGGGGTCACCTCCAGGTTTCGTTTCAAACTTTTTGAAACCCTAATTGGTGGCCT 175
                                  236 GAGGGGCGTGGGGTGAACGAAAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10666 NO. 5804
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 24-JUI
                                                                                                                                                                                                                                Local Similarity 50.3 es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92037
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VENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
VENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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UMBER: US 08/178,302
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24-JUL-1997
                                                                                                                                                                                                                                                                                                                              DNA (genomic)
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Carlos F
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US-08-899-575-170
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                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
SEQUENCE 13254 base pairs
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CITY: La JOlla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lerner, TITLE OF INVENTION: TITLE OF INVENTION:
4407 ACGGACCTTGGGGGCCCAGGAAAG 4429
                                                                          4347 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCACACCACACTAAT 4406
                                                                                                                                                     4287 GGGCAGGCATGACCTCAGCATTTGTTCCTGTAATCTTGACCCCAGCATACAAGCAGGCGC 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 0:
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                                236 GAGGGGCGTGGGGTGAACGAAAG 258
                                                                                                               176 CTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAA 235
                                                                                                                                                                           116 GGGGGTCACCTCCTCAGGTTTCGTTTCCAAACTTTTTGAAACCCTAATTGGTGGCCT 175
                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: doub
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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E: Patent Counsel
1016 No. 5804440th Torrey Pines Road, Suite 220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08899575
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170
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Carlos F
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                                                                                                                                                                                                                             Score 29.4; DB 1; Length 13254; Pred. No. 11; 0; Mismatches 71; Indels 0;
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PCT-US95-08743-156/c

Sequence 156, Application PC/TUS9508743

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RESULT 15

GENERAL INFORMATION:

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APPLICATION

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patcentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08743

FILING DATE: 11-JUL-1995

PRIOR APPLICATION NUMBER: US 08/276,852

FILING DATE: 18-JUL-1994

INFORMATION FOR SEQ ID NO: 156:

SEQUENCE CIGRACTERISTICS:

LENGTH: 13254 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

PCT-US95-08743-156
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Search completed: October 10, 2002, 18:44:40 Job time: 1790.73 secs
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                                                                                                                                                                                                                                                                       8848 ACGGACCTTGGGGCCCAGGAAAG 8826
                                                                                                                                                                                    8908 GGTAGTGAGCCTCCACGATATCCCTGCCATAGGCTTTGTCTGCGCCCACACCCACACTAAT 8849
                                                                                                                                                                                                                 176 CTGAGTGGGCCTCGTGGACTCCCGAGCTCAGTAACTCTTACCACGTCACTCAGGCCAAA 235
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                         Score
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43.2
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    Maximum Match 100%
Listing first 45 s
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AI048408
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CNS0091P
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                                                                                               AI046981 uh53d05.r
AL214492 Tetraodon
BB785045 BB785045
AI635942 tz28d09 x
BE115984 UI-R-BS1-
AI322516 mh62e08 y
                            AL054018 Drosophil
AZ187858 SP_1010_A
BE118654 UI-R-BS1-
AL053013 Drosophil
BE376636 CM3-TN006
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AI048408 uh55g06.r
AL107216 Drosophil
AZ557857 RPCI-23-2
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BB809337
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VERSION
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BB619413
LOCUS
                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 632)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Tahii, Y., Tto, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., D., Shibata, K., Shinagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Uppublished (2001)
Uppublished (2001)
Contact: Yoshihide Hayashizaki
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konro,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
Tel: 81-45-503-9216
Fax: 81-5-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB619413 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730543H16 5', mRNA sequence.

BB619413
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB619413.1 GI:16458774
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1132
305
466
645
811
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297
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AI503776
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AW009306
AQ741137
CNS006NE
BM415169
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BB809337
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AL053013 brosophil
AL065132 brosophil
AL266926 Tetraodon
BB551914 BB551914
AL503776 vm12c06.x
BH179653 015_G_08-
AL616605 T7 end of
B1645296 OP3151 Mi
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ALIO6054 brosophil

BF402451 UI-R-CA0-

AW009306 ws80f02.x

AQ741137 HS_2273_A

ALO65584 brosophil

BM415169 OP20241 M

AG04384 pan trog1

ALO74642 brosophil

BG076658 H3004C01-
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AL477266 clone BA0
BB60937 BB809337
AI324665 ms63a02.x
AL101589 Drosophil
AL053474 Drosophil
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BG561670 EtESTed98
BG324697 602422671
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 GACTT 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CTGCGAATGCGACCAGCTCGAGAGAACGCATCAGGTGAGAAGACCCGCGAGTTCCCCGCC 64
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 528)
                                                                                                                                                                                                                                                                        AI048408 528 bp mRNA linear EST 08-JUL-199 uh55g06.rl Soares_embryonic_stem_cell_NMES Mus musculus cDNA clone IMAGE:1749370 5' similar to gb:X71137 SOX-9 PROTEIN (HUMAN);, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                      AI048408.1 GI:3296695
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. Ist strand CDNA was primed with a primer [5'
GAGAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTVN 3'], CNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGTTCGGGGTTAATTAATTCGCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

09 a 226 c 210 g 85 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="5730543H16"
/clone_ib="RIKEN full-length enriched, 8 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex~"mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
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                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACCGGGCAGGCTTCCCGGGCAAGCTGCGACTCGACCAGCTCGAGAGAACGCATCAGGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                 AL10721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                              CNS016UE 1101 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16G16 of DrosbAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
                                                                                                                                                                                       Drosophila melanogaster
                                               Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                 AL107216.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                               fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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314 286 1810
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                                                                                                                                                                                                                                                                                                           genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/73 vector. Library went through two rounds of normalization, and was constructed by Bento Nodes and M.Fatima Bonaldo."

a 191 c 177 g 67 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="tMAGE:1749370"
/clone_lib="Soares_embryonic_stem_cell_NMES"
/cell_type="embryonic stem cell"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                              GI:5626210
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Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GTGAACGAAAGGGCTCCCG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 CCTCAGGTTTCGTTCCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAGTGGGCCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869 CKBGYSTGGSGGGSSCSSCSCCSCTGBGCSBSYYBCCKGGKKGGGKKKGGYGTTTTGSCC 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809 GGGGSGGSGSCTSTGCYTSCCKTSCGCGTSGTKTTGKGKTCCCCCCTSYACCCCCCHSSC 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                    Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                         Unpublished (1999)
Other_GSSs: RPCI-23-205J6.TV
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are allability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 467)
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="pBACN16G16"
/note="end: T7"
a 170 c 171 g
                                                                                                                                                                                                                                                                                         Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
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                                                                                                                                                                                                                                                                                                             Mus musculus
    Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                    The WashU-HHMI Mouse EST Project
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/strain="C57BL/6J"
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1. .467
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/clone="RPCI-23-205J6"
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BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (lnfo@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 205 row: J column: 6 Seq primer: SP6 Class: BAC ends.
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/note="Organ: Kidney/Brain: Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).

DB 12; 96; Indels Length 467; 0; Gaps 0

167 TGGTGGCCTCTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCAC 226 360 TGTTATGGACATTCTGGCTGGCATACCCGTTCCCTACCCCAAACTTTCTAGCCTAGGGAT 301 47 TGTTTTCTAAATTCCGAAGCGCCCCTCTGCCCCCTCCCCCAATCTGCCTTGCGTCGGGGG 106 TGCTGGCCTCTTGCTTGGACTCTTGGTCTCCTGGCTTCTTGGTCTCCAGGCCCTCTTCTC 181 TGGGCTGAGTCTCCTTCACCCAGCATCTCTGATTCCTGTAGAACCTAGCCATTTCGATTA 241 TGGGGGGTGGGGGGTCACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAAT 166

uh53d05.rl Soares_embryonic_stem_cell_NMES Mus musculus cDNA clone IMAGE:1749129 5' similar to SW:SOX3_HUMAN P41225 SOX-3 PROTEIN. ;, mRNA linear EST 08-JUL-1998

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 61)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

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REFERENCE
AUTHORS
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Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota, Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Netazoa; Chordata; Teleostei; Buteleostei; Neoteleostei
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                                                                                                                                       Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernott, A., Fizames,C., Wincker,P., Brottler,P., Quetler,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                 Genoscope
                                                                                                                                                                     Unpublished
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; genome survey sequence.
                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1000)
Roest-Crollius, H., J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1000)
Roest-Crollius, H., Ji
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/clone=lb="Soares_embryonic_stem_cell_NMES"
/cell_type="embryonic stem_cell"
/lab_host="DH10B"
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                                                Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,C., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tayaku-Akhilira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB785045 RIKEN full-length enriched, Nullipotent stem cell CR NE CDNA Mus musculus cDNA clone G430100E18 3', mRNA sequence. BB785045
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 461)
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http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
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/clone="157C22"
/clone=1ib="G"
/note="Genoscope sequence ID : COAG167BB11LP1-end : T7"
/ note="Genoscope sequence ID : COAG167BB11LP1-end : T7"
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Pred. No. 4.1;
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cem cell CRL-2070
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RESULT 8
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67; Conserv
                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1430 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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                                                                                                                                                                                                High quality sequence stop: 313.
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/clone=lib="RIKEN full-length enriched, Nullipotent stem
cell CRL-2070 NE CDNA"
/cell_type="Nullipotent stem cell"
/cell_tine="CRL-2070 NE"
adenocarcinoma, 3 pooled tumors
                           /clone="IMAGE:2289905"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
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                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.6;
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.ulowa.edu
The sequence contained an ollgo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tay present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized embryo at 13 dpc library cDNA Library Preparation: M.B
soares Lab Clone distribution: colones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 1-85, >(GAA)
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Rattus norvegicus
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UI-R-BS1-axy-c-02-0-UI.sl UI-R-BS1 Rattus norvegicus cDNA clone
UI-R-BS1-axy-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Iowa City, IA 52242, USA
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                                                                                                                                                                                                                                                                                                                                                             primer: M13 Forward
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319 335 9565
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/note="Organ: utorus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.85 kb. Life Technologies catalog #
11539-012"
/dev_stage="embryonic 13 dpc"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Reg (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BS1
library is derived from 13 dpc whole embryo tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BS1-axy-c-02-0-UI"
/clone_lib="UI-R-BS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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Pred. No. 10;
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catalog #:
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AI322516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 TCAGACGGTTCTTTTGCTTTTCTGTCTTGGCTAACTCCTTGGCCAGCTCTGAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAGTGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 AGCGCTTCGCTGGACTCGCCCTCACCCTTTCGGACTTTGGAGGGTTTTTTCTGGGGGGCTTC 219
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Local Similarity 53.8%;
es 77; Conservation
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                                                                                                                                                                                                                                                                                             High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   MGI:272446
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                           correct orientation)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 to 658; 1 to 658; Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMACE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project Unpublished (1996)
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TAG_TISSUE=embryo at 13 dpc
TAG_SEQ-AATCC"
TAG_SEQ-AATCC 117 g 188 t
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:45558"
                                                                                                                      /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
                                                /lab_host="DH10B"
                                                                     /dev_stage="adu]
                                                                                              /tissue_type="placenta"
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Pred. No. 11
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Best Local
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746 ARAKTKTTTGGCCAAWGCTCGDSGGGACCCCCCCCCCCCCCCCCCCCCCCCCCCCGGGGGG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 CGAGAGAACTCATCAGGTGCGAGAAGCCCGGGGTTCCTGCTGATTT 500
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                                                                                                                                                                                                                                                                                                                                                                                                              AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 777)
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a 240 c 217 g 77 t 2 others
                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                          /clone_lib="RPCI-98"
/clone="BACR20M21"
                                                                                                                                                                                                                        /note="end : T7"
128 c 154 g
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                                                                                             7.5%; Score 37.4; I
46.7%; Pred. No. 12;
Live 19; Mismatches
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Pred. No. 12;
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Survey sequence T7 end of BAC #
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                                                                                                                                                                                                                         581 GGGGGGGGG 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus.
Eukaryota, Metazoa, Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ187858 764 bp DNA linear GSS 30-AUG-2000 SP_101.AZ_E09_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1010 Col=18 Row=I, DNA sequence.
BE118654 415 bp mRNA linear E UI-R-BS1-azr-c-02-0-UI.sl UI-R-BS1 Rattus norvegicus UI-R-BS1-azr-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ187858
AZ187858.1 GI:8371037
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Class: BAC ends
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California Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 764.
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514–9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A sea urchin genome project: Sequence scan, virtual map, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=1010 Col=18 Row=I"
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                                                                                                                                  280 GCCTCCTTGGNCCCCTCTTCCAA 302
                                                                                                                                                                                           184 GCCTCGTGGACTCCCGCCTCCTA 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discovery
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Rattus norvegicus
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BE118654.1 GI:8510759
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Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/lab_host="hell08 (Life Technologies)"
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/note="vector: pT73D-Pac (Pharmacia) with a modified
/note="vector: pT73D-Pac (Pharmacia) with a modified
/note="vector: pT73D-Pac (Pharmacia) with a modified
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TAG_LIB=UI-R-BS1
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/clone_lib="UI-R-BS1"
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/db_xref="taxon:10116"
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611 SGMSSSVSSSGGRSSGSGGGGGGGGGGGGGSGSSGSGSGS 575
                                                                       460 AACTCATCAGGTGCGAGAAGCCCGCGGGTTCCTGCTG 496
                                                                                                                                                  400 CAGGTATATAAGGGGCCCAGCTAGAGCCCAGGCAGACTGTGAATGCGACCTGTTCGAGAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 CCAGCCAGGCCGAACGGGGCTCGGTAATGATTGGCCAGGGCGCATCACTGCGAACCTGT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              850 SCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASHSSSSACBS 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CCCTAATTGGTGGCCTCTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's and was constructed by the Ibrary and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be training the strain project of the BDGP from the same strain project of the same strain beautiful and the provided by the BDGP from the same strain used for the BDGP's produced the properties of the same strain used for the BDGP's produced by the BDGP from the same strain used for the BDGP's produced by the BDGP from the same strain used for the BDGP's produced by the BDGP from the SDGP from the BDGP from the BDG
                                                                                                                                                                                                                                                                                                    CAATCACGGGTCCTCCGGGGTTGCGAGGGGGGGCCGACCCCAACCCCCGGGGAATCCGAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSSSSMSTSSSNSSBCSSCSSSBSSSSSTSSMSSSSBSSSSGSSSSSSGTSSACVKCNASS 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukarýota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[bases 1 to 925]
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/db_xref="taxon:7227"
/clone_lib="RpCI-88"
/clone="BACR19D16"
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153 TTTCTCTTGAACCTCTACCTCTCTACCACCATTACCACCTCTC 196
                                            183 GGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCAC 226
                                                                                                                                             123 CACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAGTG 182
                                                                                                    93
                                                                                                                                                                                                                      Local
                                                                                                 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-TN0068-140800-286-907&t3=2000-08-14&t4=1)
Seq_primer: puc_18_forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 196.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvelho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF376636 196 bp mRNA linear EST 24-NOV-200 CM3-TN0068-140800-286-g07 TN0068 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions." 67 c 28 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: testis_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
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Search completed: October 10, 2002, 20:28:03 Job time: 702.733 secs

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Result
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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1989.DAT:
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AAX59273
AAS64084
ABI99331
                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compugen Ltd
                                                                                                                                                                  Description
                                              Human
Human
Human
                Human immune/haema
Human prostate cDN
                                                                                  Human polynucleoti
Human bone marrow
                                                                                                                 Human small cell I
 Mouse
prostate c
ischaemic
                                              polynucleoti
adenosine Al
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AAD11118
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                                                                 21-JAN-2000; 2000US-0489101.
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD11118;
                                                                                                   19-JAN-2001; 2001WO-US02015.
                                                                                                                                    26-JUL-2001.
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Drosophila melanog	ABL11612	23	4216	6.0	30	5
	AAH16206	22	2798		30	4
Drosophila melanog	ABL11613	23	2078		30	ω̈
æ	AAH68564	22	1520		30	2
Human cDNA clone (AAH06402	22	811		30	
Reference sequence	AAS19906	24	20445	•	30.2	ö
Sequence of skc st	o	6	2568		30.2	39
Propionibacterium	AAS59570	23	6779	6.1	30.4	8
Klebsiella sp. nit	AAQ80198	16	1278		30.4	37
Human immune/haema	AAK78859	22	14175		30.6	36
DNA encoding novel	AAS27814	22	14175	•	30.6	5
Drosophila melanog	ABL21296	23	11470	6.1	30.6	4
Drosophila melanog	ABL21297	23	3481		30.6	ü
Human N-copine hom	ABA08650	22	2202		30.6	ະ
Maize cinnamoy1-Co	AAX25211	20	1559		30.6	μ
Human nervous syst	ABA14411	22	16329		30.8	ö
Human immune/haema	AAK83830	22	4758		30.8	9
Megakaryocyte stem	AAQ86236	16	4548		30.8	8
Megakaryocyte stem	AAQ86237	16	4500		30.8	27
Human diagnostic a	AAS31013	22	2476		30.8	86
Human ISRE-binding	AAA08502	21	2033	6.2	30.8	5
Human secreted pro	ABA83314	22	1950		30.8	4
Human secreted pro	AAV84531	20	1950		30.8	ພ
Human cancer relat	AAS59169	22	387	•	30.8	2
Human secreted pro	AAC11389		197		30.8	2
-	AAK73863		21888	•	31	õ
Human breast cance	AAL15317		985		31	9
Human nervous syst	ABA14807		12710	•	31.2	8
coding	AAS64368		646	•	31.2	7
Human breast cance	AAL15399		994		31.6	9
Rice apoptosis ind	AAF30438		1623		31.8	5
Human foetal cDNA,	\sim		1177	•	32	4
-	AAT94535		1556		2	ω
_	AAK83469	22	16161	•	N	ฉ
immune/	46	22	16106	o.5	32.4	Ξ
Human breast cance	AAL16674	22	554		32.4	0

ALIGNMENTS

AAD11118 standard; DNA; 2509 BP.

24-SEP-2001 (first entry)

Human small cell lung cancer associated gene, SOX3.

Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; lelmyosarcoma; synovial sarcoma; cytostatic; SOX3; ds.

Location/Qualifiers 441..1773 /*tag= a /product= "Human SOX3 protein" /*tag=

WO200153349-A2.

(LUDW-) LUDWIG INST CANCER RES. (SLOK) SLOAN KETTERING INST CANCER RES (CORR) CORNELL RES FOUND INC.

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RESULT 2
AAS87738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCIC-9, encoding human SOX3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encode isolated nucleic acid comprising an NA Group 3 or 4 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2509 BP; 456 A; 818 C; 757 G; 478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 57; Page 98-99; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAE05813.
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                                                                   481
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                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTCACCTCCTCAGGTTTCGTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGGCCGGGGGATGGGGCCCGGTCTGCCTTGACAGGGTTGCAAAGTTGTTTTCTAAATTC 60
                                                                                                                                                                                                                                                                  TGGGCCTCGTGGACTCCCCGCCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGG
                                                                                                                                 TAGAGCCCAGGCAGACTGTGAATGCGACCTGTTCGAGAGAACTCATCAGGTGCGAGAAGC
                                                                                                                                                                  TAGAGCCCAGGCAGACTGTGAATGCGACCTGTTCGAGAGAACTCATCAGGTGCGAGAAGC 480
                                                                                                                                                                                                                                                                                                                                                      TGGGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCACCTCCTCAGGTTTCGTTCCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCCGGGGGATGGGGCCCCGGTCTGCCTTGACAGGGTTGCAAAGTTGTTTTCTAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-457597/49.
                                                                                                                                                                                                GCGAGGGGGGGGACCAAGCCCCAACCCCGGGGAATCCGAGCAGGTATATAAGGGGCCCCAGC
                                                                                                                                                                                                                                                                                                                                     GCGAGGGGCGGACCAAGCCCCAACCCCGGGGAATCCGAGCAGGTATATAAGGGGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 500; DB 22; 100.0%; Pred. No. 2.9e-143; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jager D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Old LJ, Gure AO, Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2509;
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AAS87738 standard; cDNA; 2378

564 GCAGG 568

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                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and CD polymeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PDR) primers. Oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CD polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful for generating annibodies against it, detecting or CC (III) is useful for generating annibodies against it, detecting or CC (III) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations CC and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and acid sequences. Ass64197-AAS94564 represent novel human CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                  Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess high-mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS87738;
                                                                                                                                                                                                                                                        Sequence 2378 BP; 590 A; 708 C; 664 G; 416 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 23542; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #23542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                           339
    399 GCAGG 403
                                                                                                           504 TCAATCACGGGTCCTCCGGGTTGCGAGGGGGCGAACCCCAACCCCCGGGGAATCCGA 563
                                                                                                                                                279 TCCAGCCAGGCCGAACGGGGGCTCGGTAATGATTGGCCAGGGCGCATCACTGCGAACCTG 338
                                                        TCAATCACGGGTCCTCCGGGTTGCGAGGGGCGGACCAAGCCCCAACCCCGGGGAATCCGA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73.
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                   24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YT;
                                                                                                                                                                                  0;
                                                                                                                                                                                                   Score 121.8; DB 23;
Pred. No. 3.2e-27;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                    2;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                     Length
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proteiferation or exhibat may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematop tissue growth factor; Immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA181822;
                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1882; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA181822 standard; cDNA; 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                             Sequence 506 BP; 151 A; 108 C; 150 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 inflammation.
                                 187 TCGTGGACTCCCGCCTCCTAA 207
                                                                                                                                                             POCUT
                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
GTGTGTTCCCCCCCCCCTTAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-514838/56.
                                                                  TCCTCAGGTTTCGTTCTTTCAAACTTTTTGAAAACCCTAATTGGTGGCCCTCTGAGTGGGCC 186
                                                                                                                                AA001891
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                             8.48;
56.08;
                                                                                                                                                                                              0,
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                                                                                                                                                                                                             Score 41.8; DB
Pred. No. 0.0067
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                              62;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                               Length 506;
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Best Local (
                                                                                                                                                                                                                                                                                  The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, after the disorders and blood coagulation disorders. The present sequence is a DNA of the disorders and blood coagulation disorders. The present sequence is a DNA of the disorders and blood coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antilnflammatory; antibacterial; immunosuppressive; vasotropic; cancer; antiparkinsonian; neuroprotectial; bootropic; haemostatic; osteopathic; antiparkinsonian; neuroprotective; antiasthmatic; antiallergic; immunostimulant; analgesic; cerebroprotective; antianaemic; infection; nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA09613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA09613 standard; DNA; 1468 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217;
23-AUG-2000; 2000US-0649167;
23-AUG-2000; 2000US-0649267;
30-NOV-2000; 2000US-250583P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed oligonucleotide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2002
                                                                                                                                                                                                                                 Sequence 1468 BP; 508 A; 255 C; 301 G; 404 T; 0 other;
                                                                                                                                                                                                                                                                        of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 184-185; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopoiesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-626375/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US10472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200174836-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              remodeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                     123 CACCTCCTCAGGTTTCGTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAGTG 182
364 TITCTCTTGAACCTCTACCTCCTCTACCACCATTACCACCTCTCCCACCTGAAGA 418
                                  183 GGCCTCGTGGACTCCCGCCTCCTAAGTAACTCTTACCACGTCACTAGGCCAAAGA 237
                                                                           increasing hematopoiesis, stem cell
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT,
                                                                                                                                                                        7.6%;
58.3%;
                                                                                                                                                         Mismatches
                                                                                                                                                                        Score 38.2; DB Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boyle
                                                                                                                                                                                            DB 22;
                                                                                                                                                         48;
                                                                                                                                                                                            Length 1468;
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RESULT 5

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ID AAI9
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Best Local (
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or activity.
                                                                                                                                                                                                                      Sequence 379 BP; 99 A; 97 C; 81 G; 102 T; 0 other;
                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humanomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 12207; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AA012216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 12207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI92147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI92147 standard; cDNA;
                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2
                            365 T 365
                                                  175 T 175
                                                                          305 GGCAGCCACACCCCTTTGGGTTGTTTTTTCCAAACATTTTAAGTCCCGGGTTTTTTGCC
                                                                                       115 GGGGGGGTCACCTCCTCAGGTTTCGTTCCTTTCAAACTTTTTTGAAACCCTAATTGGTGGCC 174
                                                                                                                        245 AAACTGGGCCGGGCACCCCCCCCCCCCCCCAGAAAACCTCTCCTTCGGGTGGTCCTGGG 304
                                                                                                                                                2001-514838/56
                                                                                                                                                                           68
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac
                                                                                                                                                                                  56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379
                                                                                                                                                                        0;
                                                                                                                                                                                  Score 36.2; DB Pred. No. 0.32;
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                DB 22;
                                                                                                                                                                      53; Indels
                                                                                                                                                                                             Length 379;
                                                                                                                                                                        0;
                                                                                                                                                                        0;
                                                                                             Db 109573 CCCACCCNNHNNNSGGGGCCCVAGNNHNNNSGGGGCCCVAGGNNHNNNSGGGGCCCVAGG 109514
                       Qγ
                                                Matches
                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyce JW;
                       280 CCAGCCAGGCCGAACGGGGGCTCGGTAATGATTGGCCCAGGGCGCATCACTGCGAACCTGT 339
                                                            Local
                                                           Similarity
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RESULT

Conservative

23;

Score 35.4; DB Pred. No. 3.9; 23; Mismatches

DB 20; 116;

Length 114955; Indels

0

7.1%;

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antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, including lung diseases, pulmonary vasoconstriction, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, beast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target coligonucleotides (specifically AAX55180-271) can be used for the
Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-229400/19.
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; pulmonary bisease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepaticcellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenosine Al receptor antisense oligonucleotide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0093972
97US-0059160
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PR 14-AUG-2000; 2000US-0225214. PR 14-AUG-2000; 2000US-0225214. PR 14-AUG-2000; 2000US-0225266. PR 14-AUG-2000; 2000US-0225267. PR 14-AUG-2000; 2000US-0225266. PR 14-AUG-2000; 2000US-0225266. PR 14-AUG-2000; 2000US-0225270. PR 14-AUG-2000; 2000US-0225447. PR 14-AUG-2000; 2000US-0225758. PR 14-AUG-2000; 2000US-0225758. PR 14-AUG-2000; 2000US-0225759. PR 14-AUG-2000; 2000US-0225759. PR 14-AUG-2000; 2000US-0225759. PR 14-AUG-2000; 2000US-0225759. PR 12-AUG-2000; 2000US-0225681. PR 22-AUG-2000; 2000US-0225681. PR 22-AUG-2000; 2000US-0225681. PR 22-AUG-2000; 2000US-0225888. PR 22-AUG-2000; 2000US-02258924. PR 01-SEP-2000; 2000US-0229344. PR 01-SEP-2000; 2000US-0229344.	31-JAN-2000) 04-FEB-2000) 24-FEB-2000) 24-FEB-2000) 16-MAR-2000) 17-MAR-2000) 19-MAY-2000) 07-JUN-2000) 28-JUN-2000) 30-JUN-2000) 30-JUN-2000) 11-JUL-2000) 11-JUL-2000) 11-JUL-2000) 14-JUL-2000] 14-JUL-2000] 14-JUL-2000]	340 CAATCACGGGTTCCCGGGTTGCGAG : : (! ! 109513 CNNHNUNSGGGGCCCCVAGGCCNNHNN 400 CAGGTATATAAGGGGCCCCAGCTAGAG 400 CAGGTATATAAGGGGCCCVAGGCCNHAN 400 CAGGTATATAAGGGGCCCVAGGCGAG 460 AACTCAGTCAGGTGCAGAAGCCCGCG 460 AACTCAGCCAGAGCCCAANHNNNSGGG 109393 GGCCCVAGGCGAGACCCANNHNNNSGGG 109393 GGCCCVAGGCGAGCCANNHNNNSGGG 109393 GGCCCVAGGTAGAGCCANNHNNNSGGG 109393 GGCCCVAGGTAGAGCCANNHNNNSGGGGCCCCANHNNNSGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGCCANHNNNSGGGGCCCANHNNNSGGGGCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCANHNNNSGGGGGCCCCANHNNNSGGGGCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCCANHNNNSGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGCCCANHNNNSGGGGGCCANHNNSGGGGGCCCANHNNNSGGGGGCCCANHNNSGGGGGCCCANHNNNSGGGGGCCCANHNNNSGGGGGCCANHNNSGGGGGCCCANHNNNSGGGGGCCANHNNNSGGGGG
		GGGGGGACCAAGCCCCAAGCCCGGGGAATCCGAG 399 :
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08 - NOV - 2000 08 - NOV - 2000 17 - NOV - 2000	02-0CT 2000 02-0CT 2000 02-0CT 2000 02-0CT 2000 13-0CT 2000 20-0CT 2000 20-0CT 2000 20-0CT 2000 20-0CT 2000 20-0CT 2000 20-0CT 2000 20-0CT 2000 00-NOV-2000 08-NOV-2000 08-NOV-2000	01 - SEP - 2000 05 - SEP - 2000 06 - SEP - 2000 08 - SEP - 2000 14 - SEP - 2000 15 - SEP - 2000 16 - SEP - 2000 17 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000
2000US-0246534. 2000US-0246534. 2000US-0246535. 2000US-0246535. 2000US-0246536. 2000US-0246537. 2000US-0246532. 2000US-0246610. 2000US-0246611. 2000US-0246611. 2000US-0246613. 2000US-0249211. 2000US-0249211. 2000US-0249211. 2000US-0249211. 2000US-0249211. 2000US-0249211. 2000US-0249211.	2000US-0237037 2000US-0237039 2000US-0237040 2000US-0239935 2000US-0239935 2000US-0239937 2000US-0241221 2000US-0241121 2000US-0241186 2000US-0241186 2000US-0241809 2000US-0244809 2000US-0244809 2000US-0244807 2000US-0246675 2000US-0246676 2000US-0246676 2000US-0246676	2000US-0229345. 2000US-0229533. 2000US-0239533. 2000US-0231242. 2000US-0231244. 2000US-0231244. 2000US-0231414. 2000US-0231414. 2000US-0231981. 2000US-023298. 2000US-0232401. 2000US-0232401. 2000US-0233644. 2000US-0234998. 2000US-0234998. 2000US-0235844. 2000US-0235844. 2000US-0235886. 2000US-023687. 2000US-023687. 2000US-023688.

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                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 95
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-
17-NOV-
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 686 BP; 164 A; 152 C; 184 G; 181 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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  122
                                           213 TCTTACCACGTCACTAGGCCAAAGAGGGGCGTGGGGGTGAACGAAAGGGCTCCCGAACTTT 272
                                                                                                                                153 TTTGAAACCCTAATTGGTGGCCTCTGAGTGGGCCTCGTGGACTCCCGCCTCCTAAGTAAC 212
                                                                                          62
                                                                                                                                                                                                                                  93
                                                                                                                                                                                    N
TTTAATTAAATGAGAAGATGAACGAGAGATGGACTTTACAGTAACACACTCCAGATTCTT 181
                                                                                       TCTCCCCTGCTACCTGGGAGCCCATAGCTGGACCTGGGTGAGCACTGGGTTTTAAATTTT 121
                                                                                                                                                                                                                          GCTTGCGTCGGGGGGGGGGGGGGGGGGGCCACCTCCTCAGGTTTCGTTCTTTCAAACTT 152
                                                                                                                                                                                 GCACGAGCCTGGGGTTATGGTTGGCAGGTCCAGCCCTGCATTGCTAATTCAGAGCATATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-483426/52.
                                                                                                                                                                                                                                                                              1 Similarity
95; Conserv
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2000US-0250391
                                                                                                                                                                                                                                                                                           6.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                 Score 34.4; DB 22; Pred. No. 1.4;
                                                                                                                                                                                                                                                                           101;
                                                                                                                                                                                                                                                                                                                      Length 686;
                                                                                                                                                                                                                                                                           Gaps
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Вb Ş

Matches

Similarity Conservative

57.68;

0; Mismatches Score 34.2; DI Pred. No. 1.6;

DB 22; Length 637; 42; Indels

0; Gaps

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09-MAY-2000; 2000US-0556100.
12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0655783.
10-MUG-2000; 2000US-0656215.
29-AUG-2000; 2000US-06551236.
                           The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polypucleotides and the antigen-presenting cells are useful for stimulating and/or expanding realls specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                   New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2001.
Sequence 637 BP; 149 A; 135 C; 149 G; 161 T; 43 other;
                                                                                                                                                                                                                                                                     Claim 1; Page 502; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639232/73.
                                                                                                                                                                                                                                                                                                                                                                                                                       Хu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2001; 2001WO-US09919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cDNA seguence #565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS64084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS64084 standard; cDNA; 637 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ACTCATCCCAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 TTTTTTTCCAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Mitcham JL, H
GR, Retter MW, Stolk JA,
                                                                                                                                                                                                                                                                                                                                                                                      Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0685166
                                                                                                                                                                                                                                                                                                                                                                                      .; Mitcham JL, Harlocker SL, Jiang Y,
.er MW, Stolk JA, Day CH, Vedvick TS,
Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288
                                                                                                                                                                                                                                                                                                                                                                                                      Kalos MD;
Carter D;
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RESULT 9
AB1993J/c
ID AB1993J/c
ID AB1993
XX AD1993
XX MOUSE
XX IS-MAY
XX IS-MA
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to AB57374) or by determining the expression profile of gene group comprising these genes. The expression profile or agene group comprising these genes. The used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                      1712 CTCCTGATTTTATTATTCAATTTCTTTTCTACTAAAAAGTAGTCTTCGGTGGCTGGGAAGC 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 579-582; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABI99331 standard; cDNA; 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1714 BP; 478 A; 396 C; 442 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-034733/04.
P-PSDB; ABB57093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2001; 2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 TGGATACCTAAATCGAGTGNGTTCATTAAAAGTAGTTGA 166
                                                                                                         129 CTCAGGTTTCGTTCTTTCAAACTTTTTGAAACCCTAATTGGTGGCCTCTGAGTGGGCCTC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GGGTCACCTCCTCAGGTTTCGTTCTTTCAAACTTTTTGA 157
                                                                                                                                                                                                                                                                                                                    6.5%; Score 32.6; DB 24; Length 1714; ilarity 54.6%; Pred. No. 6.8; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahashi Y, Nagata T,
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                 0;
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ANAL16674
ANAL16674
ANAL16674
ANAL16674
ANAL16674
ANAL16674
ANAL16674
ANAL167
ANAL16
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AAK83468/c

ID AAK83468 standard; DNA; 16106 BP
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Best Local S
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14-MAR-2000; 2000US-0189167.
24-MAR-2000; 2000US-019299.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-021315.
09-UUN-2000; 2000US-021315.
25-JUL-2000; 2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and encoded potypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human breast cancer expressed polynucleotide 9131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 554 BP; 154 A; 124 C; 123 G; 153 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1647-1648; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2001; 2001WO-US00798
Human immune/haematopoietic antigen genomic sequence SEQ ID
                                                                                07~NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                    500 TTTTTTTTTTTTT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 CTTTCAAACTTTTT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 6.5%;
1 Similarity 64.9%;
48; Conservative
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                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.4; DB 22; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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אס מים מים מים מים אינו אינו אינו אינו אינו אינו אינו אינו	אם א	מים אים היים מים מים מים מים מים מים מים מים מים	X X X X X X X X X X X X X X X X X X X
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2000US-0232081 2000US-0232081 2000US-023239 2000US-023239 2000US-023239 2000US-0232400 2000US-0233401 2000US-023363 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0233064 2000US-0233064	2000US-0225758 2000US-0225759 2000US-0226279 2000US-02268681 2000US-0226868 2000US-0227182 2000US-0227182 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-02314 2000US-023124 2000US-023124 2000US-0231244 2000US-0231414 2000US-0231414 2000US-0231414	2000US-0214886 2000US-0216647 2000US-0216647 2000US-0216880 2000US-0217487 2000US-0217496 2000US-0220963 2000US-0220963 2000US-0220964 2000US-0224519 2000US-0225213 2000US-0225214 2000US-0225214 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225264 2000US-0225266 2000US-0225266 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264 2000US-0225264	Human; immune; haematopoletic; immune/haematopoletic antigen; cytostatic; gene therapy; vaccine; metastasis; ds. Homo sapiens. W0200157182-A2. 09-AUG-2001. 17-JAN-2001; 2001WO-US01354. 117-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-018668. 24-FEB-2000; 2000US-018664. 02-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0186350. 18-PAR-2000; 2000US-0186350. 18-PAR-2000; 2000US-0186350. 19-MAR-2000; 2000US-0186350. 19-MAR-2000; 2000US-0186350.
			; immune/haemat cine; metastasi
			opoletic antigo
			n; cancer;
מי מ	תי ש מי		ק הים
** ** ** ** ** ** ** ** ** ** ** **	08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 17-NOV-2000	20-CCT-2000; 20-CCT-2000; 20-CCT-2000; 20-CCT-2000; 20-CCT-2000; 20-CCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;	
	2000US-0246611 2000US-0246611 2000US-0246613 2000US-0249207 2000US-0249209 2000US-0249210 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249249	2000US-0241786 2000US-0241787 2000US-0241808 2000US-0241809 2000US-0246174 2000US-0246674 2000US-0246476 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246478 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246523	2000US-02349 2000US-02358 2000US-02358 2000US-02358 2000US-02353 2000US-02353 2000US-02353 2000US-02353 2000US-02353 2000US-02370
99866998001.00 70998699	2996644487665432211110098.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000000000000000000000000000000000000

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CC amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) controlled the proteins and polynucleotides may be used in the prevention, diagnosis and controlled the protein that the production of controlled the production of controlled the protein of diseases associated with inappropriate (I) expression. For controlled the precipity of untations or deletions in a patient's genome controlled the activity of (I) by expressing inactive proteins or to controlled the patients own production of (I). Additionally, (I) controlled the patients own production of (I). Additionally, (I) controlled acids into a host cell and culturing the cell to express the contein. (I) proteins and polynucleotides may be used to prevent, concers and treat immune/haematopoietic related diseases, especially concers and cancer metastases of haematopoietic derived cells. AAK64703 concers from the present invention. AAK54942 to AAK54950 and AAM82169 concers and cancers used in the exemplification of the present invention.
 RESULT 12
AAK83469/c
ID AAK83469 standard; DNA; 16161 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1854 TTTCAAGAGTTCCAAATTTGAGTATAAAATTACGGCCAGGCGCGGTGGCTCATGCCTGTA 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16106 BP; 3275 A; 4801 C; 4361 G; 3669 T; 0 other;
                                                                                                                                                                                                                                                                             07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               1794 ATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGATCAGG 1749
                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                       cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38281
                                                                                      17-JAN-2001;
                                                                                                                                             WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to AAK64702 encode the human immune/haematopoietic antigen (I) id sequences given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 38280; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; ilarity 56.6%; Conservative
; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
; 2000US-0186350.
; 2000US-0189874.
                                                                                      2001WO-US01354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.4;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Indels
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    18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                       22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

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08-SEP-2000

08-SEP-2000

14-SEP-2000

21-SEP-2000

21-SEP-2000

21-SEP-2000

25-SEP-2000

25-SEP-2000
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-JUL-2000;
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0217487.
2000US-0217496.
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2000US-0232401
2000US-0233064
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2000US-0233065
2000US-0234274
2000US-0234274
2000US-0234274
2000US-0234998
2000US-0234988
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2000US-0235834
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2000US-0232080.
2000US-0232081.
2000US-0231968.
2000US-0231397.
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2000US-0231242.
2000US-0231243.
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2000US-0229513.
2000US-0230437.
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2000US-0220964.
2000US-0224518.
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2000US-0225757.
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2000US-0225213.
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2000US-0232399
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01-DEC-2000

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05-DEC-2000

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08-DEC-2000
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20-OCT-2000
20-OCT-2000
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01-NOV-2000
08-NOV-2000
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17-NOV-2000;
17-NOV-2000;
                           Disclosure;
                                                 Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers metastasis -
                                                                                     WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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17-NOV-2000
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                                                                                                         Barash SC,
                     SEQ ID NO 38281; 3071pp + Sequence Listing; English.
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2000US-0249245.
2000US-0249264.
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2000US-0246610.
2000US-0246611.
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2000US-0246525.
2000US-0246526.
2000US-0246527.
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2000US-0240960.
2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241787.
2000US-0241808.
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2000US-0254097.
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2000US-0250160
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2000US-0249297.
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2000US-0249217.
2000US-0249218.
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2000US-0249215.
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2000US-0249212.
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2000US-0249209.
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2000US-0249207.
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2000US-0246532.
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2000US-0246477.
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                                                                                                         Ruben SM;
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AAK54951 to AAK64702 encode the human i amino acid sequences given in AAM82170

immune/haematopoietic antigen (I) to AAM91921. (I) have cytostatic

Claim 1; Page 38-40; 86pp; French

polypeptides and

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AAT94535
ID AATS
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Best Local
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                                    Transformation of plants to reduce or increase lignin content using DNA encoding alfalfa or maize cinnamoyl CoA reductase or corresponding anti-sense mRNA, e.g. to improve digestibility of
                                                                                                                        WPI; 1997-226225/20.
                                                                                                                                                        Beckert M,
                                                                                                                                                                                                                                      03-OCT-1995;
                                                                                                                                                                                                                                                                   03-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic actived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK34942 to AAK94950 and AAM82169
                            fodder crops
                                                                                                         P-PSDB;
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                                                                                                                                                                                    (CNRS ) CENT NAT RECH SCI.
(INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                  WO9712982-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alfalfa; cinnamoyl CoA reductase; eucalyptus; transgenic plant; maize; lignin biosynthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize cinnamoyl CoA reductase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1796 ATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGATCAGG 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1856 TITCAAGAGTTCCAAATTTGAGTATAAAATTACGGCCAGGCGCGGTGGCTCATGCCTGTA 1797
                                                                                                                                                                                                                                                                                                  10-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT94535 standard; cDNA to mRNA; 1556 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16161 BP; 3307 A; 4825 C; 4360 G; 3669 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ATCTGCTTGCGTCGGGGGTGGGGGGGGGGGGGTCACCTCCTCAGG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                         AAW36041.
                                                                                                                                                        Boudet AM,
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                                                                                                                                                                                                                                    95FR-0011623.
                                                                                                                                                                                                                                                                   96WO-FR01544.
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
195..1310
/*tag= a
                                                                                                                                                                                                                                                                                                                                                             /product= cinnamoyl CoA reductase
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                                                                                                                                                        Briat JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 17;
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                                                                                                                                                      Gamas
                                                                                                                                                      P,
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                                                                                                                                                      Grima-Pettenati J;
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                                                       or the
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RESULT 14
AAH94477/c
ID AAH94
XX
AC AAH9.
AC AAH9.
XX
DT 05-0
XX
KW Hum
KW Hum
KW Gen
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PN WC
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Best Local :
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                                                                                                                                                                 25-JAN-2000;
15-SEP-2000;
06-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1556 BP; 304 A; 500 C; 505 G; 247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lower than in normal plants.
                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH94477 standard; cDNA; 1177
Novel fetal proteins useful associated with dysfunction
                                                                                                                                                                                                                            25-JAN-2001; 2001WO-US02723
                                                                                                                                                                                                                                                                                      WO200155339-A2
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               nervous system disorder; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 GCGCCGTGCAGGGCTGCCAGGGCGTCTTCCACACCGCCTCCCCCGTCACCGACGACCCGG
                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACCAGGAACTGGTACTGCT 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTAGAGCCCAGGCAGACTGTGAATGCGACCTGTTCGAGAGAACTCATCAGGTGCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118;
                                                             2001-465571/50
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                                                                                         Asundi V,
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                                                                                                                                                               2000US-0491404.
2000US-0663870.
2000US-0707351.
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                                                                                          Boyle BJ, Arterburn MC, Zhou P, Werhman T;
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   for the treatment and diagnosis of diseases of the protein e.g. cancers, immune {\bf r}
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1164.
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                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag;
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CS Rice
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KW Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, growth disorders, thrombolytic disorders, nervous disorders and inflammation \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a full length cDNA which was assembled using expressed sequence tags (ESTs) found to be expressed in human foetal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1177 BP; 256 A; 291 C;
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                                                New polynucleotide encoding plant apoptosis inducing factor for engineering male sterility, altering plant architecture, manipulating stress response, and influencing growth of cells and tissues in cultus
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The present sequence is that of expressed sequence tag cDNA from CC rds2c.pk(02.glf, a clone obtained from a rice developing seedling CC (from the middle of the plant) cDNA library following screening CC for homology to database sequences. The predicted full-length protein product (see AAB20309) shows 51.3% amino acid identity to C previously known monodehydroascorbate-reductase-like capoptosis inducing factors (AIFS) of Oryza sativa and Brassica C the present nucleic acid, encoding plant AIFs. Such nucleic acids, such as C the present nucleic acid, encoding plant AIFs. Such nucleic acids, cused in sense or antisense constructs, can be used to alter levels C of AIFs in plant cells, and hence to alter apoptosis and eventually C to control cell tissue culture growth, facilitate studies of C transfer, help provide more stable transformations, engineer male C sterility, alter plant architecture and manipulate stress response.
Sequence 1623 BP; 338 A; 460 C; 511 G; 314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 62; 91pp; English.
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Query Match Best Local S Matches 60 y Match 6.4%; Score 31.8; Local Similarity 56.1%; Pred. No. 12; hes 60; Conservative 0; Mismatches Mismatches DB 22; 47; Indels Length 1623; 0; Gaps

0;

В Q 1044 GAGGGCACCGGATCGGTGGGGCACATCGACTACCTGCCATTCTTCTACTCCAGGGTCTTC 1103 295 GGGGGCTCGGTAATGATTGGCCAGGGCGCATCACTGCGAACCTGTCAATCACGGGTCCTC 354

Qy 1104 TCGCTGTCGTGGCAGTTCTACGGCGACAACGCCGGGGAAGCCGTGCA 1150 355 CGGGTTGCGAGGGGCGGACCAAGCCCCAACCCCGGGGAATCCGAGCA 401

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Search completed: October 10, 2002, 15:16:17 Job time: 122 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Peterson, Michael G
APPLICANT: Henkel, Thomas
TITLE OF INVENTION: EPSTEIN-BARR VIRUS TRANSCRIPTION FACTOR
TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                 NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE, DOCKET NUMBER: A-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                    FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/246,977
APPLICATION NUMBER: US/08/246,977
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CORRESPONDENCE ADDRESS:
                                                                           MOLECULE TYPE:
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US-08-262-220-13

US-08-471-733-13

US-08-468-878-13

US-08-68-220-3

US-08-62-220-3

US-08-68-750-494-13

US-08-68-878-3

US-08-494-3

US-08-750-494-3

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US-08-95-1968-11

US-08-030-335-3
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PCT-US95-05966-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 422; Conserv
                                      FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 38-3249
TELEFAX: (415) 38-3249
             INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EPSTEIN-BARR VIRUS TRANSCRIPTION FACTOR TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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               TELEFAX: (777299
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                              STATE: Califa. .
                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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CHARACTERISTICS:
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                                                                                           FP-59233-PC/RAO
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RESULT 3
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                                                                                                                                                                                                                                  Sequence 7, Application US/08896164
Patent No. 6218521
GENERAL INFORMATION:
APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: MITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
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-- rocal Similarity
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NAME/KEY:
LOCATION:
          SOFWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: July 17, 1997
                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                        NUMBER OF SEQUENCES: E
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                                                 COMPUTER: IBM PS/2
OPERATING SYSTEM: I
SOFTWARE: Wordperfo
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CLASSIFICATION:
                                                                                            MEDIUM TYPE:
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STRANDEDNESS: double
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                                                                                                                                                  New York City
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805 Third Avenue
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100.0%; Pr
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                                                                   PC-DOS
                         US/08/896,164
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US-08-896-164-1
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Best Local S
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LEGGTH: 666 base pairs
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: OBATA, YUIChi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
                                                                                                                                                               STREET: 805 Third Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: NO. 6218521man D. Han
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LU
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 TGGATGGAAGAAAAAAAAGAACGAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA 270
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                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: F
APPLICATION NUMBER: US/08/896,164 FILING DATE: July 17, 1997
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                                                                                                                   Diskette, 3.50 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.5%;
98.9%;
                                                                                PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUD 5499 - JEL/NDH/SLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 362.6; DB 4;
Pred. No. 2.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels~ 0;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Applia Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHELFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 707 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: .No. 6218521man D.
                 ZIF: 22313-0299

COMPUTER READABLE FORM:
MEDIUM YYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 GCCTGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 CTTCATTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 CTTCATGTT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 GTCATATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: NO. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 GACAGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAA 76
                                                                                                                                                        COUNTRY:
                                                                                                                                                                                               CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 TTATTTAAAAGAGCGAGGGGATCAAACAGTNCTTATTCTTCATGCAAAAGTTGCACAGAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAAAAATGCAGCAGCTANACTTGGA 316
                                                                                                                                           22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08232463
                                                                                                                                                            USA
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        US/08/232,463
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FILING DATE:

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                                                                                                                                                                                                                                                                                                           US-08-213-419B-3/c
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                                                 SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                    sequence 3, Application US/08213419B
Patent No. 6333406
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                     APPLICANT: Inselburg, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPERENCE/DOCKET NUMBER: 30472/114 IMPELEPOMMUNICATION: 1703)836-9300
TELLEFONMUNICATION: (703)836-9300
TELLEFAX: (703)833-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harr
Type:
                                                                                                        PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1992-04-17
                                                                                       NUMBER OF SEQ ID NOS:
TYPE: DNA ORGANISM: Plasmodium falciparum
                                   ENGTH: 6124
                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      440 ACTATTGCACAGCCAAAACATTGTATATCTGACTCAGACAAGCGAAAG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGTGTG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GAMATGAMAMAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGCGGATGGM 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATATG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 AATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTAA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Practice 9.0%; Score 45.2; DB 1; Length 7218; Local Similarity 2.3%; Pred. No. 0.00028; les 8; Conservative 202.
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                                                                      PatentIn Ver. 2.0
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GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
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                                                                                                                          US 07/870,506
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RESULT 8
US-09-511-477-38
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                                                            Sequence 38, Application US/09511477 Patent No. 6337202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/302,812B
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/83,768
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
LENGTH: 29793
                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.1 Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JACOBSON, EÎBINE L.
APPLICANT: AM, Jean-Christophe
APPLICANT: LIN, Winston
APPLICANT: LIN, Winston
TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG)
TITLE OF INVENTION: THE ENCTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACT
TITLE OF INVENTION: THERENITH
TITLE OF INVENTION: THERENITH
  APPLICANT:
                     APPLICANT:
                                                                                                                                                                                             14672 CTGCATAAAAATCCCTTCTTTTTCACTAAT 14702
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                                                                                                                                                                                                                                                                             14612 TATTTCTGATGAGAAGAGGATAGAGAAAAAAAACGAGTCTAATAAAATGCATGTGATATC 14671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (3850)..(5835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (2407)..(2439)
NAME/KEY: CDS
LOCATION: (2598)..(3404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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                                                                                                                                                                                                                                  356 CTGAACAAGAGTCTCAACCGTGTGCATTTAT 386
                                                                                                                                                                                                                                                                                                                    296 TATATCTTATGGGCAGCGGATGGAAGAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693 AAATAAAA 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 AAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAATGAAAAAAAGGT 274
                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JACOBSON, Myron K. JACOBSON, Elaine L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (3580)..(3720)
JACOBSON, Myron K. JACOBSON, Elaine L.
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 32; DB 4; Length 6124; 53.1%; Pred. No. 3.9; ative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                 6.4%; Score 31.8;
59.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 29793;
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US-09-511-477-38
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CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 09/302,812
PRIOR FILING DATE: 1999-04-30
NUMBER: OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 38
LENGTH: 29793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/08503226B Patent No. 5871945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14672 CTGCATAAAAATCCCTTCTTTTTTCACTAAT 14702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14612 TATTTCTGATGAGAAGAGGATAGAGAAAAAAAACGAGTCTAATAAAATGCATGTGATATC 14671
                                                             INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lockerbie, Robert Owen, et al.
TITLE OF INVENTION: Calcineurin Inhibitory Compounds and
TITLE OF INVENTION: Anchoring Protein
                                                                                                                                                                                                           FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      FILING DATE: 15-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,731
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                           SEQUENCE CHARACTERISTICS:
                                                                                                      TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 CTGAACAAGAGTCTCAACCGTGTGCATTTAT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 TATATCTTATGGGCAGCGGATGGAAGAAAAAAAAGAACAAATGGAACGCGATGGTTGTT 355
                                                             TELEPHONE: 312-4740448
                                                                                                                                           NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32861
                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.4%;
Local Similarity 59.3%;
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/503,226B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 South Wacker Drive, 6300 Sears Tower
519 base pairs
ucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                           436
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                                                                                                                                                                                                                                                  US 08/344,227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31.8; DB 4; Length 29793; Pred. No. 11;
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US-08-503-226B-36
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US-08-721-458B-36
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Patent No. 6
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                                                                                                                                        TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
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                  TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 2786 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                        STRANDEDNESS:
                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/503,226
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                 LENGTH:
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                                                                               nucleic acid
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                                                                                                 519 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lockerbie, Robert Owen, et al. VENTION: Calcineurin Inhibitory Compounds
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                                                           single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/404,731
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6.3%; Score 31.6;

DB 3;

Length 519;

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US-08-503-226B-35/c
; Sequence 35, Application US/08503226B; Patent No. 5871945
; GENERAL INFORMATION:
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US-08-503-226B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION:
APPLICATION:
FILING DATE: 23-NOV-13-7
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
"BYLEPHONE: 312-474-6300
                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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188 GAAATTATTAAAAAGAGCGAGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCAC 247
                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                128 CATCGCCTGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGC 187
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                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                              ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lockerbie, Robert Owen, et al.
VENTION: Calcineurin Inhibitory Compounds and
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                       Score 31.6; DB 2; Length 541; Pred. No. 1.4;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312-474-630
TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Calcineurin Inhibitory Compounds
TITLE OF INVENTION: and Anchoring Protein
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/503,226 FILING DATE: 17-JUL-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 15-MAR-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                              282 GGAATTCTCTAGCCACCGACAGAAAGTCGGTCTGTCAACCTGCATG 237
                                                                                                                                                342 AAGTTGTTTATGTGTCACTGTGACAGCTCCCACTGTGGTCTCTTTTGGCAAACCTTTCAA 283
                                                                                                                                                                                                            188 GAAATTATTTAAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCAC 247
                                                                                                                                                                                                                                                                         128 CATCGCCTGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGC 187
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                                                                                       248 AGAAGTCATATGGAAATGAAAAAAGGTTTTTTTGCCCCACCTCCTTG 293
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                                                                                                                                                                                                                                                                                                                                                                                        . Match D. B. J. Length 541; Local Similarity 49.4%; Pred. No. 1.4; Local Similarity 69.4%; Pred. No. 1.4; Local Similarity 69.4%; Local Similarity 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 541 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/344,227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
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SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                Query Match
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TELEPHONE: 415/225-1896
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 05/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
EILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/197, FILING DATE: 16-FEB-1994 CLASSIFICATION: 435 PRIOR APPLICATION UMBER: 07/958414 PILING DATE: 08-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3588 bases
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PRIOR APPLICATION NUMBER: 06/827710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
07/744207
                                          2459 CCGGTCCCTTTTAACCCAAGTAGGGAAGGGGAATGAGATCTAAGAAGTGAATTTCTTGACA 2528
                                                                                                                         2409 GGCCCAAGAAATAGCAAAAAAAAAAAAAAAAAAAACCACCGTGGAGGCCCGTAGCCAGAG 2468
                                                                                                                                                               307 GGCAGCGGATGGAAGAAAAAAAAAAGAACAAATGGAACGCGATGGTTCTGAACAAGAG 366
  427 TTGGAAGGAAAGAA 440
                                                                              367 TCTCAACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAAC 426
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 12-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                             Local Similarity 52.2%;
                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 29
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                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                ropology:
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5525488
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                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                             Score 31.6; DB 1; Length 3588; Pred. No. 3.9;
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                                                                              US-08-459-850-32
                                                                                                                                      TELERAX: 415/yoz TELERX: 910/371-7168
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3'
SEQUENCE CHARACTERISTICS:
FENGTH: 3588 bases
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  Matches
                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: 07/958
APPLICATION NUMBER: 07/958
FILING DATE: 08-CCT-1992
PRIOR APPLICATION DATA:
THE DATE: 07/141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept
TITLE OF INVENTION: Using such Nucleic Acid
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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2529 GTCGCAGGCCAGAA 2542
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 06/91
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4:
FILING DATE: 02-70N-1995
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 06/827710
EILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-AUG-
PRIOR APPLICATION DATA:
                                                                                                                    LENGTH: 3588 bases
TYPE: nucleic acid
STRANDEDNESS: sing
                 Match 6.3%;
Local Similarity 52.2%;
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                  TOPOLOGY:
    70;
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    Conservative
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12-AUG-1991
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Score 31.6; DE Pred. No. 3.9; 0; Mismatches
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                                        DB 1; Length 3588;
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307 GGCAGCGGATGGAAGAAAAAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAG 366

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PATENT NO. 5716810
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-CCT-1992
PRIOR APPLICATION NUMBER: 07/744207
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-UUL-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                               TELEPHONE: 415/225-1896
TELEPHONE: 415/225-1896
TELEFAX: 415/95-981
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,214
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                        APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297P2
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LENGTH: 35% ....

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TYPE: nucleic acid

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31-DEC-1986
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Search completed: October 10, 2002, 18:15:08 Job time: 58.7333 secs
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Best Local Similarity
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Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Contact: Robert Strausberg, Ph.D.
Email: ogapbs:remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM144 row: m column: 14
High quality sequence stop: 595.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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// Lissue_type="retinoblastoma"
// Lab_host="OHDM" selve; Vector: pOTB/; Site_1: XhoI; Site_2: // Note="Organ: eye; Vector: pOTB/; Site_1: XhoI; Site_2: // Cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (Onlversity of California, Berkeley) using ZaP-cDNA synthesis kit
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Local Similarity 99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 662)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.A.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LCCM144 row: m column: 13

High quality sequence stop: 541.

Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BE253285
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Note: this is a NIH_MGC Library."
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Pred. No. 1.6e-108;
0; Mismatches 2;
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                                                          Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 716) NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BE269949
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE269949 716 bp mRNA linear EST 13-JUL-2000 601184864F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542655 5',
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adaptor: GGCACGAG(0). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubhi (University of
California, Berkelay) using ZAP-CDNA synthesis kt
/tlifetategene) and Superscript IRT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Db 4		d Market	
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Db 3:	439 AACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCCACTTCATT 498	ν	
	3/9 GCRITIATIGGGTAGGAAATAGIDACCAAGAAATGCAGCAGCAAACTTGGAAAGAAAG 505 446 GCATTTATGGGGAAAGGAAATAGTGACCAAGAAATGCAGCAGCAAACTTGGAAAGGAAAG 505	B 2	
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Qy	206 AAATTTGGTGAGCGGCCTCCACACGAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 265		
Matche	139 AAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 198	0у	
Query	146 ATGGACCACACGGGAGGGCTCGCCCGAGGAGGCCGCCTGCGCATGCTCCATCGCCCTGGG 205	Db 1	
ORIGIN	79 ATGGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGG 138	Qy	
BASE COL	19 CAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCGGATAACCGGAGCGCTCCCC 78	ОУ	
	Query Match 95.1%; Score 475.6; DB 10; Length 716; Best Local Similarity 99.2%; Pred. No. 1e-107; Matches 478; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Query Ma Best Lou Matches	
	N TO 8 TOO C TAO 8 TOO C	ORIGIN	
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JOURNA COMMENT	/organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="NIKE_BGC_B"	į	
REFERENC AUTHOR TITLE	High quality sequence's Location/Quali	FEATURES	
ACCESSIO VERSION KEYWORDS SOURCE ORGANI	rissue Procurement: Louis M. Staudt, M.D., Ph.D. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM234 Tow: p Column: 16		
BI093196 LOCUS DEFINITI	AL Unpubl	TITLE JOURNAL COMMENT	

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y Match 95.0%; Score 475.2; DB 10; Length 785; Local Similarity 99.2%; Pred. No. 1.3e-107; Length 785; Local Similarity 99.2%; Pred. No. 1.3e-107; Length 785; Local Similarity 99.2%; Similarit
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contact: Robert Strausberg, Ph.D.
contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
plate: LLAM11024 row: b column: 16
High quality sequence stop: 755.
Location/Qualifiers
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
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BI093196
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199 AAACAGCGAGGGATCAAACAGTACTTATTCTTCATGCAAAACGTGCACGAAAGTCATRAT 258
267 AAACAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAAGTTGCACAAGAGTCATAT 326
                                                                                                                                             207 AAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 266
                                                                                                                                                                                                                    139 AAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 198
                                                                                                                                                                                                                                                                                           147 ATGGACCACACGGAGGGCTCGCCCGCGGAGGAGCCGCCCTGCGCATCCTCCATCGCCTGGG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Ggapbs-remail nih gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM32B row: f column: 16
High quality sequence stop: 656.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 690)
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BE513818.1 GI:9721030
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99.2%; Pred. No. 1.8e-107;
tive 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 GRANICANANAGETTITTTGCCCACCTCCTTGTGTRINICTRATGGGCAGGGATGG 318
327 GGANATGANANAGGTTTTTTGCCCACCTCCTTGTGTRINICTRATGGGCAGCGATGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         567 T 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAAAAAAAAGAACAAATGGAACGCGATGGTTCTGAACAAGAGTCTCAACCGTGT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: Capabs-r@mail.nih.gov
Fissue Procurement: Louis M. Staudt, M.D., Ph.D.
Fissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.linl.gov
Plate: LLCM233 row: J column: 24
High quality sequence stop: 583.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                            Similarity
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/lab_host="Diplos (phage-resistant)"
/lab_host="Diplos (phage-resistant)"
/note="Organ: lymph; Vector: poTB7; Site_1: XhoI; Site_2: Rocal; cDNA made by oligo-dT priming. Directionally cloned into EconI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 136 c 182 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3542135"
/clone_lib="NIH_MGC_8"
                     90.8%;
      0;
   Score 454.2; DB 10; Length 658; Pred. No. 2.1e-102; 0; Mismatches 3; Indels 2;
Mismatches
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19 CAGTCTCCACGTACGTCCCTCAAAGCGCGCTCCCTAAAACCCGGATAACCGGAGCGCTCCCC 78

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa; Chorddta; Crausaca; vestevacaca; commanalia; Esthéria; Primates; Catarrhini; Hominidae; Homon (bases 1 to 524)

NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM35 row: h column: 02 High quality sequence stop: 524.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:3542833"
/clone_lib="NHH_MCC_8"
/clone_lib="NHH_MCC_8"
/clone_lib="NHH_MCC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; Organ: lymph; Vector poTB7; Site_1: XhoI; Site_2: EcoRI; Organ: lymph; Vector poTB7; Site_1: XhoI; Site_2: EcoRI; Site by Oligo-dT priming. Directionally cloned into EcoRIXNhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
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/db_xref="taxon:9606"
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146 ATGGACCACACGGAGGCTCGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 ATGGACCACACGGAGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 CAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCGGATAACCGGAGCGCTCCCC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGTGT 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 473)
2 (bases 1 t
                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG609533 473 bp mRNA linear 323418 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
and -minmatch 12 options. PCR PRimers
                                                                                                                  Single pass sequencing Bases of v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST discovery in swine 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG609533.1 GI:13659512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                  called and alt_trimmed with phred d by cross_match with the -minscor
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REFERENCE
AUTHORS
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SOURCE
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BI597820
                                                                        COMMENT
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Local Similarity 93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCCCCTCCGGTTTTCCTCAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGAGTCTCAACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATGGGCAGTGGATGGAAAAAAAAAAAAGAACAAATGGAACGGGATGGTTGTTCTGAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAACTTGGAAGGAAAGAACTATTGCACGGCCAAAACATTGTATATATCTGATT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAGTCTCAACCATGTGCATTTATTGGAATAGGAAATAGTGACCAGGAAATGCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGCACAGAAGTCATATGGGAATG-AAAAAGGTTTTTTTTGCCCCTCCTTGTGTGTAT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGCACAGAAGTCATATGGAAATGAAAAAAGGTTTTTTTGCCCCACCTCCTTGTGTATAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTATGCGAAATTATTTAAAAGAGCGAGGAGATCAAACAGTACTTATTCTTCATGCAAAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGCTCCATCG-CTTGGAAAATTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGCTCCATCGCCTGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAACCGGAGCACTCCCCATGGACCAGACGGAGGGCTCGCCGCGGGAGGAGGTGCCTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCCCTCCGGTTTTCCTCA--TCTCCCGTACGTCCCTC-AGGCGCGTCCCAAAACCCGG 60
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 575)

NHH-NGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                 BI597820.1 GI:15490759
                                                                                                                                                                                                                                                                                        mRNA sequence.
BI597820
                                                                                                                                                                                                                                                                                                                         BI597820 575 bp mRNA linear EST 07-SEP-2001
                                                                                                                                                                                                         Homo sapiens
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Plate: 98 row: L column: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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105 c 116 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 383.4;
Pred. No. 7.8
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GCAGCAGCTAAACTTGGAAGGAAAGAACTATTGCACAGCCAAAAACATTGTATATATCTGA 365
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                                                                                                                                                                                                               BI604083 699 bp 1603244010F1 NIH_MGC_96 Homo sapiens
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Plate: LLAM11727 row: a column: 02
High quality sequence stop: 575.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                       Homo sapiens
                                                                                                               EST
                                                                                                                                          BI604083.1 GI:15497023
                                                                                                                                                                                           mRNA sequence.
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/lisue_type="hypothalamus"
/lab_host="hypothalamus"
/lab_host="hypothalamus"
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/lab_host="hypothalamus"
/lab_host="hypothalamus"
/lab_host="hypothalamus"
/lab_host="hypothalamus"
/lab_host="hypothalamus"
/lab_rorrange for average insert size 2.3 kb and
normalized to ROT 5. This is a primary ilbrary enriched
normalized to ROT 5. This is a primary ilbrary enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
institutes of Health). Note: this is a NIH_MGC Library."

94 a 110 c 132 g 139 t
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/db_xref="taxon:9606"
/clone="IMAGE:5287561"
/clone_lib="NIH_MGC_96"
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shire
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
BI600065 748 bp mRNA linear EST 07-SEP-2001 603251452F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5303101 5',
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/db_xref="taxon:9606"
/clone="IMAGE:5286458"
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       474 CTCAGACAAGCGAAAGCACTTCATTTT 500
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CINA Libzary Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Libzary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Contact: Robert St
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="hypothalamus"
/lab_host="hildb"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamH; Site_2: SalIT XhoI (grcgag
pBluescript KS+); Site_1: SalIT XhoI (grcgag
pBluescript KS+); Site_1: Site_2: SalIT XhoI
site_2: SalIT XhoI (grcgag
pBluescript KS+); Site_2: SalIT XhoI
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/db_xref="taxon:9606"
/clone="IMAGE:5303101"
/clone_lib="NIH_MGC_96"
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99.2%; Pred. No. 1.5e-84;
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294 TGTATATCTTATGGGCAGCGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 341.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF226018.1 GI:11133663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" 94 c 124 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:3672122"
/clone_lib="NOI_CGAP_Mam6"
/sex="female, virgin"
/tissue_rype="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 to 463)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 378.2; DB : Pred. No. 1.5e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
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VERSION
KEYWORDS
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AA171575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ATCAGACAAGAGAAGACATGTCATGTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 CTCAGACAAGCGAAAGCACTTCATTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 GGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGGAA 140
                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCATCTGAACTTGGAAGGGAAGAACTACTGCACAGGCAAAACATTGGACATATTTGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGAACAAGAGTCTCAACCCTGTGCGTTATTGGAATAGGAAACAGTGACCAAGAAAT 360
                                                                             399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA171575 438 bp mRNA ilhear EST 23-DEC-199, zp23a04.rl Stratagene neuroepithelium (#937231) Homo sapiens CDNA clone IMAGE:610254 5' similar to gb:L07872_cdsl J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN (HUMAN);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissee, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Weg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Materston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags genome Res. 6 (9), 807-828 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA171575.1 GI:1750644
                                                                                                 Similarity
                                                                                                                                                                                                      137
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314 286 1810
                                                                             Conservative
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:4625513"
/db_xref="Taxan:9606"
/clone="IMAGE:510254"
/clone="Ib>"Stratagene neuroepithelium (#937231)"
/dev_stage="Neter=2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="NotCor" pBluescript SK', Site_1: EcoRI; Site_2:
/note="Poetor: pBluescript SK', Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. NMT2
cells (Ntera-2/C1.D1) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 Kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCACCAG 3' -3' adaptor
sequence: 5' CGAGTTTTTTTTTTTT 3'"
sequence: 5' CTCGAGTTTTTTTTTTTT 3'"
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                                                                                                 74.68;
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                                                                                                 Score 373; DB 9 Pred. No. 3e-82;
                                                                          Mismatches
                                                                                                                        DB 9; Length 438;
                                                                             11; Indels
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                                                                             ω,
                                                                          Gaps
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Ouery Match 72.8%; Score 364.2; DB 9; Length 599; Best Local Similarity 99.2%; Pred. No. 4.5e-80; Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="DKFZp688H1720" /clone_lib="686 (synonym: hlcc3)" /tissue_type="human skeletal muscle" /tissue_type="adult" /dev_stage="adult" /lab_host="DH10B" /note="Vector: pTriplEx2; Site_1: SfiTA; Site_2: SfiTB; CDNA-collection" 198 a 107 c 142 g 152 t	lopfe is the from arch (efformarch (ortium)) arch (ortium) arch (closed continum) arch (clo	REFERENCE 1 (bases 1 to 599) AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.) JOURNAL Unpublished (1999) COMMENT MIPS MIPS MIPS LEXT (Wambutt R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.) COMMENT MIPS MIPS MIPS LEXINGER (1999) MIPS MIPS Mambutt R	599 bp mRNA linear 6 (synonym: hlcc3) Homo sapiens c RNA sequence. 6475	OY 141 ATTGGTGAGGGGCGCCCACCTAACGACTTACTAGGAAAGTATGGG-AAATTATTAA 199
	source	COMMENT	ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 15 BG614689 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy 192 TTV Qy 192 TTV Qy 252 GTV Qy 312 CGV Qy 312 CGV Qy 312 CGV Qy 372 ACCV Qy 432 ACCV
sequence: 5'.ATP: sequence: 5'.ATP: (where B = A, C, insert size 1.75 contained insert	/organis /dbxrei /dbxrei /dbxrei /clone=" /clone_" /clone_" /lab_hos /note=" Stil (gg Double-s- and 3' a		Homo sapiens Homo sapiens Eukaryota; Metazoa; Chorda Mammalia; Eutheria; Primat 1 (bases 1 to 799) NIH-MGC http://mgc.nci.nih National Institutes of Hea Unpublished (1999)	.7 BG614689 102642184F1 NIH_MGC_61 Hom mRNA sequence. BG614689 BG614689 1 GI:13666060 EST.	GACAGGAAATTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

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omo sapiens"

con:9666"

i:4773165"

i:H_MGC_61"

i*embryonal carcinoma"

ii:DB (F1 phage-resistant)"

itestis; Vector: pDNR-LIB (clontech); Site_1: Stitegec);

sitegac); Site_2: SfiI (ggcaattatggcc);

led cDNA was prepared from cell line RNA. 5'

led cDNA was prepared from cell line RNA. 5'

sors were used in cloning as follows: 5'

nose: 5'-CACGGCCATTATGGCC-3' and 3' adaptor

'ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'

C, Or G and N = A, C, G, Or T). Average

1.75 kb (range 0.9-4.0 kb). 15/15 colonies

nserts by PCR. This library was enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                : The I.M.A.G.E. Consortium (LLNL)
te Genomics, Inc.
clone distribution information can be
G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lh.gov/.
salth, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lata; Craniata; Vertebrata; Euteleostomi;
ites; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                        column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : CLONETECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        799 bp mRNA linear EST 18-APR-2001 mo sapiens cDNA clone IMAGE:4773165 5',
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Search completed: October 10, 2002, 20:27:56 Job time: 702.733 secs
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Best Local Similarity
                                                                                                                                                                                                                                                     Matches 366;
                                                             398 CTTCATGTT 406
                                        492 CTTCATTTT 500
                                                                                            full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NHLMGC Library."

252 a 146 c 194 g 207 t
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                                                                                                                                                                                                                                                    72.8%; Score 364.2; DB 10; Length 99.2%; Pred. No. 4.4e-80; ative 0; Mismatches 3; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                  500
432.8
422
364.2
354.4
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1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/ho
3: /SIDS1/gcgdata/ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 10, 2002, 12:39:37; Search time 84.9333 Seconds (without alignments) 10107.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 1.0
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Match Length DB
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3: //SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT: *
3: //SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT: *
3: //SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT: *
5: //SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
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AAD11117
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AAH42783
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Renal cancer assoc Human small cell 1
Jk recombinant sig C-promoter binding Lung cancer associ gastric cancer ass Human prostate can Nucleotide sequenc
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Human low adenosin	AAF21288	21	13611	6.8	33.8	4 5	
Human gene regulat	AAS61396	24	10647		w	44	Ω
Human HBM gene reg	ABA82620	22	26928		34	43	o
Human immune syste	ABL32387	24	18598		34	42	c
	AAH54742	22	3769		34.4	41	
	AAH54587	22	3450		34.4	40	C
 s. epidermidis gen 	AAH54436	22	3148	٠	34.4	39	
uman gene	AAZ16396	20	1154	•	34.4	38	
Human gene regulat	AAS61276	24	8964	•	34.6	37	
Human immune syste	ABL33534	24	8964	6.9	34.6	36	
SHOX (AAV35620	19	32367		35	ω G	
Maize starch branc	AAZ35392	21	8119		35.6	34	
DNA encoding novel	AAS92571	23	3662		41.2	ω G	
	AAS71622	23	3662	8.2	41.2	32	
DNA encoding novel	AAS71624	23	276		\mathbf{L}	31	O
	AAF22649	22	819	9.5	7	30	
Human ORFX ORF2583	AAC77028	21	2370		Ġ	29	
Human transcriptio	ABA83044	22	1127		65.2	28	
Human secreted pro	AAC08033	21	303		67	27	
Drosophila melanog	ABL06268	23	5829		111	26	
Human single nucle	AAH87431	20	262	•	115.2	25	
	AAH87430	20	262		•	24	
Lic	AAX12527	19	251	٠		23	
Human biallelic po	AAX12526	19	251	23.0	•	22	
Drosophila melanog	ABL06269	23	2932			21	
	AAF22793	22	741	•	?	20	
	AAD23366	23	538	•		19	
Human lung tumour-	AAC79290	21	538			18	
Human secreted pro	AAC00786	21	229	•		17	
Human breast tumou	AAH55536	22	391	٠	•	16	o
Human prostate can	AAF22791	22	815	•		15	
Human prostate can	AAF22792	22	625	•	281.8	14	
Human prostate can	AAF22795	22	768	•	•	13	
	AAF22796	22	665	•	312.6	12	
Human colon cancer	AAH33426	22	473	63.9	319.6	11	
Breast cancer asso	AAX39641	20	1599	4	•	10	

ALIGNMENTS

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	\ (LUDW-) LUDWIG INST CANCER RES.		11-OCT-1997;	10-OCT-1997;	10-OCT-1997;	10-OCT-1997; 97US-0061599.	17-JUL-1997;	22-JUN-1998;		15~JUL-1998; 98WO-US14679.	•) 28-JAN-1999.		v W09904265-A2.		Homo sapiens.		prostate cancer; ss.	breast	Cancer associated antigen; diagnosis; research; treatment;		Renal cancer associated gene.		02-JUL-1999 (first entry)		: AAX39671;) AAX39671 standard; DNA; 1580 BP.	71	RESULT 1

cancer;

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Chen Y,

Gout I, Gure A,

O'Hare M,

Obata Y,

Old LJ;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for diagnosing a disorder characterised by expecsion of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions that accertised by the expression of various cancer associated antigen precursors expressed in human breast which are cancer associated antigen precursors expressed in human breast contacts.
              AAD11117 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 67; Page 481-482; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1580 BP; 481 A; 352 C; 359 G; 388 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for the diagnosis, monitoring or treatment of cancers
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                                                                                                                                     ATAACCGGAGCGCTCCCCATGGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCG 120
                                                                            AAGCGAAAGCACTTCATTTT 500
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Similarity 100.0%;
Onservative 0
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              DNA; 1580
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Pred. No. 2.3e-146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES (SLOK ) SLOAN KETTERING INST CI (CORR ) CORNELL RES FOUND INC.
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synovial sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000; 2000US-0489101.
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                                                                                                                                                                                                                            500;
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                                                                                                                                                                                                                          100.0%; Score 500; ilarity 100.0%; Pred. No.: Conservative 0; Mismatch
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The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a DNA encoding human J-kappa recombination signal binding protein (RBP-1). This small cell lung cancer associated gene is designated as NY-SCLC-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by isolated nucleic acid comprising an NA Group 3 or 4 molecule \dot{\gamma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1580 BP; 481 A; 352 C; 359 G; 388 T; 0 other;
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melanoma; cancer; colon; breast; head; neck; transitional cancer
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1 ATCCCCTCCGGTTTTCCTCAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCGG 60
GCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAA 240
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coma; J-kappa recombination signal binding protein;
sarcoma; cytostatic; ds.
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                                                                                                                                                                                                                                 The sequence is that which encodes Jk recombinant signal sequence (JkRS) binding protein. Using the sequence mass production of the protein is possible by genetic engineering. See also AAQ20596-Q20601.
                                                                                                                                                                                                                                                                                                                              JK recombinant signal sequence binding protein - binds specifically on immunoglobulin gene, obtd. by culturing transformant of plasmid, then collecting protein
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                                                                                                                                                                                                      Sequence 1581 BP; 460 A; 380 C; 392 G; 349 T; 0 other;
                                                                                                                                                                                                                                                                                              Claim 2; Fig 6; llpp; Japanese.
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                                                                                                           1 ATCCCCTCCGGTTTTCCTCAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTATGGGCAGCGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAAACTTGGAAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGAGTCTCAACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAAACTTGGAAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGAC
                ATGCCCTCCGGTTTTCCTCAGTCTCCACGTACGTCCCCGAGGGCGCGCCTCCCAAAACCCGG 60
                                              ATAACCGGAGCGCTCCCCATGGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCG 120
                                                                                                                                                         Similarity
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90JP-0077317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                     86.6%; Score 432.8; DB 13; 91.6%; Pred. No. 2.7e-125;
                                                                                                                                        Pred. No. 2.7e-125;
0; Mismatches 42; Indels
                                                                                                                                                                      Length 1581;
                                                                                                                                        0;
                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
AAT06947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
   C-promoter binding factor 1; CBF1; transcription factor; TF; EBWA2; Epstein-Barr virus; CBF1-TF transcription complex; virus; CBF1-TF transcription complex; virus; classes; bacterial infection; fungal infection; metabolic disease; inflammation; genetic disease; cell growth disfunction; regulatory disfunction; neoplasm; hypersensitivity; human; animal; plant; therapy; ds.
This sequence represents the cDNA encoding C-promoter binding factor-1 (CBF1). A partially purified form of the protein encoded by this sequence is used in the method of the invention. The method is used for screening a chemical library for pharmacological agents. The protein is able to
                                                                             Claim 1; Page 22-24; 34pp; English.
                                                                                                         Screening cpds. which disrupt complex formation between C-promoter binding factor and transcription factor - potentially useful for treating diseases involving the expression of a gene modulated by such complex formation
                                                                                                                                                                                       WPI; 1996-020599/02.
P-PSDB; AAR86790.
                                                                                                                                                                                                                                                                                                                                                                                                W09532307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-promoter binding factor 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT06947 standard; cDNA; 1500 BP
                                                                                                                                                                                                                                                                   (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                                                                  17-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GTTGCACAGAAGTCTTACGGAAATGAAAAACGATTTTTTTGCCCTCCTCCTTGTGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GTTGCACAGAAGTCATATGGAAATGAAAAAAGGTTTTTTTGCCCCACCTCCTTGTGTATAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GCTATGCGAAATTATTTAAAAGAACGAGGGGATCAAACAGTGCTCATTCTTCATGCAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CAAGAGTCTCAACCCTGTGCGTTTATTGGAATAGGAAACAGTGACCAAGAAATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 CAAGAGTCTCAACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAAACTTGGAAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTATGGGCAGCGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGAAAACATTTCATGTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACTTGGAAGGAAGAACTACTGCACAGCCAAAACATTGTACATATCTGATTCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selectively bind to a transcription factor (TF) (such as Epstein-Barr virus EBNA2), and a test compound. The sample is incubated under conditions that allow the protein and the TF to bind. The presence or absence of binding of CBF1 and TF is then detected. Absence of binding indicates that the test compound disrupts CBF1-TF dependent gene expression. This method is also modified to include a labelled nucleic acid sequence containing the sequence GGGA in the incubation mixture. When the nucleic acid is used, the presence or absence of the binding of the CBF1-TF transcription complex to the nucleic acid sequence is detected. The test compounds identified are potentially useful for treating diseases associated with expression of a gene modulated by a CBF1-TF transcription complex. These include viral, bacterial or fungal infections, metabolic or genetic diseases and cell growth/regulatory disfunction (such as neoplasms, inflammation or hypersensitivity), in humans animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproduproliferative disorder; wound healing; infectious disease; ds.
                                                                                                                                                   Lung cancer associated polynucleotide sequence SEQ ID 342.
                                                                                                                                                                                                       14-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                   AAF18323 standard; DNA; 5668 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1500 BP; 465 A; 319 C; 346 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 TT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGTGT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAATGAAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGCGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATAT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.4%; Sural No. 100.0%; Pred. No. 100.0%; Pred. No. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 422; DB 17;
Pred. No. 6.5e-122;
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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58166 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated protein or polynucleotide sequences are lung cancer associated colonication, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive.

C disorders such as neural, immune, muscular, reproductive gastrointestinal, pulmonary, cardiovascular, reproductive consistency and proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and content and activities and activities
Sequence 5668 BP; 1647 A; 1028 C; 1113 G; 1879 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 798-800; 1425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US05918
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                                                                                                       ldentification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-587514/55
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Matches Query Match Local 366; Similarity Conservative 72.8%; Score 364.2; 99.2%; Pred. No. 1.7 Mismatches .7e-103; DB 21; Length 5668; Indels

Homo sapiens

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492 CTTCATTTT 500

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                                                                                                                                                                                                               The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions the invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastric cancer associated gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 67; Page 691; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
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                                                                                                                                                                           Sequence 666 BP; 214 A; 120 C; 155 G; 173 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                          lung cancer.
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 192 TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 251
                                                                   132 GCCTGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAA 191
                                                 31 GACAGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCATGTT 551
                                                                                                                             h 72.5%;
Similarity 98.9%;
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                                                                                                               Conservative
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97US-0061765.
97US-0948705.
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97US-0896164
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Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Hare M, C
Scanlan MJ,
                                                                                                           0;
                                                                                                                             Score 362.6;
Pred. No. 1.1
                                                                                                               Mismatches
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                                                                                                                             1.8e-103;
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                                                                                                                                          DB 20; Length 666;
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   AAX40076
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                                                                                                                                                                                                                                                                                                                                                  10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a
                                                                                                                                                        New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                  Chen Y, Gout 1
Pfreundschuh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gastric cancer associated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX40076 standard; DNA; 707 BP.
                                                                                                                             Claim 67; Page 689-689; 787pp; English.
                                                                                                                                                                                                                        WPI; 1999-132448/11.
                                                                                                                                                                                                                                                       Turect of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 CTTCATTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 TGGATGGAAGAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 CGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GTCATATGGAAATGAAAAAGGTTTTTTTGCCCCACCTCCTTGTGTATATCTTATGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GTCATATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCA
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                                                                                                                                                                                                                                                                                    Gout 1,
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97US-0061599.
97US-0061765.
97US-0948705.
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                                                                                                                                                                                                                                                                        O'Hare M,
Scanlan MJ,
                                                                                                                                                                                                                                                                        Obata Y, C
, Stockert
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RESULT 8
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XX AAF2
AC AAF2
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OS Homo
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                               WPI; 2001-025274/03
                                                                                        Obata Y;
                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 707 BP; 227 A; 129 C; 155 G; 180 T; 16 other;
                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                 28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000WO-US14749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer associated antigen nucleotide sequence SEQ ID:369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF22790 standard; cDNA; 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GACAGGGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGATGGAAGAAAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCATGTT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCATTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATTTAAAAGAGCGAGGGGATCAAACAGTNCTTATTCTTCATGCAAAAGTTGCACAGAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAAAAATGCAGCAGCTANACTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                 99US-0136526.
99US-0153454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF22422 to AAF23626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen procursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 50; Page 395; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding breast, gastria and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                        01-OCT-2001 (first entry)
                                                                                                                                                                                                                                        AAH42783;
                                                                                                                                                                                                                                                                        AAH42783 standard; DNA; 373 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1336 BP; 400 A; 239 C; 356 G; 333 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                         771 TGTT 774
                                                                                                                                                                                                                                                                                                                                                                                       497
                                                                                                                                                                                                                                                                                                                                                                                                                       711 AGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCACTTCA 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 GGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCAT 256
                                                                                                                                                                                                                                                                                                                                                                                       TTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCACTTCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAG-AAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAGAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCAT
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Pred. No. 5.6
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2;
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18-JAN-2001; 2001WO-GB00188

26-JUL-2001. WO200153524-A2 Homo sapiens. oesophageal cancer;

Cancer associated gene;

cancer; vaccine; ss.

prostate cancer; stomach cancer;

Nucleotide sequence of JK-recombination signal binding protein gene.

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RESULT 10
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XX AAX391
XX AAX391
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH42781-AAH42846 represent the nucleotide sequences of cancer associated genes, identified using SEREX (Serological Identification of Antigens by Recombinant Expression Cloning). The genes are overexpressed in prostate cancer, and some are overexpressed in other cancers such as stomach cancer and oesophageal cancer. The nucleic acids are useful for detecting and monitoring cancer, particularly prostate cancer. They are particularly useful in the treatment or prevention of cancer, in producing DNA-based vaccines against prostate cancer or that promote anti-tumor immune responses, and to raise antibodies. The expression of genes and detection of their protects products and/or peptides may be used to monitor disease progression during therapy, or as a prognostic indicator of initial disease status of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 373 BP; 128 A; 59 C; 93 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 18; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of cancer-associated genes and their products in detecting, monitoring, treating or preventing cancer, specifically prostate cancer, and in developing DNA-based vaccines that promote anti-tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476121/51
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                Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNO-) UNIV NOTTINGHAM TRENT
                                                                           Breast cancer associated gene.
                                                                                                                                                                                         AAX39641 standard; DNA; 1599
  prostate cancer; ss.
                                                                                                               02-JUL-1999
                                                                                                                                                                                                                                                                                 432 AGGAAAGA-CTATTGCACAGCCAAAACATTGTATATATGTAGCT 475
430 AGGAAAG-ACTATTGCACAGCCAAAACATTGTATATATCTGACT 372
330 AGGAAAG-ACTATTGCACAGCCAAAACATTGTATATATCTGACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GTCATATGGAAATGAAAAAAGGTTTTTTTGCCCCACCTCCTTGTGTATATCTTTATGGGCAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 TGGATGGAAGAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 CGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GTCATATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 TTATTTAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAA 149
                                                                                                                                                                                                                                                                                                                                                           ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGA 329
                                                                                                                                                                                                                                                                                                                                                                                               ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                             (first entry)
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98.8%;
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Pred. No. 1.7e
0; Mismatches
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ves 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1599 BP; 498 A; 317 C; 358 G; 426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 67; Page 401-402; 787pp; English.
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                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                               137 GGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 196
                                                                                                                                                                                                            257
                                                        GGAAGAAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGT 376
                                                                                                                                                                                                                                                                                                    TAAAAGAGCGAGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCAT 256
                                                                                                                                                                                                                                                                                                                                                           GGAAATTTGGTAAGTGGCTTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
AGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCACTTCA
                                                                                                                                  GGAAGAAAAAAAAAAGAACAAATGAAATGCGATGGTTGTTCTGAACACAGCTCTCATCCAT 376
                                                                                                                                                                                                            ATGGCAATCAAAAATTTTTTTTTGCCCTCCCCCTTGTGTATATCTTATGGGCAGTGGAT 316
                                                                                                                                                                                                                                                                                    TAAAAGGGTAAGGGGATCAAATAGTACTTATCCTTCATGCAAAAGTTGTACAGAAGTCAT 256
                                                                                                                                                                                                                                              ATGGAAATGAAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGCGGAT 316
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97US-0061765.
97US-0948705.
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97US-0896164
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Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.68;
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Scanlan MJ,
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                                                                                                                                                                                                                              C cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene charges and vaccine production. N and P may be used in the prevention, c diagnosis and treatment of diseases associated with inappropriate P c expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing C in a patient's genome that affect the activity of P by expressing C Inactive proteins or to supplement the patients own production of P. C Additionally, N may be used to produce the colon cancer-associated P. C Additionally, N may be used to produce the colon cancer-associated P. C Additionally, N may be used into a host cell and culturing the cell construction of colorectal carcinomas and cancers. Analyzing to AAH37204 and AAB77799 represent sequences used in the exemplification of the
                                                                                                       Query Match
                                                                                                                                                             present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                      Sequence 473 BP; 142 A; 76 C; 136 G; 114 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 2571; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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03-NOV-1999;
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28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AGAACTATTGCACAGCCAAAACATTGTACATATCTGATTCAGACAAGCAAAAGCACTTCA 496
                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-235357/24.
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                                                                                        Similarity
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                                                                      Conservative
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                                                         63.9%; Score 319.6; DB 22; Leny...
97.2%; Pred. No. 4.7e-90;
4. Mismatches 4; Indels
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                                                                                                       AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleiting of the content of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                       e.g. cancer.
                                                                                      condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                          Claim 50; Page 397; 799pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF22796 standard; cDNA; 665 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 AAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AAGGAAAGNACTATTGCACAGCC-AAACMTTGTATATCTGRCTCAGCCA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 GTCATATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGTGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTT-GG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGTGTGCATTTATTGGGRTAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGG
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99US-0153454.
                                                                                                                                                nucleic
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Best Local Similarity

62.5%; 96.6%;

Pred. No. 8.9e-88; Score 312.6;

DB 22; Length 665;

Query Match

Sequence 665 BP; 218 A; 115 C; 154 G; 174 T; 4 other;

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ARESULT 1.

AAF22795
AAF22795
AAF
AXX AAF
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XX Can
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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nuclectide sequences encoding human breast, gastric and prostate cancer associated antiqen precursors (CAAP) respectively. AAB63222 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleated or anti-CAAP antibodies are useful for diagnosing and treating condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein.
                                                                                                                                                                                                                                                                                                          Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                          Claim 50; Page 396-397; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-025274/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000WO-US14749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF22795 standard; cDNA; 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAACTATTGCACA-CCAAAACATTGTATATATCTTGACTCAACAAGCCGAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGAAA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAG-AAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGAAATGAAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGNGGAT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAAGAGCGAGGGGATCAAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCAT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer associated antigen nucleotide sequence SEQ ID:374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0136526.
99US-0153454.
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antigen; cytostatic; cancer vaccine; ss.
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     RESULT 14
AAF22792
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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nu
                                                                                                                                                                                                                                                            Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
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                                                                                                                                                                                          Claim 50; Page 395-396; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF22792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer associated antigen nucleotide sequence SEQ ID:371.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-025274/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 AAACATTGTATATATCTGACTCAGACAAGCGAAAGCACTTCATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AAACATTGTATATCTGACTCAGACAAGCGAAAGCACTTCATGTT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 AAACAGTACTTATTCCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAAATGAAAAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAACAGTACTTATTCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAATGAAAAAAGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast cancer; gastric cancer; prostate cancer; diagnosis; associated antiqen; cytostatic; cancer vaccine; ss.
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99.3%;
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                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acids or anti-CAAP antibodies are useful for diagnosing and treating \mu condition characterised by expression of an abnormal amount of a protein,
AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                     Claim 50; Page 395; 799pp; English.
                                                                                                                                                                                                                                                                    28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 625 BP; 205 A; 103 C; 142 G; 164 T; 11 other;
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                                                                                                                                                             WPI; 2001-025274/03.
                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000WO-US14749
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cancer associated antigen nucleotide sequence SEQ ID:370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF22791 standard; cDNA; 815 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 AAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 GNGTGCATTTATTGGGATAGGAAATAAGTGCCNAAAAATGCACCA-CTTAACTTGGAAGG 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 GGAAATTTGGTGAGCGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATT 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAAATGAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATATCTTATGGGCAGTGGAT 387
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Search completed: October 10, Job time: 90 secs

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nest Local Similarity
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63722 to AAB637270 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 815 BP; 261 A; 149 C; 179 G; 218 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. cancer.
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                               487 AAGCACTTCATTTT 500
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AAGCACTTCATGTT 253
                                                                TTGGAAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGA 239
                                                                               TTGGAAGGAAAGAACTATTGCACAGCCAAAACATTGTATATATCTGACTCAGACAAGCGA 486
                                                                                                                                                                                                          GGCAGCGGATGGAAGAAAAAAAAAAAAAACAACTGGAACGCGATGGTTGTTCTGAACAAGAG
                                                                                                                                                                                         GGCAGTGGATGGAAG-AAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAG
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98.8%;
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Pred. No. 1.
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Perfect score:
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1: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/2/1na/5B_COMB.seq:*
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     168 TGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGGATGTCAT 227
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ე	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5. 5	5 5	ហ ហ	5.5	5. 5	5.5	5 .5	5 .5
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Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Seguence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 257, App	Sequence 3, Appli				

Sequence 3, Application US/08200232 Patent No. 5721349 APPLICANT: Cover, Timothy L. APPLICANT: Blaser, Martin J. TITLE OF INVENTION: VACCOLATING TOXIN-DEFICIENT H. PYLORI TITLE OF INVENTION: AND RELATED METHODS NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: TELEFAX: 404/588-9860 INFORMATION POR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1541 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOTICEY: 154----CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Spratt, Gwendolyn D. REGISTRATION NUMBER: 36,016 REGISTRATION NUMBER: 32,016 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC com TELEPHONE: 404/688-0770 CURRENT APPLICATION DATA: US MOLECULE TYPE: DNA (genomic) MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palan-STREET: 127 Pe CITY: Atlanta STATE: Georgia REFERENCE/DOCKET NUMBER: Georgia E: NEEDLE & ROSENBERG P.C. 127 Peachtree Street, Suite 1200 PatentIn Release #1.0, Version #1.25 linear us/08/200,232 2200.023 Score 29.8; DB 1; Pred..No. 5.2; 0; Mismatches 42;

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                                                                                                                                                                                                                                       RESULT 3
                                                                                                       Sequence 3, Application PC/TUS9502219A GENERAL INFORMATION:
APPLICANT: Cover, Timothy L.
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GENERAL INFORMATION:
APPLICANT: Cover, Timothy L.
APPLICANT: Blaser, Martin J.
TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
TITLE OF INVENTION: AND RELATED METHODS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 3:
                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                1339 CAGAAATATTGTCATAACTAGCGCCTTGCACTCCCAC 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1399 TGTTGTTGTTATAAAGGGCTAGGCGCTCTTTGAATTGCTCTTGCAGATTGGTGTTGCTTG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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ADDRESSEE: NEEDLE & ROSENBERG P.C.
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1339 CAGAAATATTGTCATAACTAGCGCCTTGCACTCCCAC 1303
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LENGTH: 1541 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         228 CTCAAACATCAATATCACCAGAGCCCTTGAGGAACAC 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STRANDEDNESS: doub
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Similarity 56.7%;
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                                          Tummuru, Murali KR
Cao, Ping
                 Thompson, Stuart A.
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; LOCATION:
PCT-US95-02219A-3
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Patent No. 5654397
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1541 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local S
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: CROSTON, Glenn E.
APPLICANT: GOEDDEL, David V.
APPLICANT: GOEDDEL, D
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVERVION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
TITLE OF INVERVION: AND THE RELATED METHODS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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CITY: Atlanta
STATE: Georgia
                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                   COUNTRY:
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REGISTRATION NUMBER:
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                                                                                                       94111-4187
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OPERATING SYSTEM: SOFTWARE: PatentI

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FILING DATE:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-60916
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
"""FLEAT (415) 494-8771
"""FLEAT (415) 494-8771
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE: JAN 16
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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               REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
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                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                               CLASSIFICATION:
APPLICATION NUMBER:
FILING DATE: JUNE 23
CLASSIFICATION:
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Similarity 55.2%;
58; Conservative
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(415) 494-8700
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JAN 16 1996
                                                                                                                                      JUNE 23 1995
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                                                                                                                                                          U.S. Serial No. 08/494,006
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Sequence 6, Application US/09417822
Patent No. 6344549
GENERAL INFORMATION:
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                                                                                                                                                              RESULT 7
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Sequence 7. Application US/09417822
Patent No. 6344549
GENERAL INFORMATION: ARTHY
APPLICANT: Keegan, Kathy
TITLE OF INVENTION: ATR-2
FILE REFERENCE: 27866/35633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.9%; Score 29.6;
Best Local Similarity 45.6%; Pred. No. 10;
Matches 104; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/417,822
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 43
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TELEX: 910 277299
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3590 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4495
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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DEDNESS: double
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Pred. No. 7.8;
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US-09-417-822-8/c
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CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ 1D NOS: 43
SOFTMARE: Patentin Ver. 2.0
SEQ 1D NO 8
LENGTH: 4535
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Patent No. 6344549
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CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Keegan, Kathy
TITLE OF INVENTION: ATR-2
FILE REFERENCE: 27866/35633
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ORGANISM: Homo sapiens
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135 GCTAAAAGGCCTTTGCAAAATTTATGGAAAGACGGAAGAGAGAATAAA 88
                                                                                     195 AGAGCATGTAGACTGCTGCATGCCTGCAGACAGATATTCACATCTTCAACGAGAGTGTTG 136
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45.6%; Pred. No. 10;
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Pred. No. 1
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RESULT 10
PCT-US95-05512-1/c
; Sequence 1, Application PC/TUS9505512
; GENERAL IMPORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
Density Enhanced Protein Tyrosine
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Patent No. 6114140
GEMERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
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US-08-854-585-1
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Best Local 9
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                                                                                                           TITLE OF INVENTION: Density burner TITLE OF INVENTION: Phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5117 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, MICHAEL F.
REGISTRATION NUMBER: 25,447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        2295 TCAAAGTTCTGCCAACTTAAAGTTGCTGCTGTGTGTTGGTACTTACATCAATGTTGGAC 2236
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CITY: Chicago
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STATE:
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    Illinois
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                                       233 South Wacker Drive, Suite 6300
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                                                                            Marshall, O'Toole, Gerstein, Murray &
                                                           Borun
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COUNTRY:

United States of America

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; LOCATION:
PCT-US95-05512-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Keegan, Kathy
APPLICANT: Keegan, Kathy
TITLE OF INVENTION: ATR-2
TITLE REFERENCE: 27866/35633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09417822 Patent No. 6344549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                  Matches
                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5117 base pairs
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/417,822
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (31)..(8820)
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                     LENGTH: 8838
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2235 ACATTGCTGGGCCGTGTGTACTGTGCAGTGGA 2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2295 TCAAAGTTCTGCCAACTTAAAGTTGCTGCTGTGGTGTTGGTACTTACATCAATGTTGGAC 2236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 CGATCACTGGGAGATGTCCTCCGTGATGTTGA 176
                                                                                                                                                                                                                                                                                                                                              ID NO 1
314 AAAGGAATTGATTTCAACAGTTTTCCAAATGCTTGTCGAATACGAGTTCCACTGTGCACT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/05512 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 TCAAAGTGGTGCCGCCCTACATCTCTCAATGTTGGTTCGAATAATTACATCAGAGCTCTAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27
                                      62 AAATCAAAGAACATTTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTC 121
                                                                                               Match 5.98;
Local Similarity 45.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oca1
                                                                                  104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 5.9%; Score 29.6; DB 5; Length 5117; Similarity 57.6%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                               Score 29.6; DB 4; Length 8838; Pred. No. 14;
                                                                             Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Indels
                                                                           0; Gaps
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US-08-463-115-89/c
; Sequence 89, Application US/08463115
; Patent No. 5703221
; GENERAL INFORMATION:
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                                                                                                 STRANDEDNESS: Sir
TOPOLOGY: linear
US-08-463-115-89
          Matches
                                                   Query Match
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: APPLICATION UNMER: 06.157,811
FILLING DATE: NO. 5703221ember 23, 1993
APPLICATION NUMBER: 07/7687,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/764,814
FILLING DATE: May 33, 1991
APPLICATION NUMBER: 07/763,039
APPLICATION NUMBER: 07/763,039
APPLICATION NUMBER: 07/763,039
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLATED STEALTH VIRITITLE OF INVENTION: AND RELATED VACCINES NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAAAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 AGAGCATGTAGACTGCTGCATGCCTGCAGACAGATATTCACATCTTCAACGAGAGTGTTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 AGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAATA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 AGTTGAACACGGCAAACATCGACACATCTCTGTAAAAAGATCATCTGGCAAGGAAGAAGAGCAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.U. 7TP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
y Match 5.9%; Score 29.4; DB 1; Length 663; Local Similarity 60.8%; Pred. No. 4.6; hes 48; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Riche REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                    (: (213) 955-0440
67-3510
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                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                            Richard J.
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158 ATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATG 217

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567 ACGTACTGGGAGATGAAAGTCCACATTCTTCACAGCACTCTGACTCGCTGCTGGAGGATG 508

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                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: June 5, 1993
FILING DATE: June 5, 1993
FLASSIFICATION: 435
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: PRIOR APPLICATION NUMBER: 087157,811
**PRIOR APPLICATION NUMBER: 087157,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 20, 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                          158 ATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTTCTGGTGTATG 217
                                   507 AGGAACTCTCCACAGACAT 489
                                                                                                  218 GGGATGTCATCTCAAACAT 236
                                                                                                                                                           567 ACGTACTGGGAGATGAAAGTCCACATTCTTCACAGCACTCTGACTCGCTGCTGGAGGATG 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/465,388 FILING DATE: June 5, 1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Los Angeles : California
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90071-2066
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633 West Fifth Street
Suite 4700
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WENTION: ISOLATED STEALTH VIRUSES
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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May 24, 1994
May 25, 1994
May 2
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                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                               Score 29.4; DB 1; Length 663; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                      31;
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INFORMATION FOR SEQ ID NO: 8

SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-115-88
; Sequence 88, Application US/08465388
; Patent No. 5753488
; GENERAL TWOCK
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US-08-463-115-88/c
                                                                                                                               RESULT 15
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GENERAL INFORMATION:
GENERAL THOOMATION:
GENERAL THEOMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
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FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 07/763,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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MEDIUM TYPE: 3.5" Diskette, 1.44 mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                       513 AGGAACTCTCCACAGACAT 495
                                                                                                                                                                                                                                                                               218 GGGATGTCATCTCAAACAT 236
                                                                                                                                                                                                                                                                                                                                                  573 ACGTACTGGGAGATGAAAGTCCACATTCTTCACAGCACTCTGACTCGCTGCTGGAGGATG 514
                                                                                                                                                                                                                                                                                                                                                                                                              158 ATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTTGGTGTATG 217
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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Local Similarity 60.8%;
les 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
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DB 1;

31; Indels Length 669;

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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEG VERSION 1.5
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: NO. 5753488ember 23, 1993
APPLICATION NUMBER: 07/767,811
FILING DATE: NO. 5753488ember 23, 1993
APPLICATION NUMBER: 07/768,039
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/763,039
FILING DATE: MAY 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: WALDURG, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION SEQUENCE: (213) 489-1600
TELECOMMUNICATION SEQUENCE: (213) 55-0440
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
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Search completed: October 10, 2002, 18:14:28 Job time: 38.7333 secs
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TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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STREET: 633 West Fifth Street
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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BE384912 601276436
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AL556496 AL556496
AL549090 AL549090
AL527428 AL527428
AL532402 AL532402
BM464486 AGENCOURT
AL518699 AL518699
BG478628 60255515
BE409507 601303024
AL553746 AL553746
BE976694 602243611
BG688786 602637891
BH755143 60302599
BG33881 602460213
BE740422 601595455
BG476370 602521874
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BG420072	вғ310996	BI693233	BF314366	BF312821	BI258553	BE874220	в1600224	BG475925	BI602244	BE409885	BG340922	BG820903	в1915099	BG325760	BG337550	BE902069	BG282087	вм083375	BM464540		BI824942	BE409574	BG478857	BE727120	BF307478	вм008455	6238
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ALIGNMENTS

	FEATURES source		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BE384912 LOCUS DEFINITION
/db_xref="taxon: 50.6" /db_xref="taxon: 50.6" /clone="ib="NIH_MGC_20" /clone_1ib="NIH_MGC_30" /clone_1ib="NIH_MGC_30" /clone_1ib="NIH_MGC_30" /tissue_type="melanotic melanoma" /tissue_type="melanotic melanoma" /lab_bost="MH10B (phage-resistant)"	High quarter stop: oil. Cocation/Qualifiers 1. 713 Arganism "Homo capions"	Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/CTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM284 row: h column: 10 High cmailty sequence stop: 611.		mRNA sequence. BE384912 BE384912.1 GI:9330277 EST. human. Homo sapiens Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;	BE384912 713 bp mRNA linear EST 21-JUL-2000 601276436F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617337 5',

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RESULT 2
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AL549103 LTI_NFL006_PL2 Homo
prime, mRNA sequence.
                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 872)
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AL549103.1 GI:12884761
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Location/Qualifiers
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(Stratagene) and Superscript II RT (Life Technologies)."
162 c 170 g 195 t
/clone="CSODIO51YK06"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                              /db_xref="taxon:9606"
                                                         organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://fulllength.invitrogen.com"
1 212 c 236 g 216 t
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AL556496 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK006YK17 5
prime, mRNA sequence.

PESSION AL556496
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AL556496.1 GI:12899223
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PINE
ERENCE 1 (bases 1 to 928)
UTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
URNAL Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                            EST
                                                                             AL549090.1 GI:12884735
                                                                                            prime, mRNA sequence.
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Location/Qualifiers
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/clone_11b="ITI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMYSPORT 6; Site_1: NotI; lst strand
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Eull-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
  AL527428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: segref@genoscope.cns.fr,
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/note="Vector: pCMV5PORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMV5PORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMV5PORT 6
/rector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
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1 (bases 1 to 865)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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AL527428
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/lab_host="DH10B"
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/clone_lib="LTI_NFL003_NBC3"
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/db_xref="taxon:9606"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Location/Qualifiers
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/lab_host="DH10B"
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121 CGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCCTCCGTGATGTTGATGCC 180
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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AGENCOURT_6439009 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5535574
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/tissue_type="lelomyosarcoma"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                              /note-"Organ: brain; Vector: pcMVSPORT 6: 1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fullength.invitrogen.com"
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                                  Score 493.2; DB 9; Length 920; Pred. No. 3.3e-142;
       Mismatches
       Indels
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                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                               http://image.llnl.gov
Plate: LLCM1414 row: n column: 04
High quality sequence stop: 792.
                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organiam="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4643907"
/clone=lib="NHL_MGC_20"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 743)
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                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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99.8%;
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AL553746.1 GI:12893867
EST.
                               prime, mRNA sequence.
AL553746
                                                            AL553746 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI080YF09
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Clone distribution: MGC clone distribution information can be
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/clone_lib="NIH_MGC_21"
/clone_lib="NIH_MGC_21"
/tissue_type="choriogarcinoma"
/lab_host="DH10B (phage resistant)"
/note="0cygan: placenta; Vector: poTB7; Site_1: XhoI;
/note="0cygan: placenta; Vector: poTB7; Site_1: XhoI;
/note="0cygan: placenta; Vector: poTB7; Site_1: XhoI;
/note="0cygan: placenta; Vector: poTB7; Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
92 a 170 c 174 g 207 t
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181 AAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAAT 240
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/note="Vector: pcWvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcWvSpORT 6; Site_1: NotI; 1st strand cDNA
vas primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
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/clone_lib="LTI_NFL006_PL2"
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/db_xref="taxon:9606"
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Pred. No. 1.4e-140;
O; Mismatches 0;
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                                                                                       241 ATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAAAAATGTTTCTGTG 300
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                                                                 ATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAAAAATGTTTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: gapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1204 row: f column: 03
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1. (bases 1 to 700)
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602243611F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334594 5',
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/tlssue_type="primary B-cells from tonsils (cell line)"
/tlssue_type="primary B-cells from tonsils (cell line)"
/lab_host="BH10B (phage-resistant)"
/lab_host="BH10B (phage-resistant)"
/lab_host="primary B-cells; Vector: pOTB7; Site_1: XhoI;
/lab_host="primary Site_1: Yector: pOTB7; Site_1: XhoI;
/lab_host="primary total yellog-driving from the B-cells; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dr primary:
/site_2: EcoRI; cDNA made by oligo-dr primary:
/site_1: Claifornia Site_1: Alboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
/site_1: Note: this is a NIH_MGC_Library."
/site_1: Note: this is a NIH_MGC_Library."
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
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plate: LLCM1634 row: f column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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NIH-MGC http:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               /tisue_type="prinary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; DCNA made by Oligo-dT prinning.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCG Library."
66 a 172 c 167 g 185 t
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/clone="IMAGE:4765463"
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Pred. No. 3.9e-140;
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Plate: LLAM11491 row: p column:
High quality sequence stop: 809.
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BI753143
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Tissue Procurement: Life Technologies, Inc
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              /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is ollgo-dy primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note:
                                                                                                                                                                                     /clone="IMAGE:5196551"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 GAATTCCTGACTGCCACAGGTGTACAGGAAACATTTGTCTTTTGTTGCTGGAAAGCTGCT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAAATCAAAGAACATTTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCGGCG-TTTGCATTTCCTCTGAGCCTGTTTCAGGGCAGTAGCGATGGAGTTGGAGGTT
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           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLCML290 row: j column: 04
High quality sequence stop: 598.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 936)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG333881 936 pp mixes integral 551 602460213F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4576995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG333881.1 GI:13140319
                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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BASE COUNT
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Best Local (
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411 GTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCATTTTCAGAAGACCCCAGGGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                  171 CGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 CAAATCAAAGAACATTTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTT 170
                                                                                                                                                                                                                                                                       361 GTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCATTTTCAGAAGACCCCAGGGT 420
                                                                                                                                                                                                                                                                                                                              351 ATGACGATGATCTTCAAGGAGTCATCCCCCAGCCACCCCAACTCGTTGCCACGAAGACAAT 410
                                                                                                                                                                                                                                                                                                                                                                              301 ATGACGATGATCTTCAAGGAGTCATCCCCCAGCCACCCAACTCGTTGCCACGAAGACAAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAAT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4576995"
/clone="IMAGE:4576995"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies)."
237 a 235 c 249 g 215 t
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99.8%;
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Pred. No. 1.2e-139;
0; Mismatches 0;
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Search completed: October 10, 2002, 20:27:49 Job time: 702.733 secs

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                     Result
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                                                                                                                                                                                                                                                                                                                                                   Score
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2: SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*

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23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA199B.DAT:*

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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA200D.DAT:*

24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20DB.DAT:*
       100.0
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10107.424 Million cell updates/sec
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22: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001b.DAT:*
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                                                                                                                                                                       AAD11116
AAI58623
AAI60409
ABA08061
                                                                ABA08062
AAL06787
AAL06788
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                                                                                                                                 Human small cell l
Human polynucleoti
Human polynucleoti
Human ovarian and
Human ovarian and
                                                                                                                                                                                                                                                                                                                                           Description
                                                                    Human reproductive
Drosophila melanog
Drosophila melanog
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DNA encoding novel	AAS92572	23	2868		9.	G
Human retinoblasto	AA169735	22	1677		9	4
₩.	AAC79952	21	1583		9	ω
Drosophila melanog	ABL26428	23	7957		9.	N
Drosophila melanog	ABL26429	23	4378		9	ш
Ĭ.	AAT62551	18	3590		29.8	0
Helicobacter pylor	AAT04133	16	1541		9.	9
Human neuroblastom	AAI93960	22	842		9.	œ
richia co	ABA89022	22	16066		30	7
	ABA15345	22	12758		30	σ
nervous sys	ABA15344	22	10899		30	G
isome	ABA03787	24	3571		30	4
L776_	AAX90855	20	3546		30	ω
coli	ABA89030	22	1422	٠	30	N
breast	AAL17265	22	735	٠	30	- -3
breast	AAL09376	22	710		30	0
_	AAK85314	22	32476		0	٥
	ABL15542	23	12161		0.	æ
	ABL15550	23	12138		0.	7
DNA fo	AAS97010	24	1663		0.	σ
	AAH10947	22	555		0.	ŲΊ
\circ	AAI96719	22	769		0.	.4.
	ABL17884	23	3813			w
	ABL04958	23	3748		ŗ.	N
Drosophila melanog	ABL04959	23	1574	6.3		-
reproductiv	AAL05000	22	5151		۳.	0
Human nervous syst	ABA18681	22	5151		۲.	ø
Drosophila melanog	ABL10434	23	12126		ω	80
sseria mening	AAF21608	21	349980		2	7
N. meningitidis pa	AAA81520	21	30078		2	o,
Human transcriptio	ABA83052	22	2187		2	u
Pseudomonas sp nod	AAF26310	22	936		۲,	**
Human kidney relat	AAI63294	22	m		۰	ω
Human excretory re	AAI98944	22	18301		2	N
Human cancer assoc	AAF26953	22	3635	6.7	33.6	ш.
Drosophila melanog	w	23	6162		8	0

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ALIGNMENTS

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RESULT 1
AAD11116
Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; eukaryotic translation initiation factor; eIF2B;
                                                                                                             26-JUL-2001.
                                                                                                                                                Homo sapiens.
                                                                                                                                                                   synovial sarcoma; cytostatic; ds.
                                                                                                                                                                                                              Human small cell lung cancer associated gene, eIF2B.
                                                                                                                                                                                                                                 24-SEP-2001 (first entry)
                                                                                                                                                                                                                                                      AAD11116;
                                                                                                                                                                                                                                                                       AAD11116 standard; DNA; 2291 BP
                                                                                                                               WO200153349-A2
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ABL06740

WPI; 2001-457597/49 Stockert E, Scanlan MJ,

Jager D,

Old LJ,

Gure AO,

Chen Y;

21-JAN-2000; 2000US-0489101. 19-JAN-2001; 2001WO-US02015

(LUDW-) LUDWIG INST CANCER RES (SLOK) SLOAN KETTERING INST C. (CORR) CORNELL RES FOUND INC.

CANCER RES

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AC AAI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or translational cancer, leinwyosarcoma or synovial sarcoma. The present sequence is a DNA encoding human entaryotic translation initiation factor eIFDB. This small cell lung cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encode isolated nucleic acid comprising an NA Group 3 or 4 molecule \alpha
                   22-OCT-2001
                                                                                     AAI58623 standard; cDNA; 2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2291 BP; 588 A; 540 C; 630 G; 533 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene is designated as NY-SCLC-7
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                                                                                                                                                                                                                                                                                                                    CGATATGATTTACTGGATTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGCTTTGGTGCGCTCTGACTTTCTTCTTGTTGTTATGGGGATGTCATCTCAAACATCAAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATTCCTGACTGCCACAGGTGTACAGGAAACATTTGTCTTTTGTTGCTGGAAAGCTGCT 60
                                                                                                                                                                             CGATATGATTTACTGGATTG 500
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                 (first entry)
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                                                                                       ВP
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                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzhelmer's, Parkinson's disease, Huntington's disease, such as Alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitys cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; cls; parkinson's disease; Huntington's disease; hamenostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                          Sequence 2907 BP; 734 A; 703 C; 810 G; 653 T; 7 other;
                                                                                                                                                                                                                                                                          specification.
                                                                                                                                                                                                                                                                                                        C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 826; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia; ss.
121 CGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCC
                                               659 CAAATCAAAGAACATTTACTGAAGTGAAGTGGTGCTGCCCCTACATCTCTCAATGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
                                                                                                                                                                                            Local
                                                                                                                                 QA,
                                                                                 CAAATCAAAGAACATTTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCCAATGTGGTT 120
                                                                                                               GAATTCCTGACTGCCACAGGTGTACAGGAAACATTTGTCTTTTGTTGCTGGAAAGCTGCT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-442253/47.
DB; AAM39467.
                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                            Similarity
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2000US-0598042
2000US-05620312
2000US-0653450
2000US-0663151
2000US-0693036
2000US-0727344
                                                                                                                                                                              Conservative
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Wehrman T, X
, Goodrich R,
                                                                                                                                                                                          100.0%; Score 500; DB 22; 100.0%; Pred. No. 3.7e-159;
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Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
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09-JUL-2000;
19-JUL-2000;
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14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; parkhalmer's; parkhason's disease; Huntington's disease; hemeostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                               P-PSDB; AAM41253
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                                                           WPI; 2001-442253/47.
                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                  29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                          leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                 Liu C,
Wang Z,
                                                                                    Zhou P,
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; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
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2000US-0662191.
2000US-0693036.
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Wehrman T,
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                                                                                     Goodrich R, Drmanac
                                                                                               Chen R, Ma Y,
, Xu C, Xue AJ,
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Yang Y,
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                                                                                                                                                                         Query Match
                                                                                            Matches
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                                                                                                                                                                                                                                                                           Sequence 2968 BP;
                                                                                                                                                                                                                                                                                                                                                             specification.
                                                                                                                                       local
                                                                                                 499;
                                                                                                                                       Similarity
                                                                                                 Conservative
                                                                                                                                                                                                                                                                           728 A; 719 C; 825 G; 696 T; 0 other;
                                                                                                                                       99.78;
                                                                                                 0;
                                                                                            Score 498.4; DB 22; Length Pred. No. 1.3e-158; 0; Mismatches 1; Indels
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                           CGATATGATTTACTGGATTG 500
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CGATATGATTTACTGGATTG 761
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ABA08061 standard; DNA; 2898

ABA08061;

11-JAN-2002 (first entry)

SX SX FX SX SX S Human ovarian and breast cancer associated polynucleotide SEQ ID NO 856

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

PR 21-SEP-2 PR 25-SEP-2 PR 25-SEP-2 PR 25-SEP-2 PR 26-SEP-2 PR 26-SEP-2 PR 26-SEP-2 PR 27-SEP-2 PR 29-SEP-2 PR 29-SEP-2 PR 02-OCT-2 PR 02-OCT-2 PR 20-OCT-2 PR 20-		No. 15-984 2000 2000 -01987 2000 -01981	31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000;	<pre>KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; XX neurological disease; infection; human; secreted protein; ds. XX PD WO200155325-A2. XX PD 02-AUG-2001. XX PD 02-AUG-2001. 2001WO-US01345.</pre>
	2000US-0234223 2000US-0234223 2000US-0234223 2000US-0234949 2000US-02358364 2000US-02358364 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0237039 2000US-0241109 2000US-0241109 2000US-0241109 2000US-0241109 2000US-0241221 2000US-0246676 2000US-0246676 2000US-0246676 2000US-0246676 2000US-0246611 2000US-0246612 2000US-0246612 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246234 2000US-0249234 2000US-0259234	13-0CT 20-0CT	02-001 02-001 02-001 02-001	21-SEP 21-SEP 25-SEP 25-SEP 26-SEP 27-SEP 29-SEP 29-SEP 29-SEP 29-SEP

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -
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11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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76 TTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTCGAATAATTACATCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 52.4%; Local Similarity 79.4%;
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                                                                                                                                                                                                              AAAAAAATGTTTCTGTGATGACGATGATCTTCAAGGAGTCATCCCCCAGCCACCCAACTC 343
                                                                                                                                                                                                                                                    TGAGACTGCTTTTTTGCAGTTCTGTCCCTCCTGTCCTTTATAGGTTGAGACGGAAGCTAG
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                                                                                                          GTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCATT 403
                                                                                                                                                                                                                                                                                                                                       GAGGAACACAGGTCAGGATGGGAAAATGACAGGAACAAGGGTTAAAAGACCAGCAGAGCCC 405
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                                                                                   GTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCATT 225
                                                                                                                                                                      AAAAAAATGTTTCTGTGATGATGATGATCTTCAAGGAGTCATCCCCCAGCCAACCCC
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                                                                                                                                                                                                                                                                                            ----AGGTTGAGACGGAAGCTAG 283
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08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

2000US-0231414. 2000US-0232080. 2000US-0232081. 2000US-0231968.

2000US-0232397 2000US-0232398 2000US-0232399 2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064 2000US-0233064 2000US-0233064 2000US-0234223

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                                                                                                                                                                                                                                                                                    76 TTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTCGAATAATTACATCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGC
404 TGAGACTGCTTTTTTGCAGTTCTGTCCCTCCTGTCCTTTATAGGTTGAGACGGAAGCTAG 345
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2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0256719.
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2000US-0249300
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79.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 262.2; DB 22; Pred. No. 2.8e-78; 0; Mismatches 3;
                                                                      ----AGGTTGAGACGGAAGCTAG
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2000US-0235484 2000US-0225834 2000US-0225836 2000US-0236367 2000US-0236368 2000US-0236368 2000US-0236369 2000US-0236802 2000US-0236802 2000US-0236802 2000US-0237033 2000US-0237033

2000US-0237040. 2000US-0239935. 2000US-0239937. 2000US-0240960.

20-CCT-2000;
01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;

2000US-0246525. 2000US-0246524.

2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246477. 2000US-0246478.

2000US-0246526 2000US-0246527 2000US-0246532 2000US-0246619 2000US-0246611 2000US-0246611 2000US-0246611 2000US-0249613 2000US-024920 2000US-024920 2000US-024920 2000US-0249210 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214

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7 standard; DNA; 2898 BP. 2001 (first entry) 2001 (first entry) 2001 (first entry) gene therapy; ds. pleas. 5230-A2. 2001.	TTCAGAAGACCCAGGGTCTCCGGCGTTTTGCATTTCCTCTG 444 	AAAAAAATGTTTCTGTGATGACGATGATCTTCAAGGAGTCATCCCCGAGCCAACTC 343 [
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2000US -02231968. 2000US -0223397. 2000US -0223491. 2000US -023400. 2000US -0234063. 2000US -0234063. 2000US -0234404. 2000US -0234497. 2000US -0234998. 2000US -0234998. 2000US -0234998. 2000US -0234988. 2000US -0235370. 2000US -0234567. 2000US -0234988. 2000US -02441785. 2000US -02441785. 2000US -0246478. 2000US -0246477. 2000US -0246478. 2000US -0246478. 2000US -0246477. 2000US -0246478. 2000US -0246477. 2000US -024667. 2000US -02467. 2000	20000S-0231244. 20000S-0231413. 20000S-0231414. 20000S-0232080. 20000S-0232081.	2000US-0229345. 2000US-0229509. 2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231242.

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01-DEC-2000;
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01-DEC-2000;
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08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9475; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                          344
                                                                                      284 AAAAAAATGTTTCTGTGATGACGATGATCTTCAAGGAGTCATCCCCCAGCCACCCAACTC
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                                                                                                                                                                   404
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                                                                                                                                                                                                                                                                                                                                                                                                             196 TCTGACTTTCTGGTGTATGGGGATGTCATCTCAAACATCAATATCACCAGAGCCCTT 255
                                                                                                                                                                                                                                                                                                                             256 GAGGAACAC
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                                                                                                                                                                TGAGACTGCTTTTTTTGCAGTTCTGTCCCTTCCTGTCCTTTATAGGTTGAGACGGAAGCTAG
                                                       AAAAAAATGTTTCTGTGATGACGATGATCTTCAAGGAGTCATCCCCCAGCCACCCAACTC
                                                                                                                                                                                                                    -----AGGTTGAGACGGAAGCTAG
                                                                                                                                                                                                                                                                         GAGGAACACAGGTCAGGAATGGGAAAATGACAGGAACAAGGGTTAAAGACCAGCAGCAGCCC 405
                                                                                                                                                                                                                                                                                                                                                                                 TCTGACTTTCTTGGTGTATGGGGATGTCATCTCAAAACATCAATATCACCAGAGCCCTT 465
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2000US-0249217
2000US-0249218
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249264
2000US-0249265
2000US-0249297
2000US-0249297
2000US-0249297
2000US-0249297
2000US-0249297
2000US-0249300
2000US-0250160
2000US-0250391
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Pred. No. 2.8e-78;
0; Mismatches 3
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      403
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      RESULT 7
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ID AAL06788 standard;
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14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

15-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

21-AUG-2000

23-AUG-2000

24-AUG-2000

25-AUG-2000

27-AUG-2000

28-AUG-2000

29-AUG-2000

29-AUG-2000

20-AUG-2000

20-AU
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 9476.
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2000US-0179065
2000US-01180628
2000US-01186464
2000US-01186350
2000US-01186370
2000US-0118133
2000US-0125515
2000US-01255135
2000US-0215135
2000US-0215135
2000US-021518290
2000US-021518290
2000US-021518290
2000US-021518290
2000US-021518290
2000US-021518290
2000US-021518290
2000US-022511
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225217
2000US-0225275
2000US-0225757
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2000US-0225775
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08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0231242 2000US-0231243 2000US-0231413 2000US-0231414 2000US-0232081 2000US-0232081 2000US-0232397 2000US-0232397 2000US-0232399 2000US-0232340 2000US-0232401 2000US-0232401 2000US-0232401 2000US-0232401 2000US-0232401 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-023423 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-023403 2000US-0235484 2000US-0235834 2000US-0235834

08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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2000US-0236802.

2000US-0237037.

2000US-0237038.

2000US-0237038.

2000US-0237030.

2000US-0239937.

2000US-0239937.

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2000US-0239937.

2000US-0241221.

2000US-0241785.
2000US-0246611

2000US-0246613

2000US-0249207

2000US-0249208

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01-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 9476; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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 404 TTCAGAAGACCCAGGGTCTCCGGCGTTTTGCATTTCCTCTG 444
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                         TCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAATATCACCAGAGCCCTT
                                                                                                                                                                                                                                                                                                                                                                           TTACTGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTCGAATAATTACATCA 135
                                           GTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCATT
                                                                                                                                                TGAGACTGCTTTTTTGCAGTTCTGTCCCTCCTGTCCTTTATAGGTTGAGACGGAAGCTAG
                                                       GAGGAACACAGGTCAGGATGGGAAAAATGACAGGGAACAAGGGGTTAAAGACCAGCAGAGCCC
                                                                                                                                                                                                                               GAGGAACAC
                                                                                                                                                                                                                                                       TCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAATATCACCAGAGCCCTT
                                                                                                                                                                            -----AGGTTGAGACGGAAGCTAG
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2000US-0249264.
2000US-0249265.
2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249390.
2000US-0259160.
2000US-0259189391.
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2001US-0259678
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2000US-0251989
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2000US-0251856
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2000US-0256719
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79.48;
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Pred. No. 2.8
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2.8e-78;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
21-SEP-2000;
22-SEP-2000;
23-SEP-2000;
23-CCT-2000;
23-CCT-2000;
23-CCT-2000;
23-CCT-2000;
23-CCT-2000;
23-CCT-2000;
24-SEP-2000;
25-CCT-2000;
26-CCT-2000;
27-CCT-2000;
28-NOV-2000;
28-NO

2000US-0236368. 2000US-0236369. 2000US-0236370.

2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246478.
2000US-0246528.
2000US-02465234.

2000US-0246528. 2000US-0246532. 2000US-0246609. 2000US-0246610.

2000US-0246525. 2000US-0246526. 2000US-0246527.

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RESULT 9
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                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ0176-ABLJ0511), expressed DNA sequences (ABLJ0184-ABLJ0513) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                               (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   Sequence 2010 BP; 463 A; 548 C; 596 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 14705; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABB62638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                     382 GATCTGCGCCCAGTGCTGGAGCAGCACAAGCGGCAGGCCAAGTTCGACAA 431
                                                                                                                                         322 AATAAGGCGCTGATCCGTGGCCACTTCATTCTGCTCGGCGCCGATACGGTGACCAATGCC
                                                                                                                                                           178 GCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATC 237
                                                                                                                                                                                                                                             118 GTTCGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 TTCAGAAGACCCAGGGTCTCCGGCGTTTTGCATTTCCTCTG 184
                                                                                                     238 AATATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAA 287
                                                                                                                                                                                                           262 GTCCATGTGATTGGCGGCGAGGGTTGTCGCTGCTTCGGCGATGCCATGCGTGATTTGGAC 321
                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                               7.8%;
Similarity 51.8%;
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                               Score 38.8; DB 23;
Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                               Length 2010;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
26-MAR-2002
                                                                   ABL06328 standard; cDNA; 6162 BP
                                 ABL06328;
                                                                                                                                                         2755 GATCTGCGCCCAGTGCTGGAGCAGCCACGAGCCGCCAAGTTCGACAA 2706
                                                                                                                                                                                                                             2815 AATAAGGCGCTGATCCGTGGCCACTTCATTCTGCTCGGCGCCGATACGGTGACCAATGCC 2756
                                                                                                                                                                                                                                                                                                 2875 GTCCATGTGATTGGCGGCGAGGGTTGTCGCTGCTTCGGCGATGCCATGCGTGATTTGGAC 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4272 BP; 1069 A; 1157 C; 1092 G; 954 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 14702; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 14702.
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                                                                                                                                                                                                                                                                                                                   118 GTTCGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGAT 177
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                                                                                                                                                                                                                                               178 GCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTGATGGGGGATGTCATCTCAAACATC 237
                                                                                                                                                                                       238 AATATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Score 38.8; DB Pred. No. 0.034; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG171), expressed DNA sequences (ABLIG175) and the encoded proteins (ABB70377-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 13466; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 13466
Human; cancer associated antigen precursor; cancer associated antigen;
seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
                                                        Human cancer associated antigen precursor HOM-TES-84/6 cDNA SEQ ID NO:5
                                                                                                 10-APR-2001
                                                                                                                                                                       AAF26953 standard; cDNA; 3635 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6162 BP; 1591 A; 1658 C; 1564 G; 1349 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ABB62225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                     178 GCCAAGGCTTTGGTGCGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GTTCGAATAATTACATCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGAT 177
                                                                                                                                                                                                                                                                      302 GATCTGCGCCCAGTGCTGGAGCAGCACAAGCGGCAGGCCAAGTTCGACAA 253
                                                                                                                                                                                                                                                                                                         238 AATATCACCAGAGCCCTTGAGGAACACAGGTTGAGACGGAAGCTAGAAAA 287
                                                                                                                                                                                                                                                                                                                                                362 AATAAGGCGCTGATCCGTGGCCACTTCATTCTGCTCGGCGCCGATACGGTGACCAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.8; DB Pred. No. 0.041;
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ID AAI98
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for diagnosing a disorder characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group I nucleic acid molecule (NI) comprising contacting the biological sample with an agent (A) that specifically binds to NI, (I) or its fragment, complexed with an human leukocyte antigen (HLA) molecule and determining the interaction between the agent and NI or (I). (I) has cytostatic activity and can be used in gene therapy and vaccine production. The method can be used for treating a subject with a condition characterised by expression of (I) in cells of a subject. The present sequence which is used in the exemplification of the present condition of the method can be used to condition of the present sequence which is used in the exemplification of
                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; excretory system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing a disorder characterized by expression of a human cancer associated antigen precursor, comprises detecting interaction of an associated antigen precursor, comprises detecting interaction of an agent with a nucleic acid molecule encoding the antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3635 BP; 1162 A; 741 C; 797 G; 935 T; 0 other;
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    Homo sapiens
                                                                                                                                                                                                           Human excretory related polynucleotide SEQ ID NO 708.
                                                                                                                                                                                                                                                  07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                          AAI98944;
                                                                                                                                                                                                                                                                                                                              AAI98944 standard; DNA; 18301 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 48; Page 90-91; 126pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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	001553 AUG-20 JAN-20 JAN-20 JAN-20 FEB-20 FEB-20 MAR-20	
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13-0C21 13-0C21 13-0C21 20-0C1 20-0C1 20-0C1 20-0C2	27-SE 29-SE) 1
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2000US-0249937 2000US-0239937 2000US-0241920 2000US-0241920 2000US-0241808 2000US-0241808 2000US-0241808 2000US-0241808 2000US-0241808 2000US-0244677 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246610 2000US-0246611 2000US-0246611 2000US-0246611 2000US-0246611 2000US-0246611 2000US-0246221 2000US-0246221 2000US-0246211 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249215 2000US-0249215 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0251988 2000US-02519886 2000US-02519869 2000US-02519869 2000US-02519869 2000US-02519899 2000US-02519899 2000US-02519899 2000US-02519899 2000US-02519899 2000US-02519990 2000US-02519899		2
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9937, 9937,	5836. 6327. 6368. 6369. 6370. 5802. 7037. 7038.	,

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AA163294/c
ID AA1632
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    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel excretory system related human CC polynucleotides (AAI98567-AAI99503) and the encoded proteins (AAI99594-AAM99913) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy, especially CC disorders related to the excretory system. The specification. The CC the diagnosis, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as myocardial ischaemias; and parasitic infectious diseases such as viral, bacterial, fungal cand parasitic infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-465569/50
                                                                                                                                                                                                                                      Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidabetic; antiallergic; hepatotropic; antidabetic; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 708; 574pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA,
  31-JAN-2000; 2000US-0179065
04-FEB-2000; 2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA163294 standard; DNA; 18301 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18301 BP; 5076 A; 4392 C; 3842 G; 4991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding excretory system antigen is
used in preventing, treating or ameliorating a medical condition -
                                                            17-JAN-2001; 2001WO-US01343.
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                    gene therapy; cancer;
neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                 Human kidney related polynucleotide SEQ ID NO 609.
                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
                                                                                                                                        WO200155323-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 AACTGTGTGTTTAAGCTGTTGCATTAAAAAGCTTTCTTCTACATCAATATCTGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 CGCTCTGACTTTCTTCTGGTGTATGGGGATGTCATCTCAAACATCAATATCACCAGAGC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 TCCGGGCTTCATAGTTCTTTGTAATATGTTGAAGTTAATTTGAATTGAACTGATTTTGTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 TCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.5%;
Similarity 54.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                         infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
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Pred. No. 9.5;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18301;
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    24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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01 - S
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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02-OCT-2000;
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08-SEP-2000;
12-SEP-2000;
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25-SEP-2000;
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19-MAY-2000;
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2000US-0186350.
2000US-0189874.
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2000US-0220963.
2000US-0220964.
2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-0231243.
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2000US-0232399
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A RATE OF THE PROPERTY OF THE 
                    Disclosure; SEQ ID NO 609; 564pp + Sequence Listing; English.
                                                               New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders - \ 
                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 - NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VON-
                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-02
                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
AAF26310/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel kidney related polynucleotides

(AA162971-AA163793) and the encoded polypeptides (AAM42417-AAM42691)

(C) collectively known as kidney antigens and the use of such kidney antigens

(C) collectively known as kidney antigens and the use of such kidney antigens

(C) concer metastases. The polynucleotides and proteins are also

(C) useful for preventing, treating or ameliorating medical conditions

(C) concerned the protein or gene therapy. The genes are isolated from a range

(C) of human tissues disclosed in the specification. The nucleic acids,

(C) treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,

(C) curdinate the protein of: (a) cancer, e.g. breast and ovarian cancer,

(C) cardother cancers of the adrenal gland, bone, bone marrow, breast,

(C) castoinnes thyroiditis, diabetes mellitus, Croth's disease, multiple

(C) cardovascular disorders such as mycoardial ischemias; (d) wound

(c) cardovascular disorders such as woral and epilepsy;

(c) cardotyascular diseases e.g. cerebral anoxia and epilepsy;

(c) cardotyascular diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                    WPI; 2001-182785/18
                                                                                         Fraser CM,
Timmis KN,
                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000WO-EP07001
                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200107588-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nodulation factor; transgenic plant; growth promoter; plant yield; development promoter; Leguminosae; root formation; ORF00968; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF26310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF26310 standard; DNA; 936 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18301 BP; 5076 A; 4392 C; 3842 G; 4991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parasitic infections.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                     Peterson J;
                                                                                                                                                                                (TIGR-) TIGR INST GENOMIC RES.
(QIAG-) QIAGEN GMBH.
(GERB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                   23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas sp nodulation factor encoding DNA ORF00968.
                                                                                                                                                            (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 CGCTCTGACTTTCTCTGGGGTATGGGGATGTCATCTCAAACATCAATATCACCAGAGC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 TCCGGGCTTCATAGTTCTTTGTAATATGTTGAAGTTAATTTGAATTGAATTTGTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 TCAGAGCTCTATCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 AACTGTGTTTTAAGCTGTTGCATTAAAAAGCTTTCTTCTACATCAATATCTGCTGTGC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                      Tuemmler B, Hoheisei
Moore E, Straetz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                 99DE-1034718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%;
                                                                                                              Hoheisel J, Duesterhoeft A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.6; DI
Pred. No. 9.5;
0; Mismatches
                                                                                         Heim S,
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                                                                                            Nelson K,
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54;

Indels

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Hickey E; Hilbert H;

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      This invention describes novel DNA sequences (1) that express products CC having the biological function of nodulation factors. The invention also describes (1) recombinant expression vectors containing (1); (2) cc describes (1) recombinant expression vectors containing (1); (2) cc the vector of (1); (3) production of nodulation factors by culturing cc delts of (2); (4) (partial) expression products (II) of (I), and cc synthetic proteins or peptides with the same sequences; (5) monoclonal or cp produce monoclonal Ab; and (7) transgenic plants that contain cells that cc produce monoclonal Ab; and (7) transgenic plants that contain factors or synthetic protein as probes and primers for detection, cc isolation and amplification of fill-length cDNA sequences and are used to produce transgenic plants. Cells transformed with (I), and recombinant cc nodulation factors or synthetic peptides or proteins with the same activities, are used to promote growth, development and yield of plants, cartivities, are used to promote growth, development and yield of plants, cartivities, are used to promote growth, development and yield of plants, containing the promote growth of factors encoded by (1) promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  Hillman JL,
Azimzai Y,
                                                                                                                                                                                                                                                                                                       Human; transcription factor; TRFX; cell proliferative disease; autolimmune disease; inflammation; neurological disease; developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV; neuroprotective; antiinflammatory; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                             Human transcription factor TRFX-79 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA83052 standard; DNA; 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 936 BP; 182 A; 293 C; 279 G; 182 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         particularly Leguminosae. The nodulation factors encoded by (I) promote root formation in plants and improve yield, particularly when grown on soil contaminated with xenobiotics injurious to plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3a; Page 14; 16pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA encoding a bacterial nodulation protein, useful e.g. for promoting root formation and yield of plants, and producing transgenic
                                                                                                                                               13-MAR-2001; 2001WO-US08117
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                       13-MAR-2000;
                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 GGGAGTGGGCTGCATCTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 AGTGATGGAGTGGAGGTT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 CGAGGCCACCAGGGGGAAGTGTCGCTTGCTTGCTGGCCGGATCGAACACCGGCTTGGCCGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 CGTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCACAAACAGGGTTCTCCAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCGAGGCGCGAATGGTCAGCAGCACCTCGCGTACCGGCTTGGCCAGTTCCAGAGCATA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAGAAGACCCAGGGTCTCCGGCGTTTTGCATTTCCTCTGAGGCCTGTTTCAGGGCAGT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 6.5%;
Similarity 52.2%;
  Baughn MR,
Bandman O,
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                                                                                                       2000US-0188986.
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Yue H,
Tang YT,
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Pred. No. 2.3;
0; Mismatches 66;
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  Lal P,
Mathur
  P, Shal
      Shah
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  Patterson C;
P, Au-Young
  Au-Young J;
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Search completed: October 10, 2002, 15:15:35
Job time: 118 secs

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                                                                                                                                                                                                                                                                                                         including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the coding sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, including associated with the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity -
                                                                                                                                                                                                                                                                  Sequence 2187 BP; 386 A; 697 C; 737 G; 367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-570896/64.
P-PSDB; ABB50228.
                                                                                  788 TGGCAGCACCTCCAGGGTGCTCAGCTCTGAGAAGCCGCCGCGCGCTGCCAGCGCCTGGCATG 729
                                           438 TCCTCTGAGCCTGTTTCAGGGCAGTAGTGATGGAGTGGAGG 478
                                                                                                                              378 TAGTACCACAAACAGGGTTCTCCATTTTCAGAAGACCCAGGGTCTCCGGCGTTTTGCATT 437
                                                                                                                                                                                                  Local Similarity
TGCGTTGCACCTGCTCGATGCACGGTGAGAAGGAGCAGAAG
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                6.48;
57.48;
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                                                                                                                                                                                                Score 32.2; DB 22;
Pred. No. 4.2;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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        US-09-489-101A-8_COPY_1_500 500 1 gggacgtgagccgctgccc.
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*

1: //gn2_6/ptodata/2/ina/5A_COMB.seq:*

2: //gn2_6/ptodata/2/ina/5B_COMB.seq:*

3: //gn2_6/ptodata/2/ina/6A_COMB.seq:*

4: //gn2_6/ptodata/2/ina/6B_COMB.seq:*

5: //gn2_6/ptodata/2/ina/FCTUS_COMB.seq:*

6: //gn2_6/ptodata/2/ina/Dackfiles1.seq:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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        4800
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30001
90001
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20137
20138
23071
1789
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2089
3708
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1293
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12924
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2547
                 US-08-232-463-14
US-08-246-849-1
US-08-293-284A-1
US-08-293-284A-1
US-08-961-810-19
US-08-961-083-15
US-08-961-083-15
US-08-961-083-15
US-08-961-083-7
US-08-961-083-7
US-08-961-083-7
US-08-968-878-7
US-08-968-878-7
US-08-968-681-129-1
US-08-968-62
US-08-968-62
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US-08-958-1558-116
US-08-958-1558-116
US-08-910-973-1
US-08-910-973-1
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US-08-910-973-1
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Sequence 14, Appli sequence 1, Appli sequence 1, Appli sequence 19, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli sequence 1, Appli sequence 206, Appli sequence 206, Appli sequence 210, Appli sequence 210, Appli sequence 210, Appli sequence 210, Appli sequence 211, Appli sequence 211, Appli sequence 211, Appli sequence 11, Appli
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                                     ; CLONE: pTZgpt-F1s
US-08-232-463-14
      Query Match
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                               STRANDEDNESS: single TOPOLOGY: linear
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(703)836-9300 AX: (703)83-4109 : 899149

30472/114 IMMU

US/08/232,463

linear

10.6%;

Score 53;

DΒ 1;

Length 7218;

C 28 32 6.4 3708 1 US-08-416-523-1 C 29 32 6.4 3708 3 US-08-789-789-74-78-1 31 31.6 6.3 3011 2 US-08-328-111-712 31 31.6 6.3 3211 2 US-08-574-95A-8 32 31.6 6.3 3211 2 US-08-574-95A-8 32 31.6 6.3 3211 2 US-08-574-95A-8 33 31.6 6.3 3211 2 US-08-574-95A-8 33 31.6 6.3 3211 2 US-08-78-328-11 C 37 31.4 6.3 3207 4 US-09-357-014-6 34 31.4 6.3 32207 4 US-08-728-323A-1 C 37 31.4 6.3 32207 4 US-08-728-323A-1 C 39 31.4 6.3 32207 4 US-08-75-66A-20 C 40 31.2 6.2 2458 3 US-08-6611-587-6 41 31 6.2 2458 3 US-08-611-587-6 42 30.8 6.1 1041 4 US-09-337-31A-20 43 30.6 6.1 1041 4 US-09-337-120-10 C 43 30.6 6.1 13987 2 US-08-804-227C-13 45 30.6 6.1 US-08-32463 5 Patent NO SCHEIFLINGER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESS: 52 CORRESPONDENCE ADDRESS: 52 CORRES	RESULT 1 US-08-232 Sequence Patent No GENERAL APPLIG APP		44	c 42	41		c 38		ນ ຜ	34	ω u w k	υ L	30	c 29	
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-416-523-1 -789-478-11 -789-478-1 -789-478-1 -574-959A-8 -574-959A-6 -577-914-6 -357-014-6 -357-014-6 -357-69A-20 -230-371A-20 -611-587-6 -371-913A-10 -371-913A-10 -393-07261-10 -804-227C-13 IGNMENTS IGNMENTS IGNMENTS IGNMENTS IGNMENTS IGNMENTS	/082 / F. G. OMB:		N 05	4	, 2 - (4 w	. 4	N	J N	4	N #	- K	4	ωŀ	_
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RESULT 2
US-08-346-849-1
                                                                                       NAME: Brook, David E. 22,592
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08346849 Patent No. 5670483
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                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: BIOOK, DAVID E.
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1163 RRRRRRRRRRRRRRRR 1147
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                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PATENTIN Release #1.0, Version #1.25
                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                  STRANDEDNESS:
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  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Lockshin, Curtis
  linear
                    double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STABLE MACROSCOPIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4%;
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80; Mismatches 120;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 123; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                           REFERENCE/DOCKET NUMBER: 22,592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAY. (617)
                                                                                                                                                                 FILING DATE: 28-DEC-1992
ATTORNEY/AGET INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1550 ACTCATGATGCTAGAGACTGGAAAAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAG 1609
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1724 TTCAAGATTATTCAAAAGGCCTTTGAAACTTTGACTGATTC 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER
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                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Relaccompatible
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LOCATION: 1292..29
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
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STRANDEDNESS:
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                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         02173-4799
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                nucleic acid
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                                  3083 base pairs
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Rich, Alexander
DiPersio, C. Michael
Lockshin, Curtis
                                                                                         (617)
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                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
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1292..2590
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28-DEC-1992
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Pred. No. 1.6e-06;
0; Mismatches 92;
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                                                                                              TELEFAX: (503) 295-6679
TELEX: 360619
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA TITLE OF INVENTION: MISMATCH REPAIR GENES NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
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                                 SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
TYPE: nucleic acid
                                                                                                                                                        REFERENCE/DOCKET NUMBER: OH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-6655
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                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1292..2590
OTHER INFORMATION: /product= "zuotin"
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ADDRESSEE: Heuser
TOPOLOGY:
                 STRANDEDNESS:
                                                                                                                                                                                                                     NAME: Van Rysselberghe, Pierre C. REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Bronner, C. Eric
Baker, Sean M.
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linear
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                 single
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US-08-352-902D-19/c
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                                                                                                                                                                 Matches
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
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128 AAATAAAACCAAAAAACAGGTAAGTAAT 101
                                          422 TGGTGAACCAATAAAAGAAGGAGATAAT 449
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                                                                                188 GATTCACACAGCCCACGAAGGAGTGGTTATGCAACATCTCCCGGAGAACTGCAAAACAAA 129
                                                                                                                      362 GATCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAGC 421
                                                                                                                                                                                     Local Similarity
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CLASSIFICATION: <Unknown>
ATTORNEY_AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE_POCKET NUMBER: 306B
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
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                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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STATE: Oregon
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TELEFAX: (503) 295-6679
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                                                                                                                                                                 Conservative
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Baker, Sean M.
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                                                                                                                                                                                   Score 35.2; DB . Pred. No. 0.088;
                                                                                                                                                                                                    DB 4; Length 377;
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Sequence 1, Application US/09309682
Patent No. 6214348
GENERAL INFORMATION:
APPLICANT: Black, Michael T.
TITLE OF INVENTION: No. 6214348el Ftsy
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Frice & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 6072032
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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LENGTH: 1293 base pair
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NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
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APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                    314 TGCAGTTCTTGGAC 327
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                                                                                                                                                                                                                                                   TGAAGTTCTTGAAC 346
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4000 Bell Atlantic Tower, 1717 Arch Stre
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53,7%;
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Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                           Sequence 159, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                 COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VESTEMARE: ASCIT Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
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LENGTH: 1293 base pair
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                CITY: Rockville
STATE: Maryland
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STRANDEDNESS: double
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CLASSIFICATION: 435
                 FILING DATE:
                                 APPLICATION NUMBER:
                                                                                                                                                                              COUNTRY:
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REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM
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72; Conserv
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                                                                                                                                                                                                                                  E: Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1293 base pairs
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IBM Compatible
                                                                                                                        Diskette, 3.50 inch, 1.4Mb storage
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                                                                                     MSDOS version 6.2
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                                   US/08/961,083
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INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1924 base pairs
TYPE: nucleic acid
STRANDENESS: double
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NAME: Brookes, A. Ander.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB34

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 109-8504
                                                                                                                              SOFTWARE: Patentin ReleacURENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
                                APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
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APPLICATION NUMBER:
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                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
COFFWAREN DATASET.
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                New York
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US 07/672,183
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Patent No. 6054296
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 4:
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REFERENCE/DOCKET NUMBER: 454
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2172 AGAAGAAGAAGAATAGTACCAGAAAATTTGACAACTGAAGAATCAAAA 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1932 TCAAGAAACGGAAGAAAATGGAAAAACAAGTTGAAGCAATCACCAAGCAAATAGAAGC 1991
                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 TCAGGAACTGGAGGATAAGAAGAGTTATCCGAGGAATCAGAAGATGAAGAATTGCAGTT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         STREET: ***
CTTY: WASHINGTON
                                                                                                                                    APPLICATION NUMBER: US/08/262,220 FILING DATE: 20-JUN-1994
                                                                                                                                                                                                 SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Pred. No. 0.39;
0; Mismatches 159; Indels
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BERGSTROM=3

TELEX: 248633 INFORMATION FOR SEQ ID NO:

7:

SEQUENCE CHARACTERISTICS:

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US-08-471-733-7/c

Sequence 7, Application

Patent No. 6068842

GENERAL INFORMATION:
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                                                                CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/262,220
FILING DATE: 20-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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STRAIN: 1p90
IMMEDIATE SOURCE:
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                 REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   STREET:
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LOCATION:
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                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2547 base pairs TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                     20004
                                                 COOPER, IVER P.
                                                                                                                                                                                                                                                                                                                                     WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08471733
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419 SEVENTH STREET, N.W.
                                                                                                                                                                                                                                                                                                                    USA
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443..2242
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380..442
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380..2245
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                                28,005
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Pred. No. 0.49;
0; Mismatches 61;
               BERGSTROM=3
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/262,220
                                                                                                                                                                                                                                                                                                                            APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2547 base pairs
TYPE: nucleic acid
               APPLICATION NUMBER: 08/2
FILING DATE: 20-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P,
                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2355 AAAATTCAAGATGCTTATGAAAAGATTT 2328
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IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         STREET: 419 SEVEN CITY: WASHINGTON
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LOCATION:
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NAME: COOPER, IVER REGISTRATION NUMBER:
                                                                                                                 FILING DATE:
                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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443..2242
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380..442
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380..2245
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                                                                                                               06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.8%;
                                                                                                                               US/08/468,878
28,005
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Pred. No. 0.49;
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US-08-750-494-7/c

; Sequence 7, Application US/08750494
; Patent No. 6204018
; GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2547 base pairs
                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,494
                                                                                                                                                                                                                                                                       APPLICANT: BARGOUR ALAN G.
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
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                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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IMMEDIATE SOURCE:
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                           CITY: WASHINGTON
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380..2245
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443..2242
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380..442
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INFORMATION FOR SEQ ID NO:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                             APPLICANT: Kanji NAKAMURA
APPLICANT: Hiroaki ISHIDA
TITLE OF INVENTION: GENE RECOMBINANT WITH BIODEGRADABILITY
TITLE OF INVENTION: FOR CHLORINATED ETHYLENE AND BIO-TREATMENT OF
TITLE OF INVENTION: CHLORINATED ETHYLENE THEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                 CURRENT APPLICATION DATA
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IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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                                              SOFTWARE:
                                                                                                                                                                  CITY: Shinjuku-Ku
STATE: Tokyo
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                                                                                                                                  COUNTRY: Japan
ZIP: 160-0023
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FILING DATE:
                 APPLICATION NUMBER:
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443..2242
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380..442
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7, Nishi-Shinjuku 3-Chome
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Pred. No. 0.49;
0; Mismatches 61;
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                                                                                                  3.5 inches, 1.44Mb storage
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RESULT 15
US-08-681-129-1
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                                                           Sequence 1, Application US/08681129
Patent No. 5738854
GENERAL INFORMATION:
APPLICANT: Mettenleiter, Thomas Cristoph
TITLE OF INVENTION: Pseudorables virus va
                                                                                                                                                                                                                                                                                                                                            Matches
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IDENTIFICATION METHOD: 1
OTHER INFORMATION: pheD
FEATURE:
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NAME/KEY:
LOCATION:
                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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LENGTH: 4800 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: 174990
FILING DATE: 30-June-1997
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ORIGINAL SOURCE:
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APPLICATION NUMBER: 174997/1997, Japan
FILING DATE: 30-June-1997
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LOCATION: 1754..3268
IDENTIFICATION METHOD:
OTHER INFORMATION: phe
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LOCATION: 127..345
IDENTIFICATION METHOD:
OTHER INFORMATION: ph
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                                                                                                                                                                                                                                                                                           36 GGCGCCATCATGCTGCTTCTGCCAAGCGCCGGGACGGCCGGGGCACCGCCATCACCCAC 95
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OTHER INFORMATION: pheE of phenol-hydroxylase
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LOCATION:
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les 47; Conserv
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LOCATION:
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LOCATION: 434..1429
IDENTIFICATION METHOD:
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                   ADDRESSEE:
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E: Organon Teknika Corporation
1330 Piccard Drive
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3689..4756
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1440..1712
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 92.203.079.6 FILING DATE: 06-OCT-1992 ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2.
FILING DATE: 02-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                    RIGLM: FSC. ORGANISM: FSC. TONTN: Kaplan
                                                                     834 GGACGACGCCTCGGCCGCCGTGGTCGAGGCCGTGTCCGCCGTCGC 878
                                                                                                                                           774 GATGCTCTGCGACCTCGTGGCCGGGGCGGACGCCATCCTGCGGCGGGCCGCGGGCGCCTC 833
                                                                                                     68 GGACGGCCGGGGCACCGCCATCACCCACGCTCTGACCTCTGCCTC 112
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CLASSIFICATION: 424
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STATE: Maryland
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57.1%;
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Result
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IDENTITY_NUC
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Copyright (c) 1993 ~ 2002 Compugen Ltd.
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gb_est1:*
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BC012376 Homo sapi
BG720251 602692311
AL548837 AL548837
B1460193 603201794
BG39661 602459730
AL517760 AL517760
BG71844 502269473
AV655598 AV655598
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ALIGNMENTS

REFERENCE AUTHORS TITLE LOCUS DEFINITION RESULT 1 BF037074 COMMENT BASE COUNT FEATURES SOURCE ORGANISM KEYWORDS ACCESSION VERSION source cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9595 row: 1 column: 09 High quality sequence stop: 738. 1. .761 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 761) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) BF037074 761 bp mRNA linear EST 20-OCT-2000 601456938Fl NTH_MGC_66 Homo sapiens cDNA clone IMAGE:3860504 5', Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP Homo sapiens Contact: Robert Strausberg, Ph.D. BF037074 BF037074.1 GI:10745303 mRNA sequence. Jnpublished (1999) 233 a /tissue_type="adenocarcinoma" /lab_host="DH10B (phage-resistant)" /note="Organ: ovary; Vector: pcMV-SpORT6; Site_1: NotI; /notI, NotI, Not Technologies. /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3860504" /clone_lib="NIH_MGC_66" 186 g 179 t tionally. Primer: Oligo dT. Library constructed by Life

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           Email: genomics@hri.co.jp
HRI human cDNA project; 5'~& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                        Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3951
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 844)
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AU121047 HEMBB1 Homo
                                                                                                                                            Contact: Takao Isogai
                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                       Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
                                                                                                                                                                                                                                                            Homo sapiens
                                                                             Fax: 81-438-52-3952
                                                                                                                                                                                            Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
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iens cDNA clone HEMBB1001966
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Homo sapiens, clone IMAGE:3860504,
BC012376
BC012376.1 GI:15214504
HTC.
                                                                                                                                                       Homo sapiens
                                                                                                     Strausberg, R.
Email: cgapbs-r@mail.nih.gov
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                                                             Direct Submission
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 920)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBB1001966"
/clone_lib="HEMBB10"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME185FL3"
179 c 205 g 204 t 4 others
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Pred. No. 4.8e-117;
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                                                  AAATGTTATCTGATCCAGTG 500
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                                                                                                     CTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTATG 480
                                                                                                                                                                                                       AGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAG
                                                                                                                                                                                                                                AGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to protein
This clone
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Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D.M., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3860504"
/tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pCMV-SPORT6"
180 c 222 g 214 t
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Pred. No. 5e-117;
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                    301 ACCAAGATCATTATGCAGTTCTTGGACTTGGCCATGTGAGATACAAGGCTACACAGAGAC
                                                                     334 AAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGA
                                                                                                               241 AAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGA 300
                                                                                                                                                                274 CTTCTGCCTCTTTTCAGGAACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGATG
                                                                                                                                                                                                                                                                                                 121 GTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATG 180
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                                                                                                                                                                                       CTTCTGCCTCTTTTCAGGAACTGGAGGATAAGAAAAGAGTTATCCGAGGAATCAGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500;
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 666) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov plate: LLAM10736 row: e column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG720251.1 GI:13999438
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site1: BamHI; Site2: SalI-MDI (9tcgs); Oligo-df primed using primer 5. "TTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National constitutes of Health). Note: this is a NIH_MGC Library." Institutes of Health). Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 489; DB 10;
Pred. No. 2.8e-114;
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ORIGIN
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AUTHORS
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                                  180 GCTTCTGCCTCTTTCAGGAACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGAT 239
                                                                                                   249 TGTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAAT 308
                                                                                                                                                                   120 TGTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAAT 179
                                                                                                                                                                                                                                                                                                                                                                              129 GGGACGTGAGCCGCTGCGCCCACCGGGCTAGACCCGGCGCCATCATGCTGCTTCTGCCAA 188
                                                                                                                                                                                                                                        189 GCGCCGCGGNACGGCCGGGGCCATCACCCACGCTCTGACCTCTGCCTCTACACTC 248
                                                                                                                                                                                                                                                                                                             61 GCGCCGCGG-ACGGCCGGGGCACCGCCATCACCCACGCTCTGACCTCTGCCCTCTACACTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGACGTGAGCCGCCTGCGCCCACCGGGCTAGACCCGGCGCCATCATGCTGCTTCTGCCAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATGTTATCTGATCCAGTG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGAACCAATAAAAGAAGGAGATAATGACTTCACTTCCATTAAAACTAAAAGCTTAT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCAAGATCATTATGCAGTTCTTGGACTTGGCCATGTGAGATACAAGGCTACACAGAGAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCAT-AACTAAAGCTTAT 479
BP 191 91006 EVRY cedex - rrance
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 bp mRNA linear EST 16-FEB-2001
AL54488 77 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI043YJ07 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 780)
Li.W.B., Gruber, C., Jessee, J., and Polayes, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="LITI_NPI006_PL2"
/clone=lib="LITI_NPI006_PL2"
/clone=lib="LITI_NPI006_PL2"
/clone=lib="LITI_NPI006_PL2"
/clone=lib="LITI_NPI006_PL2"
/clone=lib="lidenta"
/clone="Topoly prime" Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the pCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6 encounter the Not I and Eco RV sites of the PCMVSPORT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 489; DB 9;
Pred. No. 3e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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SOURCE
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                                                                                                                                                                           BASE COUNT
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                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
Matches 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 GARATGITATCTGATCCAGTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 GCTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 CAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 CAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 GAAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGGTGAACCAATAAAAGAAGGAGGAGATAATGACTACTTCACTTGCATAACTAAAAGCTTAT 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIENN)

Toshiyuki and Piero Carninci (RIENN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 689)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 bp mRNA linear EST 21-AUG-2001 663201794F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267854 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11075 row: k column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 687
Conservative
                                                                                                                                                                /note-"organ: testis; Vector: pBluescriptR (modified /note-"organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-Xhol (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVTV-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMI/NHGRI, Mational Institutes of Health). Note: this is a NIH_MGC Library." a 156 c 176 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5267854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                  97.6%;
99.8%;
   0,
                                  Score 488; DB 10; Length 689; Pred. No. 5.2e-114;
   Mismatches
   Indels
   1;
   Gaps
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GCGCCGCGGACGGCCGGGGCACCGCCATCACCCCACGCTCTGACCCTCTGACCCTCTACACTCT 191
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                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM1303 row: 1 column: 07
High quality sequence stop: 758.
Location/Qualifiers
                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 937)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602459730F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4582038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
/clone="IMAGE:4582038"
/clone=lib="NHH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 955)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                       AL517760.1 GI:12781253
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505 CTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTATG
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AL517760 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA004YE24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGORI; CDNA made by oligo-dT priming. Directionally cloned into EGORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Pred. No. 5.8e~114;
0; Mismatches 0;
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469 GCTGGTGAACCAATAAAAGAAGGAGGACTACTTGACTTCACTTGCATAACTAAAGCTTAT 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGACGTGAGCCGCCGCCCACCGGGCTAGACCCGGGCGCCATCATGCTGCTTCTGCCAA 60
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                                                                                                    BG718443 829 bp mRNA linear EST 08-MAY-2001 602656473F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828339 5', mRNA sequence.
BG718443 BG7:18443.1 GI:13997630
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="raxon.9606"
/clone="CSODA004YE24"
/clone_liba"tri_NFL011_NBC1"
/sexa"male"
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/lab_host="DH10B"
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                                               CTGGTGAACCAATAAAAGAAGGAGATAATGACTTCACTTCACTTGCATAACTAAAGCTTATG
                                                                                                    CTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTATG 480
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIREN)
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
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1 (bases 1 to 829)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be
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/db_xref="taxon:9606"
/clone="IMAGE:4828339"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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Pred. No. 2.5e-113;
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                                                                                                      AAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGA 300
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chinese National Human Genome Center at Shanghai
551 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
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1 (bases 1 to 665)
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Fax: 86-21-50801922
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clone is available at CHGC in
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/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
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Pred. No. 8.5e-113;
0; Mismatches 3;
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121 GTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGC~TTTGTTAAGAGGAGAAACAGAAATG
                                        121 GTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATG 180
                                                                                       61 GCGCCGCGGACGGCCGGGGCACCGCCATCACCCACGCTCTGACCTCTGCCTCTACACTCT
                                                                                                                          61 GCGCCGCGGACGGCCGCGACCCCCATCACCCACGCTCTGACCTCTGCCTCTACACTCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10246 row: d column: 15
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BG165721.1 GI:12672424
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602344558F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4454366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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1 (bases 1 to 859)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
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/tissue_type="hypernephroma, cell line"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4454366"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qz41h10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2029507 3'
similar to TR:Q99543 Q99543 M-PHASE PHOSPHOPROTEIN 11 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
//note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with Anotis="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                       /clone="IMAGE:2029507"
/clone_lib="NCI_CGAP_Kid11"
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AW161245

au70d01.yl Schneider fetal brain 00004 Homo sapiens cDNA clone au70d02.781601 5' similar to TR:060415 060415 WUGSC:H_RG276003.1A
                                                                                                                       White,Y., Wylie,T., Watersto
WashU-NCI human EST Project
Unpublished (1997)
Other_ESTs: au70d01.x1
                                                                                                                                                                         Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Email: est@watson.wustl.edu This clone is available royalty-free through \ensuremath{\mbox{LNL}} ; contact the
                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 579)
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AW161245.1
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Fax: 314 286 1810
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               AAATGTTATCTGATCCAGTG 500
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                                                                     CTGGTGAACCAATAAAAGAAGGAGATAATGACTACACTTCACTTGCATAACTAAAGCTTATG 480
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GAATTTTATCTGATGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov) for further information
Seq primer: -40RP from Gibco
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 417.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and 3' adaptor sequence: 5'-GAGAGAGAGAGTTTTTTTTTTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Tipalu) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: brain; Vector: pBluescript SK (Stratagene);
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="ItARGE:2781601"
/clone_lib="Schneider fetal brain
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RESULT 14 AU128589

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AUTHORS
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                      GCTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTAT
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AU128589
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1532-3 Yana, Kisarazu, Cl
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/db_xref="taxon:9606"
/clone="NT2RP2003763"
/clone_lib="NT2RP2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
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Pred. No. 5.1
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5.1e-107;
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Qy	pb 05	Db .5	מם מס	Query Best 1 Match	BASE C	FEATURES SOU		AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISH	RESULT 15 BI562033 LOCUS DEFINITION	Qу	ф
181	271	212	1 152		N COUNT	RES		AUTHORS TITLE JOURNAL	CESSION RSION YWORDS ÜRCE ORGANISM	r 15 033 ITIO	480 569	509
CTTCTGCCTCTTTCAGGAACTGGAAGAAGAAGAAGATTATCCGAGGAATCAGAAGATG 240	GICAGGIIGAACCIGIGGAAGAIGGIITIGAAGCITIIGTIAAGAGGAGAAACAGAAAIG 180 			<pre>match 87.6%; Score 438.2; DB 10; Length 656; socal Similarity 96.8%; Pred. No. 2.6e-101; socal Similarity 96.8%; Pred. No. 2.6e-101; socal Similarity 96.8%; Pred. No. 2.6e-101;</pre>	/Organism="Nomo Sapiens" /db_xref="taxon:9606" /clone="IMAGE:5297303" /clone="IMAGE:5297303" /clone="IIM-"NIH_MGC_97" /lab_host="Dellos" /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgag points); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Plate: LL/ High qual:	Email: cgapbs r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	I (bases 1 to 656) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	2033.1 2033.1 n. sapie ryota;	BI562033 656 bp mRNA linear EST 05-SEP-2001 603255091F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5297303 5',	GAAATGTTATCTGATC 495 1 1 1 1 1 1 1 1 1 1	

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    481 AAATGTTATCTGATC 495
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Search completed: October 10, 2002, 20:27:42 Job time : 702.733 secs

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                                                                                                                                                                                                     Score
    500
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2: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT: *
3: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT: *
4: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT: *
4: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT: *
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Zuotin gene. Sacc
Human zuotin codin
Drosophila melanog
                                                          Drosophila melanog
C albicans apoptos
S cerevisiae apopt
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Human small cell l
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Human cDNA encodin	AAS26008	22	1565		34.4	45
S. pneumoniae deri	AAZ96236	19	1372		34.4	44
lasmodium fa.	AAQ80908	16	2223		34.6	43
Streptococcus pneu	AAV27403	19	1924		34.6	42
Novel human diagno	AAS39178	22	393		34.6	41
Borrelia burgdorfe	AAX20248	20	910715	7.0	34.8	40
Streptococcus pneu	AAX30135	20	1293		34.8	39
	AAA70225	21	4056		35	38
Mycoplasma hyopneu	AAA56820	21	1125		35	37
	AAQ03633	11	450		35	36
AL021529 cDNA clon	AAC90077	22	38734		35.2	35 5
Human METH1 relate	AAZ32020	20	38734		5	34
Plasmodium falcipa	AAA70099	21	3579		5	<u>3</u>
Wild type hMLH1 ge	AAQ90828	16	377		35.2	32
Nucleotide sequenc	AAA58471	21	58857		5	31
Human stromal anti	ABA08622	22	2987		5	30
DNA mismatch repai	AAT29628	17	1510		5	29
Drosophila melanog	ABL06648	23	3935		5	28
Drosophila melanog	ABL06649	23	1305		5	27
Human immune/haema	AAK64825	22	330		5	26
Human immune/haema	AAK64824	22	330		5	25
Human immune/haema	AAK64823	22	330		Ģ	24
	AAS32675	22	1386		36	23
Human genomic DNA	AAS32671	22	1384		36	22
0	AAS32674	22	1381		ω	21
	AAQ87587	16	1686			20
	AAS90709	23	843			19
	AAD17186	22	125401		•	18
Streptomyces nours	AAD17184	22	65140		•	17
ERD48 insert DNA i	AAD17193	22	2700	8.0	40.2	16
Chicken leucocytoz	AAT05868		3399		•	15
Borrelia burgdorfe	AAX20252		35515		•	14
. burgdorferi an	181		1125		•	13
B. burgdorferi ant	_				•	12
Mycoplasma genital	5884		580073		•	11
Drosophila melanog	ABL16648		5071		•	10

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ALIGNMENTS

RESULT 1 AAC98111

AAC98111;

AAC98111 standard; cDNA; 876

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Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne; fimunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal dis Human colon cancer antigen nucleotide sequence SEQ 09-MAR-2001 (first entry) Rosen CA, Ruben SM; (HUMA-) HUMAN GENOME SCI INC 12-MAR-1999; 08-MAR-2000; 2000WO-US05883. 21-SEP-2000 WO200055351-A1 Homo sapiens. infectious disease; cardiovascular disorder; ss. 99US-0124270. renal disorder; ID NO:121. vulnerary;

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RESULT 2
ABK09776
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                                                                                                                                                                                                                                                                                                                AAATGTTATCTGATCCAGTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No. 1.3e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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ABK09776 standard; cDNA; 1845 BP

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181 CTTCTGCCTCTTTTCAGGAACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGATG

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                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide encoding a comparising a portion of an ovarian tumour protein. The comparise comprising a portion of an ovarian tumour protein. The comparise comparising a portion of an ovarian tumour protein. The comparise comparise comparison of an ovarian tumour protein. The collater that expresses the sequences is useful for treating ovarian cancer by comparison the patient. An antigen presenting cell chart expresses the sequences is useful for treating ovarian cancer by comparison to find the patient to inhibit the comparison of cancer. The DNA sequences are useful as probes or primers comparison of a concer in a patient to involve cold hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient comportion to a protein that binds to the apprix, contacting the content of protein that binds to the apprix, comparing the amount of comportion to a predetermined cut-off value and determining the presence of cancer. Sequences ABK09404-ABK09802 represent PCR primers and cDNA content of the content of
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
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13-JUN-2000; 2000US-211457P.
21-JUN-2000; 2000US-213673P.
03-AUG-2000; 2000US-223288P.
01-MAR-2001; 2001US-272790P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian tumour protein; cancer; cytostatic; immunostimulant; ss; gene therapy; CD4+ T cell; CD8+ T cell; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding polypeptide comprising portion of ovarian tumour protein, useful for detection, diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-097641/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 256; 285pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Algate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian tumour protein encoding cDNA #309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001; 2001WO-US16895
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                                                                                                                                                                                                                                 1 GGGACGTGAGCCGCGCCCACCGGGCTAGACCCGGCGCCATCATGCTGCTTCTGCCAA 60
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                           GTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATG
                                                                                                                                                    GCGCCGCGGACGGCCGGGGCACCGCCATCACCCACGCTCTGACCTCTGCCTCTACACTCT 120
  GTCAAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATG
                                                                                                  GCGCCGCGGACGGCCGCGGCCATCACCCACGCTCTGACCTCTGCCTCTACACTCT
                                                                                                                                                                                                     GGGACGTGAGCCGCCCCACCGGGCTAGACCCCGCCCATCATGCTGCTTCTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitcham JL, Ha
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        BP; 723 A; 312 C; 413 G; 397 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker SL, P, Mannion J,
                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                              Score 500; DB 24;
Pred. No. 1.9e-142;
                                                                                                                                                                                                                                                                                                        Mismatches
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Benson DR,
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Carter D;
                                                                                                                                                                                                                                                                                                        Indels
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RESULT 3
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           The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a necoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, broast, head and non-small cell lung cancer, melanoma, colon, broast, head
                                                                                                                                                                                                                                            Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; helix-loop-helix; head; protein-binding factor; MPP11; synovial sarcoma; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD11115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD11115 standard; DNA; 1860 BP
                                                                                                                                                                                                          Claim 57; Page 94-95; 152pp; English.
                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                      Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2000; 2000US-0489101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JAN-2001; 2001WO-US02015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human small cell lung cancer associated gene, MPP11.
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                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES (SLOK ) SLOAN KETTERING INST C.
                                                                                                                                                                                                                                                                                                                                                                                       (CORR ) CORNELL RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTATG
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or transitional cancer, leimyosarcoma or synovial sarcoma.
                                                                                                                                                                                                                                                                                                                                                    Scanlan MJ, Jager D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                      Gure AO,
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Best Local
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                                       23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                               pharmaceutical; gene;
                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 1414.
                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                ABL16647 standard; DNA; 2225 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1860 BP; 738 A; 312 C; 413 G; 397 T; 0 other;
              (PEKE ) PE CORP NY
                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                               WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                AAATGTTATCTGATCCAGTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                             (first entry)
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Pred. No. 1.9e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 155;
                                                                                                                                                                                                                                                                                                                            C albicans apoptosis associated coding sequence #48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of cell-cell interactions in higher eukaryotes for the development of
                                               01-JUL-1999;
                                                                                                                                                                                                                        Candida albicans
                                                                                                                                                                                                                                                                                                                                                                           27-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH29904 standard; DNA; 1876 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1414; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
  (JANC ) JANSSEN PHARM NV
                                                                                          03-JUL-2000; 2000WO-BE00077.
                                                                                                                                  11-JAN-2001
                                                                                                                                                                                                                                                                   vaccine; autoimmune
                                                                                                                                                                                                                                                                                   Yeast; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2225 BP; 623 A; 560 C; 632 G; 410 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 CATAACTAAAGCTTATGAAAT 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                               99EP-0870141.
                                                                                                                                                                                                                                                                                   apoptosis; infection; proliferative disease;
                                                                                                                                                                                                                                                              disease; ischaemia; neurodegeneration;
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Yeast and fungal nucleic acids encoding proteins involved in a pathway
                                                                                                                                Contreras RH,
                                                                                                                                                                                                                   01-JUL-1999;
                                                                                                                                                                                                                                                                                                         11-JAN-2001
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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
WPI; 2001-367042/38.
P-PSDB; AAG70739.
                                                                                                                                                                                                                                                                                                                                                              03-JUL-2000; 2000WO-BE00077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S cerevisiae apoptosis associated coding sequence YGR284C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH29775 standard; DNA; 1802 BP.
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                                                                                                                                                                                                                (JANC ) JANSSEN PHARM NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-367042/38.
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                                                                                                              Reekmans
                                                                                                                                                                                                                                                                                           99EP-0870141
                                                                                                                                             De Backer MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Backer MD,
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                                                                                                                                             Luyten WHML,
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                                                                                                                                                 Malcorps IKL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae
                                                                                                                                                                                                                                                                                                                                Membrane-forming peptide; amphiphilic; monovalent metal cation; suture; internal lining; slow-diffusion drug delivery vehicle; erythropoletin; tissue-type plasminogen activator; haemoglobin; insulin; artificial skin; separation matrix; dialysis membranes; filter; collagen; cell migration; hazphaimen; s disease; scrapie infection; therapy; proteolytic disestion; acidic pH resistant; stomach acid; cell adhesion; cell monolayer; zuotin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1802 BP; 593 A; 346 C; 368 G; 495 T; 0 other;
                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zuotin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          certain diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis
                                                                                             28-DEC-1992;
                                                                                                                               23-SEP-1997
                                                                                                                                                                US5670483-A.
                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT90969 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding sequences of the invention.
           (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                     tissue
                                             30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 ACACTTGATCCCAAAGACTGGAAGAACCAAGATCATTATGCAGTTCTTGGACTTGGCCAT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTAC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCGTTTCAGAGCTACTGAAAGTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAG 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCATGATGCTAGAGACTGGAAAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAG 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCAAGATTATTCAAAAGGCCTTTGAAACTTTGACTGATTC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCACTTGCATAACTAAAGCTTATGAAATGTTATCTGATCC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACCATCCAGACAAGCAATCTGCTGCTGGTGGTAGTTTGGACCAAG-----
                                                                                                                                                                                                                                                                                                                   culture; differentiated cell; stratified cell layer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                             92US-0973326.
94US-0346849.
                                                                                             92US-0973326
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                              /product= zuotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; 55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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This sequence represents the yeast zuotin gene. Fragments of the encoded CC protein can be used as the amphiphilic peptides used in the macroscopic membrane (MM) of the invention. The MM is formed by self-assembly of the containing monovalent metal cations. The MM are stable in serum, are containing monovalent metal cations. The MM are stable in serum, are containing monovalent metal cations. The MM are stable in serum, are containing monovalent metal cations. The MM are stable in serum, are containing monovalent metal cations. The MM are stable in serum, are containing products (e.g. sutures), or internal linings. The MM are useful as slow-diffusion drug delivery vehicles for protein-type drugs, cincluding erythropoietin, tissue-type plasminogen activator, synthetic containing articles (e.g. dialysis membranes). Collagen may be combined with the peptides to produce membranes for use as artificial skin. The MM compared the self assembly of the produce membranes for use as artificial skin. The MM could be useful for treating Alzheimer's disease or scrapie infection. As they are resistant to proteolytic digestion and alkaline and acidic phecomology as the containing and migration. The permeability of the MM could be call adhesion and migration. The permeability of the MM also permits collarers which is made of the MM could be collarers of differentiated cells and/or stratified cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membranes formed by self-assembly of amphiphilic peptide(s) - useful as bio:material(s), separation matrices, drug delivery vehicles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Column 29-34; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-479506/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lockshin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang
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밁 Ş g Š ᅜ Š В Ş Query Match Matches 123; 1550 ACTCATGATGCTAGAGACTGGGAAAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAG 1609 1724 1670 TACCATCCAGACAAGCAATCTGCTGCTGGTGGTAGTTTGGACCAAG-----1610 TTGCGTTTCAGAGCTACTGAAAGTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAG 1669 456 TTCACTTGCATAACTAAAGCTTATGAAATGTTATCTGATCC 496 396 CATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTAC 336 GTGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAA 395 276 ACACTTGATCCCAAAGACTGGAAGAACCAAGATCATTATGCAGTTCTTGGACTTGGCCAT 335 Local TTCAAGATTATTCAAAAGGCCTTTGAAACTTTGACTGATTC 1764 Similarity Conservative 10.4%; 0; Score 51.8; Pred. No. 3. Mismatches .1e-05 DB 18; 92; Indels Length 3083; -ATGGCTTT 1723 6, Gaps 455

Sequence 3083 BP; 1026 A; 578 C; 627 G; 852 T; 0 other;

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AAZ11218 standard; DNA; 3083 BP
                                 Human zuotin coding sequence.
                                            09-NOV-1999
                                           (first entry)
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Membrane forming peptide; cell culturing; macroscopic membrane; amphiphilic peptide; slow-diffusion drug delivery system; cell growth; artificial skin; separation matrix; artificial tissue; scraple infection; alzheimer's disease; liver cirrhosis; kidney amyloidosis; protein conformational disease; human; zuotin; ZUO1; ss.

Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitro cell attachment and growth and for supporting artificial tissue

(e.g. for in vivo use as implants). They are particularly useful as

experimental models for Alzheimer's disease and scrapie infection and so

may be used in disease modelling experiments and to assay for agents

which modulate the disease processes. Additionally, they may be used in

this way to study liver cirrhosis, kidney amyloidosis and other protein

conformational diseases. The membrane in the membrane/cell mixture

produced in the method: (i) supports cellular attachment and growth;

(ii) self-assembles to form large, macroscopic membranes that are

insoluble and stable in aqueous solutions, serum and ethanol; (iii) is

highly resistant to heat, alkaline/acidic pHs, chemical denaturants and

proteolytic digestion; (iv) is non-cytotoxic and non-immunogenic; (v) is

constituted by the method of the structures with

simple structures, high tensile strength and a porous structure;

(vii) may be metabolised by humans and animals; (viii) is inexpensive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the human zuotin (ZUO1) protein. Fragments of the protein can be used in the in vitro method of the invention. The method is for culturing cells utilising stable macroscopic membranes formed by the self-assembly of amphiphilic peptides. The peptides are salt-induced to form insoluble and protease-resistant protein filaments with a beta-sheet secondary structure. The membranes may be may be useful in a wide variety of medical, research, industrial and biomaterial applications such as slow-diffusion drug delivery systems, artificial applications such as slow-diffusion drug delivery systems, artificial skin and separation matrices. The membranes may be used to support in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell cultures utilising stable macroscopic membranes formed by the self-assembly of amphiphilic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5955343-A.
1670 TACCATCCAGACAAGCAATCTGCTGCTGGTGGTAGTTTGGACCAAG-----ATGGCTTT 1723
                                                                                                                                                     1610 TTGCGTTTCAGAGCTACTGAAAGTCAAATCATCAAGGCTCACAGAAAAACAAGTTGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3083 BP; 1026 A; 578 C; 627 G; 852 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 33-38; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DiPersio CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1994;
28-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produce; and (ix) can be produced and stored in sterile conditions
                                                                    396 CATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTAC 455
                                                                                                                                                                                                                             336 GTGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAA 395
                                                                                                                                                                                                                                                                                                                                                                                   276 ACACTTGATCCCAAAGACTGGAAGAACCAAGATCATTATGCAGTTCTTGGACTTGGCCAT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                      ACTCATGATGCTAGAGACTGGAAAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAG 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0293284
92US-0973326
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1292..2593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 51.8; DB 20; Length 3083; 55.7%; Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lockshin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rich A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0130511), expressed DNA sequences (ABL0130737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1724 TTCAAGATTATTCAAAAGGCCTTTGAAACTTTGACTGATTC
                                                                 3205
                                                                                                                                 3265 TTAGATACGAGGCCAGCGAGGATGATGTTCGACGGGCTTACAGGCGCATGGTTCTGCTGC 3206
                                                                                                                                                                                                                                                                 Sequence 4791 BP; 1218 A; 1152 C; 1049 G; 1372 T; 0 other;
                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1411; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 1411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL16646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL16646 standard;
3148 TCACATGCATAACCAAAGCTTACGAGATACTGGGTG 3113
                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001.
                               457 TCACTTGCATAACTAAAGCTTATGAAATGTTATCTG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 TTCACTTGCATAACTAAAGCTTATGAAATGTTATCTGATCC 496
                                                                                                                                                                   337 TGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAAGCAATGGTTTTAAAAC 396
                                                                                                                                                                                                                  local
                                                               ACCATCCCGATAAGCGGAAAGCCAAGGGCGAGGAAGTCATCCA---GGACGATGATTACT 3149
                                                                                             ATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTACT 456
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4791
                                                                                                                                                                                                     0
                                                                                                                                                                                                                  Score 42.4; DB 23;
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1764
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                 Length 4791;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention is signalling and
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                                                                                                                                                                                                     Gaps
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RESULT 10

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RESULT 11
AAT58840
ID AAT5
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AC AAT5
XX
AC AAT5
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Z7-1
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                                                                                                                         В
                                                                                                                                              γQ
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB73737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1417; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 1417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL16648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL16648 standard; DNA;
                                                                                                                         4951 TCACATGCATAACCAAAGCTTACGAGATACTGGGTG 4916
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                                                                                                                                                                                                                                  5068 TTAGATACGAGGCCAGCGAGGATGATGTTCGACGGGCTTACAGGCGCATGGTTCTGCTGC 5009
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   27-MAR-1997
                           AAT58840;
                                                                                                                                                                                                                                                                                                                                            Sequence 5071 BP; 1321 A; 1255 C; 1155 G; 1340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                       AAT58840 standard;
                                                                                                                                                   457
                                                                                                                                                                                                       397
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                                                                                                                                                                                                                                                           TGAGATACAAGGCTACACAGAGACAGATCAAAGCAGCTCATAAAGCAATGGTTTTAAAAC 396
                                                                                                                                                 TCACTTGCATAACTAAAGCTTATGAAATGTTATCTG 492
                                                                                                                                                                              ACCATCCCGATAAGCGGAAAGCCAAGGGCGAGGAAGTCATCCA---GGACGATGATTACT
                                                                                                                                                                                                     ATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTACT 456
                                                                                                                                                                                                                                                                                                   similarity 59.0%;
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                                                                                                                                                                                                                                                                                        Conservative
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2000US-0614150
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(first entry)
                                                     DNA; 580073 BP
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                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                    Score 42.4; DB Pred. No. 0.03;
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                                                                                                                                                                                                                                                                                       61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Previously identified as MORF-20079, encoded protein shows 25.73 percentage identity to DNA primase (dnaE) from Clostridium acetobutylicum" complement (13570..14247)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Previously identified as MORF-20078, the encoded protein shows 35.43 percentage identity to the Bacillus subtilis hypothetical protein covered in accession number GB:D26185_102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Previously identified as MORF-20076, the encoded protein shows 27.59 percentage identity to thymidylate kinase (CDCB) from Saccharomyces cerevisiae"
 *Previously identified as MORF-20099, the encoded protein shows 26.82 percentage identity to ATP-dependent nuclease (addA)
                                                                                 "previously identified as MORF-19826 and MORF-20093, the encoded protein shows 46.84 percentage identity to GTP-binding protein from E. coli"
                                                                                                                                                                                                                                                                         "Previously identified as MORF-20084, the encoded protein shows 32.23 percentage identity to transport ATP-binding protein (msbA) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                        "Previously identified as MORF-19823, MORF-20080 and MORF-20081, the encoded protein shows 33.04 percentage identity to 5.10-methylene-tetrahydrofolate dehydrogenase (folD) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Previously identified as MORF-20080, the encoded protein shows 31.50 percentage identity to the ribosomal protein S6 modification protein (rimK) from Escherichia
                                                                                                                                                                           "Previously identified as MORF-20092, the encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (tsr) from B. subtilis"
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мG023
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method; open reading frame; ORF; ss.
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52366.,53220
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 complement
                                                                                       54658..55605
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/note= "
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                                                                                                                                                    abel= MG044
"Previously identified as MORF-20112, the encoded protein shows 36.60 percentage identity to sialoglycoprotease (gcp) from Pasteurella haemolytica" ment (56970..58310)
                                                                                                "Previously identified as MORF-20111, the encoded protein shows 29.45 percentage identity to spermidine/putrescine transport system permease protein C (potC) from E. co.
                                                                                                                                                                                   "Previously identified as MORE-20110, the encoded protein shows 26.51 percentage identity to spermiddine/putrescine transport system permease protein (potB) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                           "The encoded protein shows 48.86 percentage identity to phosphohistidinoprotein-hexose phosphotransferase (ptsH) from Mycoplasma cappicolum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Previously identified as MORF-20102, the encoded protein shows 30.71 percentage identity to histidyl-tran synthetase (hiss) from Mycobacterium leprae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Previously identified as MORF-19831 and MORF-20106, the encoded protein shows 43.20 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Previously identified as MORF-20105, tencoded protein shows 46.83 percentage identity to glycerol kinase (glpK) from E. coli"
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            AAX61812;
                                   AAX61812 standard; DNA;
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                                                                                                                                                                          403
                                                                                                                                                                                                                                                              Local
                                                                                                AGGTTAATGAAGCATATGAAGTTCTAAGTGATGAAG 22589
                                                                                                                        GCATAACTAAAGCTTATGAAATGTTATCTGATCCAG 498
                                                                                                                                                                        CAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAGAAGGAGATAATGACTACTTCACTT 462
                                                                                                                                                                                                 AAAACGCTAGTTCTCAAGACATAAAAAGAGCTTTTAGAAAGCTTGCAATGCAATATCACC
                                                                                                                                                 CCGATCGTCATAAAGCAGAAAATGAAACTACTCAAAAAACAAAATGAGGAAAAGTTTAAAG 22553
                                                                                                                                                                                                                                                  85;
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/note= "
                                                                                                                                                                                                                                                                                                                                                                        /note= "Previously identified as MORF-19845, the encoded protein shows 28.84 percentage identity to glutamic acid specific protease (Spase) from Staphylococcus aureus 91065..91919
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/label=
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encoded protein shows 38.90 percentage
   identity to the protein disclosed in
        GB:D26185_104 from B. subtilis"
81047..82597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Previously identified as MORF-20122,
encoded protein shows 30.25 percent
identity to the protein disclosed in
GB:D26185_99 from B. subtilis"
complement (65713..66249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Previously identified as MORF-20117, the encoded protein shows 83.03 percentage identity to deoxyribose-phosphate aldolase (deoC) from Mycoplasma pneumoniae" complement (64898..65731)
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20-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 202; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic protein; vaccine; Lyme disease; infection; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. burgdorferi antigenic protein coding sequence, t5-14.nt.
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                                                                                                                                                                                                                                                                                                                                  Sequence 1039 BP; 526 A; 94 C; 212 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                         be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                  can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases
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                                 GTGAACCAATAAAAGAAGGAGATAAT 449
                                                        AACAAGAAGACCAAAAAGCAAAAGAATCTAAAGATAAAGTTGAGGAAGAAAAAGAAGTTG 344
                                                                                                                          AAGATCATTATGCAGTTCTTGGACTTGGCCATGTGAGATACAAGGCTACAGAGACAGA 363
                                                                                                                                                                                                                  CTGCCTCTTTTCAGGAACTGGAGGATAAGAAGAGTTATCCGAGGAATCAGAAGATGAAG 243
                                                                                                                                                                                                                                          AAGGGAAAATTAAAGGATTTTTAGATAAGGTTTTAGATCCAGCAAAAGATAAAATTACTT 104
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                                                                               TCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAGCTG 423
                                                                                                                                                 AATTAATGCAGGGCGATGATCCTAATAACAGAGCAATAGCACTGTTACCAGTATTGCCGG 224
                                                                                                                                                                        AATTGCAGTTGGAAGAGTTTCCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGAACC
                                                                                                                                                                                              CAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAATTACAAGAAGAAGATGAAGATAAATG 164
                                                                                                    AAAATAGTCATGACAATCCACCAGTACCAAAAGTAAAAGCAGCAGCACAAAGTGGTGGTC 284
                                                                                                                                                                                                                                                                                       148;
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Similarity 45.4%;
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97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson MS,
                                                                                                                                                                                                                                                                                      0; Mismatches 178;
                                                                                                                                                                                                                                                                                                 Score 41.2;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lathigra
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                                                                                                                                                                                                                             Matches 148;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-)
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                                                                                                                                                                                                                               Conservative
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RESULT 13

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424 GTGAACCAATAAAAGAAGGAGATAAT 449

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B. burgdorferi antigenic protein coding sequence, f5-14.nt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for elicting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also infection caused by a member of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic protein; vaccine; Lyme disease; infection; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1125 BP; 565 A; 101 C; 223 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 202; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATGCTT 183
368 AACAAGAAGACCAAAAAGCAAAGAATCTAAAGATAAAGTTGAGGAAGAAAAAGAAGTTG
                                                                   TCAAAGCAGCTCATAAAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAGCTG 423
                                                                                                                                       AAAATAGTCATGACAATCCACCAGTACCAAAAGTAAAAGCAGCAGCACAAAGTGGTGGTC 367
                                                                                                                                                                                                          AAGATCATTATGCAGTTCTTGGACTTGGCCCATGTGAGATACAAGGCTACACAGAGACAGA 363
                                                                                                                                                                                                                                                                                      AATTAATGCAGGGCGATGATCCTAATAACAGAGCAATAGCACTGTTACCAGTATTGCCGG
                                                                                                                                                                                                                                                                                                                                                         AATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGAACC 303
                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAAATTACAAGAAGAAGATGAAGATAATG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCCTCTTTTCAGGAACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGATGAAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGAAAATTAAAGGATTTTTAGATAAGGTTTTAGATCCAGCAAAAGATAAAATTACTT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 45.4%;
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MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lathigra
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Best Local Similarity
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                         AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes endemic and spiral shaped bacteria called Spirochetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                       9281 AAGGGAAAATTAAAGGATTTTTAGATAAGGTTTTAGATCCAGCAAAAGATAAAATTACTT 9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
9161 AATTAATGCAGGGCGATGATCCTAATAACAGAGCAATAGCACTGTTACCAGTATTGCCGG 9102
                                                                    9221 CAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAATTACAAGAAGAAGAAGATGAAGATAATG
                                                                                                                                                                                                                                                                              Sequence 35515 BP; 10795 A; 5947 C; 4439 G; 13907 T; 427 other;
                                                                                                                                                                                                                                                                                                                                endemic relapsing fever, and Lyme borreliosis, more commonly known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 831-851; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPT; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
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                                244 AATTGCAGTTGGAAGAGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGAACC 303
                                                                                                     184 CTGCCTCTTTTCAGGAACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGATGAAG 243
                                                                                                                                                                       124 AAGTTGAACCTGTGGGAAGATGGTTTGAAGCTTTTGTTAAGAGGAGAAACAGAAATGCTT 183
                                                                                                                                                                                                             148;
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dougherty BA,
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                             8.2%;
45.4%;
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                                                                                                                                                                                                           0;
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                                                                                                                                                                                                          Mismatches 178; Indels
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                                                                                          Best Local Sin
Matches 132;
                                                                                                                         Query Match
                                                                                                                                                                                                ART05868 encodes a chicken leucocytozoan immunogenic protein, this plor or a fragment of it can be used in a recombinant vaccine to immunise against chicken leucocytozoan disease. The DNA is used in a vector and operatively linked to an expression regulatory sequence as in
                                Sequence 3399 BP; 1577 A; 508 C; 798 G; 516 T; 0 other;
                                                                                                                                                                                     standard practice.
                                                                                                                                                                                                                                                                             Claim 6; Page 6-9; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07284392-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicken leucocytozoan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9101 AAAATAGTCATGACAATCCACCAGTACCAAAAGTAAAAGCAGCAGCACAAAGTGGTGGTC 9042
                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1995.
                                                                                                                                                                                                                                                                                                          vaccine against chicken leucocytozoan disease
                                                            199 AACTGGAGGATAAGAAAGAGTTATCCGAGGAATCAGAAGAATGAAGAATTGCAGTTGGAAG 258
                                                                                                                                                                                                                                                                                                                                                                                                 (DOBU-) DOBUTSUYO SEIBUTSUGAKU
(KITA ) KITASATO KENKYUSHO SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunisation; vaccination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AAGATCATTATGCAGTTCTTGGACTTGGCCATGTGAGATACAAGGCTACACAGAGACAGA 363
 259 AGTTTCCCATGCTGAAAACACTTGATCCCAAAGACTGGAAGAACCAAGATCATTATGCAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 TCAAAGCAGCTCATAAAGCAATGGTTTTAAAAACATCACCCAGACAAACGGAAAGCAGCTG 423
                                                                                                                                                                                                                                                                                                                                                       1996-006311/01.
DB; AAR97866.
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                          leucocytozoan immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                DOBUTSUYO SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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1150..3218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "fragment referred to in the claims, for use as insert in a recombinant vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                        46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against chicken leucocytozoan disease"
                                                                                            0; Mismatches
                                                                                                          Score 40.8; DB Pred. No. 0.075;
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	2951 TAACACATGAAGAAGAAGAAATGTAACATATGAAGAAGAAGAA 2994	439 AAGGAGATAATGACTACTTCACTTGCATAACTAAAGCTTATGAA 482	ACP	LAGC	AG.	- ACA	AGA
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			AAA	379 AAGCAATGGTTTTAAAACATCACCCAGACAAACGGAAAGCAGCTGGTGAACCAATAAAAG 438	3CA1	319 TICTTGGACTTGGCCATGTGAGATACAAGGCTACACAGAGAGAG	
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			2891 AGAAGAAGTAACACATGAAGAAGAAGAAGAAAAGTAACACATGAAGAAGAAGAAAAAAG 2950	138	2831 ATGAGGAAGAAGAAGAAGAAGAAATAAGGAAGAAGAAGAA	378	2771 AGATGAGGAAGAAGAAGAAGAAGAAGAAGGAGGAAGAAGA
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1: /cgn2_5/ptodata/2
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     14.1 319 4
14.0 1028 4
13.8 4411529
13.8 8438 1
13.7 12001
13.7 12001
13.4 4403755
13.3 4411529
13.2 4362
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                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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1 US-08-194-087-1
1 US-08-194-088-15
2 US-08-194-087-1
2 US-08-194-087-1
3 US-09-165-264-1
4 US-09-165-264-7
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      US-08-455-073A-1
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                                                                                                                                                                      Sequence 2, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 15, Appli
Sequence 15, Appl
Sequence 17, Appli
Sequence 182, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 8, Appli
Sequence 1, Appli
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Sequence
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15, Appl
15, Appl
18, Appl
11, Appl
11, Appl
7, Appl
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12, Appl
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	1439 494 9957 4257 4257 4257 4257 4257 2846 321 321 321 321 321 2289 6530 6530 6530 6530 6530 6530 6530 6530
	4440444400004404
ALIGNMENTS	US-09-056-556-167 US-09-056-556-176 US-09-056-556-182 US-08-690-473-1 US-08-690-473-1 US-09-135-944-1 US-09-135-94-1 US-09-135-94-1 US-09-135-159 US-09-253-691-3 US-09-312-038-4 US-09-312-038-3
	Sequence 167, App Sequence 176, App Sequence 182, App Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli

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US-09-103-840A-2/c
                                                                                                                                                                              Db 3938100 CCGCCGGTGCCGCCGCCGCCGGATCCGCCGACCCGGGGTCGCCGAGGCCGCCGGTG 3938041
                                                                                                                                                                                                                                                                                                                                                           US-09-103-840A-2
Db 3937920 TCGCCGCCGGTACCGCCGTTGCCGCCGTTGCCGCCGTCGCCGCCAGTGTCGCCGCCAAGG 3937861
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Patent NO. 6294328
GENURAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWER R.
APPLICANT: WHITE, OWER R.
APPLICANT: VENTER, JOHN C.
APPLICANT: VENTER, JOHN C.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE DEFORMED SECOND ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4403765
                      443 TCGGCGCCG--CGGCCGAGGCCGCGCCCCCCCCGCCGCGCGCCACTATCGCCGCGGCGG 500
                                                                                                                                                                                                                                                                                          266 CAGGTGGACTTGCTCCCGGTGCTCG--CCGCCGCGCAGGAGTCCGCCGGGGGGCTGCCGGG 323
                                                                                                                                 384 CGGTGGAC-ACAGCGGCCCTGAAGCAGCCTCCGGCGCCCCCTCCGCCACCCCCGCCAGTG 442
                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80.8; DB 4;
Pred. No. 3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4403765;
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US-09-128-155-16
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                                                                                                                                                                                                       US-09-050-863-2/c
                                                                                                                                                                                                                              RESULT 3
                                                                                                                                      Sequence 2, Application US/09050863
Patent No. 6114111
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 203; Conservative
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Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DAYE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22199 CCCCGCCGGCGCGCGCCCCCCCCCCCCAGCCCCGACCGC 22243
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22026 GCC-----CCCCCGCCCCCCCCCCCCCCCCCCCCCACACCCGGCCCACACGCAC 22078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)...(15233
             APPLICANT: Lao, Ying
APPLICANT: Hinng, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 152331
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  328 TGCCGCCGCTGCCGCCGCCCTGCCGCCCCCCCGCCCCTCTACGGT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 GGTGGACTTGCTCCCGGTGCTCGCCGCCGCCCAGGAGTCCGCCGCCGCCGCTGCTGCGCCGC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 GCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTCC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 GGGGGTGGGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCCCT 147
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Pred. No. 3.2e-05;
0; Mismatches 195; Indels 7;
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RESULT 4
US-09-359-081-2/c
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Best Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIEVE: 30-MAD: 107-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       1238
                                                                                                                                                                                                                                                                                                                                                                                                                               447 CGCCCGCGCGAGGCCGCGCCCCCCCCCCCCGCCGCCACTATCGCCGCGGC 498
                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 GGGGGGTGGCCGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 TCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCCTTCCCCGTGCTGGGCCTGGACTCCC 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                     CTGCCGCCGCTGCCGCCGTCGCTGCCGCCCCCGCCCTCTACGG 386
                                                                                                                                                                                                                                                 CATTCCAGGCCGCGCCGGCCCCGCCCACGCCCCAGGCCCCGGCCGGCCGAGCCCCTCC 266
                                                                                                                                                                                                                                                                                                                                                                       TGCAGGTCGGGGCTGAGCTCCAGTCCCGCCTTCTTTGCCTCCCAGGGCTGCGCCCCAGAGTC 206
                                                                                                                                                                                                                                                                             230;
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 74.4; DB 3; Length 2580;
; Pred. No. 6.4e-05;
0; Mismatches 241; Indels 1; Gaps
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; Sequence 2, Application US/09359081 ; Patent No. 6316223

GENERAL INFORMATION:

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US-09-359-081-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          1118 TGCCCCTCCTGCTCCTGCCCCTC-CTGCTCCTGCCCCTCCTGCCCCCTCCTGCCC 1060
                                                                                                                                                                                                                                                                                                                      147 TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCCAGAGTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                       87 GGGGGGTGGGCGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/050,863
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
PROFESSOR (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-ull-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Mammalian Protein Interaction Cloning
                                    CATTCCAGGCCGCCGCGCGCCCCCGCCCACGCCCAGGCCCCGGCCGAGCCCCTCC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                              AGGTGGACTTGCTCCCGGTGCTCGCCGCCCCAGGAGTCCGCCGCGGCTGCTGCGGCCG 326
                                                                           230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Hiang, Betty
Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA
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48.7%;
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Pred. No. 6.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2580;
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; Sequence 1, Application US/0891064; Patent No. 6251433; GENERAL INFORMATION:
APPLICANT: Zuckermann et al.; TITLE OF INVENTION: Compositio; TITLE OF INVENTION: Polynuclec; NUMBER OF SEQUENCES: 4

US/08910647

Polynucleotide Delivery

4

Compositions and Methods

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APPLICANT: HOTLICK, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Ger
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE RETERENCE: 0867/10903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
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; ORGANISM: VEBNA
US-09-130-114-1
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Patent No. 5976807
GENERAL INFORMATION:
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                                                             1866
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Local Similarity 48.7%;
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Pred. No. 6.1e-05;
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RESULT 7
US-07-884-811-15/c
: Sequence 15, Application US/07884811
: Patent No. 5316921
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: FU]ILA, ShATON M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 12:
TELECOMMUNICATION INFORMATION:
                                                                                                                                            1164 TGCCCCTCCTGCCCCCTC-CTGCTCCTGCCCCTCCTGCCTCCTGCCCCTCCTGCCC 1106
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
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Local Similarity 48.7%;
es 230; Conservative
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Pred. No. 5.9e-05;
0; Mismatches 241;
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Best Local Similarity
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APPLICANT: Godowski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US, FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 2818
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CURRENT APPLICATION DATA:
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207
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CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-98
TELEX: 910/371-7168
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                                                                                                             TGGACACAGCGGCCCTGAAGCAGCCTCCGGCGCCCCTCCGCCACCCCCGCCAGTGTCGG 446
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                                                                                                                                                                                                                                     CATTCCAGGCCGCCGCCGCCCCCCCCCCCCCCGGCCCCGGCCGGCCGAGCCCCTCC
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                                                                                            GGGGGGTGGGCCGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCCC 146
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48.78;
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Pred. No. 5.9e-05;
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US-07-885-971-15/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           2818
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TITLE OF INVENTION:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415/225-3216
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/8
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CITY: South San Francisco
STATE: California
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les 230; Conservative
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                              AGGTGGACTTGCTCCCGGTGCTCGCCGCCCGCCCAGGAGTCCGCCGGCCTGCTGCGGCCG 326
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 5.9e-05;
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                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 18 MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 10596 base pai
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                  447 CGCCCGCGGCCGAGGCCGCCGCCCCCCCCCCCCACTATCGCCGGC 498
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TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 13-Jul-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 460 Point San Bruno Blvd CITY: South San Francisco
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                                                                                                                                                                                                                                Local Similarity 48.7
les 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,600
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                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Marschang, Diane
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   CATTCCAGGCCGCGCCGCCCCCCCCCCCCCAGGCCCCGGCGGCCGAGCCCCTCC 266
                                  TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTC 206
                                                                                                   GGGGGTGGGCGGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
                                                                                                                                                                                                    TCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCCCTTCCCCGTGCTGGGCCTGGACTCCC 86
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                                                                                                                                                                                                                                 Score 74.4; DB 1; Length 1
Pred. No. 5.9e-05;
0; Mismatches 241; Indels
                                                                                                                                                                                                                                                                  Length 10596;
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: Sequence 15, Application US/08194088B

; Patent No. 5580963
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                                                                                                         Matches
                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 34000
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-2614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 09-FEB-1994
                                                                                                                     Local Similarity
                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/884811 FILING DATE: 18-MAY-1992
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1: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                              nucleic acid
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                                                                                                       Conservative
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48.7%;
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                                                                                                      Score 74.4; DB 1;
Pred. No. 5.9e-05;
0; Mismatches 241;
Length 10596;
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US-08-194-087-15/c
; Sequence 15, Application US/08194087
; Patent No. 5879910
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                                                                                                             US-08-194-087-15
Query Match
Best Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
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                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          linear
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   Score 74.4; DB 2;
Pred. No. 5.9e-05;
                                    Length 10596;
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PCT-US93-04648-15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application PC/TUS9304648 GENERAL INFORMATION:
                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Genentech, Inc., Godowski, Paul J., Lokker, Natalie A., Mark, Melanie TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2519 CTCCTGCCCCTGCCCCCTCCTGCTCCTGCCCCCTCCTGCTCCTGC 2468
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                                                                                                            NAME: Dreger, Ginger R. REGIZION NUMBER: 33,055 REFERENCE/DOCKET NUMBER: 75 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,
FILING DATE: 18-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDLIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 182, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                              FILING DATE:
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STRANDEDNESS: single
                                                                                                                  CLASSIFICATION:
                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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   REFERENCE/DOCKET NUMBER:
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Pred. No. 5.9e-05;
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                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                               Query Match
Best Local
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 985 base pairs
TYPE: nucleic acid
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CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE;
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic
                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
237 CGCCCCAGGCCCGGCGGCCGAGCCCCTCCAGGTGGACTTGCTCCCGGTGCTCGCCGCCG 296
                                     273 GGTGGCGCCGACAACGCCGCCGGTGCCG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 CCGGCGCCCCCCCCCCCCCCCCCAGTGTCGGCGCCGCGGCCGAGGCCGCGCCCCC 472
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                                                                                                                         14.5%; Score 72.6; DB 4; 51.7%; Pred. No. 0.00014;
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NUMBER OF SEQ I
SOFTWARE: Pate
; SEQ ID NO 14
TENGTH: 320
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FILE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
                      477 CCGCCGCCACTATCGCCGC 495
                                                                        477 CCGCCGCCACTATCGCCGC 495
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51.7%;
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Search completed: October 10, 2002, 18:13:55 Job time: 1173.73 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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Perfect score:
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190
182.2
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1 cggctcagcgggggccgagg.....cgccactatcgccgcggcgg 500
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2002 Compugen Ltd.
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em_htc:*
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BE988668
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BG773423
AI509985
BE410524
AW015921
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AL524850
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AI426137
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AW763155
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AL561632 AL561632

BE514418 501315642

AW763155 ur60e04.y

BC004758 Mus muscu

BE98866 UI-M-CG0p

BG773423 602720325

AL509985 mf18620.y

BE410524 601301958

AW015921 UI-H-BIO-

BG340017 602438171

AL426137 mf18f03.x

BI198991 602759069

AW572635 xx69f05.x
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AL555273 AL555273
AW572635 xx69f05.x
AI018189 ou15g11.x
                                                                                                                                                                                                                        Description
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AUTHORS
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KEYWORDS
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AW629721
                                                                                                                                                                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                        JOURNAL
                                                                                 source
                                                                                              High quality sequence stop: 433.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         EST
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tumors"
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/db_xref="taxon:9606"
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ALIGNMENTS

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BM129350	AW592036	AI181776	AA032984	BF000610	AW469674	BM129635	AW297757	AI391563	AA509355	AI141095	AI370109	BI909543	AI651289	AI738419	AI915985	AI827731	AA476545	BF732504	AW292088	BF516485	AW204295	AI333867	AW592700	AI831058	AI990450	AI193293	AI470340	
BM129350 if21b04.x	hf37f01.	ub87c06.	AA032984 mh89c06.r	BF000610 7h33e08.x	d32f06.x	BM129635 if21b04.y		AI391563 tg16a10.x	AA509355 vg18a08.r	AI141095 ge22g07.x	_					AI827731 wflle01.x	zx02d10.	BF732504 nae11g09.	_	BF516485 UI-H-BW1-		AI333867 qp99c05.x	0	wj62d02.	0	AI193293 qe57c08.x	AI470340 tj42d05.x	

Unpublished (1997) Unpublished (1997) Other_ESTS: hh70a04.xl Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.lln1.gov/image/html/iresources.shtml Seq primer: 40RP from Gibco Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 526) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), AW629721 526 bp mRNA linear EST 31-MAR-2000 hh70a04.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968110 5 similar to gb:M94046 Human zinc finger protein (HUMAN);contains FTR5.b2 TAR1 repetitive element; mRNA sequence. Tumor Gene Index AW629721.1 GI:7376511

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 921)
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                                                                                                                                                                                                                                                                                                                                                                                                          EST
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                                                                                                                                                                                            seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/tissue_type="placenta"

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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
life Technologies. Contact: Feng Liang Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: Sail; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
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/db_xref="taxon:9606"
                                                                                                                                   /clone="CS0DK007YN22"
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1 (bases 1 to 954)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL524850 LTI_NFL003_NBC3 Homo
                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
/tissue_type="neuroblastoma cells"
/lab_host="0H10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
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                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="CS0DC008YH16"
                                                                                                                                                                     /clone_lib="LTI_NFL003_NBC3"
                                                                                                                                                                                                                                       /organism="Homo sapiens"
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92.6%;
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Pred. No. 5.5e-31;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/tissue_type="B cells from Burkitt lymphoma"
/note="Vector: pcMvSpORT 6; Site_1: NotI; ist strand cDNA
/note="Vector: pcMvSpORT 6; Site_1: NotI; ist strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODL008YE09"
                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_NFL010_BC2"
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Pred. No. 1.8e-30;
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RESULT 4 AL561632

REFERENCE AUTHORS

TITLE

SOURCE

ORGANISM

KEYWORDS VERSION

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                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM328 row: d column: 12
                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 902)
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902 DP HIRMS
601315642F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634139
                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                        quality sequence start: 33 quality sequence stop: 344.
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375 c 286 g 141 t 1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3634139"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
                                                                                                                    Location/Qualifiers
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88.0%;
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Pred. No. 1.
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RESULT 6
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                                                                                                     Unpublished (1997)
Other_ESTs: ur60e04.xl
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Ilssue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW763155 439 bp mRNA linear EST 04-MAY-2000 ur60e04.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3154686 5' similar to gb:M94046 Human zinc finger protein (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW763155
AW763155.1 GI:7695091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                               image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmalia; Eutheria; Rodentia; (bases 1 to 439)
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/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by Oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected-$500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 315 c 266 g 171 t 1 others
-40RP from Gibco
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Best Local :
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                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282;
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@nail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Denn
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                2152 bp
Mus musculus, clone IMAGE:3154686,
BC004758
                                                                                                                                                                 Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                     Strausberg, R
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                          house mouse
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/strain="129 - C57/86 - FVBN"
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/clone="IMAGE:3154686"
/clone_Iib="NCI_CGAP_Mam3"
/tissue_Type="tumor, gross tissue"
/dev_stage="10 months"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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87.0%;
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Pred. No. 4.
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                                                              Chu-Xia Deng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTC 12-JUL-2001
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VERSION
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                                                                                     TITLE
                                          JOURNAL
                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                     BE988668 379 bp mrNA linear EST 05-OCT-2000 UI-M-CG0p-bhy-g-11-0-UI.sl NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bhy-g-11-0-UI 3', mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: k Column: 1
This clone has the following problem: frame shifted.
Location/Qualifiers
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Center code: BCM-HGSC
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.M., Gibbs, R.A.
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 379)
Bonaldo, M. F., Lennon, G. and Soares, M. B.
Contact: Chin, H
                                                                                                                                                                                                                                                               BE988668.1 GI:10665238
                                          Genome Res. 6 (9), 791-806 (1996)
                                                                                  Normalization and subtraction: two approaches to facilitate gene
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/db_xref="taxon:10090"
/clone="IMAGE:3154686"
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692 c 619 g 406 t
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                                                                                                                                                                                                                                                                                                                                                                                     414 CGGCGCCCCTCCGCCACCCCCGCCAGTGTCGGCGCCCGCGGCCGAGGCCGCGCCCCCCG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCGAGGAATCAGCCGCGGCGGCGGCGGCTGCTGCGGCGGCTGCAGTGGTTA 130
                                                                                                                                                                                                                              Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
-118, >(CGG)n#Simple_repeat 133-177, >(CGG)n#Simple_repeat 220-269
Seq primer: M13 Forward
mRNA sequence.
BG773423
BG773423.1 GI:14084076
                                                 POLYA-No.
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Fax: 301 443 9890
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Similarity 87.7%;
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TAG_SED=None found" 43 t
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/clone="UI-M-CG0p-bhy-g-11-0-UI"
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/strain="C57BL/6J"
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Pred. No. 5e-22;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCGGCCCCTGCCGCCCCCTCTACGGTGGACACAGCGGCCCTGAAGGCAGCTCCGGCGGC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234;
                                                                                                                                                                                                               AT509985 337 bp mRNA linear EST 15-MAR-mj18f03.yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476477 5' similar to gb:M94046 Human zinc finger
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Email: Ggapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                          protein (HUMAN);, mRNA sequence. AI509985
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                Mus musculus
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Plate: LLAM10769 row: a column: 08
High quality sequence stop: 240.
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone_lib="NIMGE:4837135"
//clone_lib="NIH_MGC_97"
//lab_bost="DH10B"
//lab_bost="DH10BB"
//lab_bost="DH10B"
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307 GCCGCCGAGGCCGCGCCCCCCGCCGCCGGCCG 337
                                                                                                                                                                            187 GCGGCTGCCGCTGCAGTGGTTACTGCACCCCCGGCCCTGCCGCCGCCTCCACAGTGGAC 246
                                                                                                                                                                                                                                                                                             127 GACTTGCTCCCGGTTCTCGCCGCCGCGGCGGAGGAATCAGCCGGCGGCGGCGGCGGCTGCTGCG 186
                                                                                                                                                                                                                                                                                                                                                                                   272 GACTIGCICCCGGTGCTCGCCGCCGCCGCCCAGGAGTCCGCCGCCGGCTGCTGCGGCCGCTGCC 331
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                                                                                                                    ACAGCGGCCCTGAAGCAGCCTCCGGCGCCTGCCTCCGCCACCCCTGCCGTCTCCGTACCA 306
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Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40RP from Gibco POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded CDNA was ligated 1 Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.Fatima Bonaldo.
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M.Fatima Ronaldo.
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/sex="unknown"
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/db_xref="taxon:10090"
/clone="IMAGE:476477"
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/dev_stage="13.5-14.5
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Pred. No. 3.8e-18;
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                                                                                                                                                                                                         AGGTGGACTTGCTCCCGGTGCTCGCCGCCGCCCAGGAGTCCGCCGCCGCCGCAGCGGCAG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM334 row: c column: 16
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="choriocarcinoma"
/lab_bost="pH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 250 c 194 g 144 t
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_21"
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Pred. No. 5.2e-18;
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Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 64-113,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 bp mRNA linear EST 10-SEP:
UI-H-BIO-aao-h-01-0-UI.S1 NCI_CGAP_Sub1 Homo sapiens cDNA clone
IMAGE:2710128 3', mRNA sequence.
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1 (bases 1 to 235)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_tib="NAT_CGAP_Subl"
/lab_bst="DH1DE (Life Technologies)"
/lab_bst="DH1DE (Life Technologies
                                                                                     29
                                                                                                                                Research 6, 791-800.
TAG_LIB-NCI_CGAP_LU5
TAG_TISSUE-lung
                                                                               TAG_SEQ=CAAC"
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   Score 211.2; DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 721)
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Plate: LLCM1257 row:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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//db_xref="taxon:9606"
//clone=lib="NAMGE.4555884"
//clone=lib="NAMGE.4555884"
//clone=lib="NAMGE.455884"
//clone=lib="NIH_MGC_46"
//tissue_type="leiomyosarcoma cell line"
//tissue_type="leiomyosarcoma cell line"
//lab_host="DHIOB (phage resistant)"
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//corkI; CDNA made by Oilgo-dT prining. Directionally cloned
into EcoRI/XhoI sites using the following 5, adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                             Library
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Pred. No. 3.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1426137 264 bp mRNA linear EST 09-MAR-mj18f03:x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476477 3' similar to gb:M94046 Human zinc finger protein (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 264)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: polyT not found. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
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314 286 1810
/tissue_type="embryo"
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                                                                                                                                                                                                                                                                                                                             /sex="unknown
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 GACTTGCTCCCGGTGCTCGCCGCCGCCGCCGAGGAGTCCGCCGCGCGGCTGCTGCTGCCGCTGCC 331
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (199)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 7 High quality sequence stop: 642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1778 row: i column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BI198991
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/note="neuroblastor: pot organ; Site_1: XhoI; Site_2:
/note="neuroblastor: pot organ; Site_1: XhoI; Site_2: Yhoing the following 5;
/note: GCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
/note laboratory of Gerald M. R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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Pred. No. 7.3e-15;
0; Mismatches 25; Indels
Score 182.2; DB 10;
Pred. No. 5.8e~14;
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                               Length 670;
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                                               169 AACCCCCTGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCA~GGCTGCGCC
                                                           140 AACCCCCTGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCC 199
                                                                                                109 GACTCCCGGGGGGTGCGCGTGCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAG
                       200 CAGAGTCCATTCCAGGCCG
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Search completed: October 10, 2002, 20:27:35 Job time : 702.733 secs

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Maximum DB seq
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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13: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT: *
14: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT: *
15: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT: *
16: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT: *
17: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT: *
18: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT: *
20: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT: *
21: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT: *
22: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT: *
23: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20001.DAT: *
24: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20011.DAT: *
25: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20011.DAT: *
26: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20011.DAT: *
27: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20011.DAT: *
28: \SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA20011.DAT: *
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                                                                                                                                             SUMMARIES
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ult No.	Score	Query Match	Query Match Length DB	DB	ID	Description
٦	500	100.0	2389 22	22	AAD11114	Human small cell l
2	90.6	18.1	2561		AAH26500	Rabbit low density
ω	81.2	16.2	37856		AAA11992	S. cellulosum DNA
4	80.8	16.2	4403765		AA199683	Mycobacterium tube
u	78.8	15.8	1614		AAH26499	Human low density
6	78.8	15.8	12425		AAH26495	Human low density
7	77.4	15.5	114955	20	AAX53491	Human adenosine Al
œ	77.2	15.4	1337		AAZ17263	Human gene express
9	75.6	15.1	3198	20	AAX02974	Human IL-1ra BAC c

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4 U	C 44	43	c 42		40	39					c 34					29				c 25				21				c 17		15	14		c 12		
68	89	68.6	68.8	68.8	68.8	68.8	69	69.2	69.8	70.2	70.2	70.2	70.6	70.8	71.2	72				73.2		•	73.2	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4
	13.6	•			•	•	8	&	0			14.0		14.2	'n	.4	5	ს	5	o	ი		6	.9	.9	9	.9	9	9	14.9		٠	14.9	14.9	14.9
2188	795	12001	2049	1698	1007	955	8438	1411529	1102	1028	1028	1028	318	2668	320	114955	1000	320	320	985	985	985	985	16080	10596	10596	10596	10380	9600	8705	5452	2580	1926	1926	799
20	19	16	23	23	22	22						13	21	22	21	20	21	21	21	20	20	19	19	21	20	17	14	20	19	20	20	21	22	21	19
AAZ77506	AAV55830	AAQ76213	AAS76210	AAS84408	AAS01022	AAS01024	AAQ73500	AA199682	AAZ16923	AAS01347	AAA91542	AAQ27091	AAA38184	AAK75409	AAA38185	AAX53491	AAA02484	AAA38186	AAA38183	AAZ19137	AAZ19349	AAV44439	AAV64548	AAA59553	AAX15650	AAT40348	AAQ51731	AAZ22248	AAV21683	AAZ23778	AAX90923	AAA75454	AAF82902	AAA50254	AAV55831
Human ovarian tumo	FLGA insert stabil	HSV L/ST region.	DNA encoding novel	DNA encoding novel	Sugarcane plant ge	Sugarcane plant ge	DNA encoding Pseud	Mycobacterium tube	Human gene express	Human Fragile X Sy	1.0kb PstI fragmen	XTY26 probe. Homo	Primer used in the	Human immune/haema	Primer used in the	Human adenosine Al	Human colon cancer	Primer used in the	Primer used in the	M. tuberculosis re	M. tuberculosis an	Mycobacterium tube	M. tuberculosis im	DNA clone pCEK C1.	Nucleotide sequenc	Plasmid pCisEBON f	Plasmid pCisEBON f	Nucleotide sequenc	Vector plasmid pCM	Vector pShuttle DN	Anti-sense strand	Nucleotide sequenc	EBV tethering prot	Epstein Barr virus	Nucleotide sequenc

ALIGNMENTS

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RESULT 1
AAD11114
Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; myc-associated Zinc-finger protein; MAZ; cytostatic; synovial sarcoma; ds.
                                                                                                                                                                                                                                                                                               AAD11114;
                                                                                                                                                                                                                                                                                                                     AAD11114 standard; DNA; 2389 BP.
WPI; 2001-457597/49
                     Stockert E,
                                                                                                         19-JAN-2001; 2001WO-US02015.
                                                                                                                                                                                                                                                  Human small cell lung cancer associated gene, MAZ
                                        (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
                                                                                  21-JAN-2000; 2000US-0489101.
                                                                                                                                                    WO200153349-A2
                                                                                                                                                                                                                                                                          24-SEP-2001 (first entry)
                                                                                                                               26-JUL-2001.
                    Scanlan MJ,
                     Jager D,
                     Old LJ,
                      Gure
                      ÃO,
                      Chen
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RESULT 2
AAH26500
ID AAH2
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AC AAH2
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DT 12-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention relates to nucleic acids and encoded polypeptides which CC are cancer associated antigens expressed in patients afflicted with CC small cell lung cancer. The molecules provided by the invention can be CC used in the diagnosis, monitoring, research or treatment of conditions CC characterised by the expression of one or more cancer associated CC expression of a hCAAP, and determine regression, progression or onset CC of a condition characterised by expression of an abnormal amount of a CC of a condition characterised by expression of an abnormal amount of a CC are small and non-small cell lung cancer, melanoma, colon, breast, head CC and neck, or transitional cancer leimyosarcoma or synovial sarcoma. CC The present sequence is a DNA encoding human myc-associated Zinc-Tinger CC protein MAZ. This small cell lung cancer associated gene is designated CC as NY-SCLC-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
          12-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                               AAH26500;
                                                    AAH26500 standard; cDNA; 2561 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2389 BP; 419 A; 805 C; 731 G; 434 T; 0 other;
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                                                                                                          CGCCACTATCGCCGCGGCGG
                                                                                                                                                                                                                                        CCAGGCCCCGGCCGAGCCCCTCCAGGTGGACTTGCTCCCGGTGCTCGCCGCCGCCGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCTCAGCGGGGCCGAGGCCATGTTCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCC 60
                                                                                                                              CGCCACTATCGCCGCGGCGG 500
                                                                                                                                                     CCCGGCCCCTGCCGCCGCCTCTACGGTGGACACAGCGGCCCTGAAGCAGCCTCCGGCGCC
                                                                                                                                                                                                                                                                                     CCAGGCCCCGGCGGCCGAGCCCCTCCAGGTGGACTTGCTCCCGGTGCTCGCCGCCCCCC
                                                                                                                                                                                                                                                                                                                                                     CTTCCCCGTGCTGGGCCTGGACTCCCGGGGGGGTGGGCGGCCTCATGAACTCCTTCCCGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTCAGCGGGGGCCGAGGCCATGTTCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCC 60
                                                                                                                                                                                               CCCGGCCCTGCCGCCGCCTCTACGGTGGACACAGCGGCCCTGAAGCAGCCTCCGGCGCC
                                                                                                                                                                                                                                                                                                                               ACCTCAGGGTCACGCCCAGAACCCCCTGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCCCCGTGCTGGGCCTGGACTCCCGGGGGGGGGGCGGCCTCATGAACTCCTTCCCGCC 120
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llarity 100.0%;
Conservative 0
          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 500; DB 22;
Pred. No. 1.5e-63;
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein i (LBP-2, see AAB82807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 2A; 143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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14-JUL-2000;
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614 GGCGGCGCCGCCCACGCCCGCCCGCCGCCGCCGCCGCCCGTCGCCGCCGCCGC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCCAGAACCCCCTGCAGGTCGGGGCTGAGCTCCCAGTCCCCGCTTCTTTGCCTCCCAGGG 192
                                                                                         GGCCGAGCCCTCCAGGTGGACTTGCTCCCGGTGCTCGCCGCCCCAGGAGTCCGCCGC
                                                                                                                                                                                                                                                                                                                         CTGCGCCCAGAGTCCATTCCAGGCCGCGCCGGCGCCCCGCCCACGCCCAGGCCCCGGC 252
                                                                                                                                                200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2561 BP; 372 A; 937 C; 879 G; 373 T; 0 other;
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2000US-0616289.
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54.8%;
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Pred. No. 2.7e-05;
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AAA11992 standard; DNA; 37856 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "gtg start codon complement (6374..7111)
                                   /product= "ORF12-regulation element"
complement (35255..35616)
                                                                                                                                                                                                                                                                                                            /product= "ORF8-transpeptidase" complement (30040..31720)
                                                                                                                                                                                                                                                                                                                                                                                                             /product- "ORF6-polyketide synthase"
2003..27889
/*tag- q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (8433..9550)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "ORF4~ tyrosine/DOPA-Decarboxylase"
/note= "GTG start codon"
                                                                                                                 /product= "ORF11-regulation
/note= "GTG start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF5-3-oxoacyl-ACP-reductase"
/note= "ACC start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /#tag= a
/product= "ORF1-tRNA_synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                 product= "ORF9-regulation element"
                                                                                                                                                                                                                                                                                                                                                                                          product ** ORF7-peptide synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2212..13658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product= "ORF3-aminotransferase"
note= "AGT start codon given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    855..11393
                                                                                                                                                                              128..33613
                                                                                                                                                                                               duct- "ORF10-transcription regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressant; antibiotic; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "ORF2-monooxygenase"
"ORF13-transcription regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the specification"
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RESULT 4
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Best Local :
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                                                                                                                                                                                                                                       29970 CCCGCCAGGGGCCACGTGGGAGGAGGCCGCCGCGCGCACGAGGCG
                                                                                                                                                                                                                                                                                                                  30030
                                                                                                                                                                                                                                                                                                                                                                                              30090 GGCCGCGGAGCCGCCCGCGCCCCCGCGGCGCCGCCTTCCGTGGCCGCGAGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel DNA sequence (I) whose expression products effect or are involved in the enzymatic biosynthesis, mutasynthesis or partial synthesis of polyketide or heteropolyketide compounds (II). (I) can be inserted into an expression vector and used to transform or transfect prokaryotic or eukaryotic cells with the aim of obtaining strains that produce large amounts of polyketide or heteropolyketide compounds, especially epothilones, which have cytotoxic and/or immunosuppressant and antibiotic and antifungal activities and are useful as plant-protection agents. This sequence represents the DNA sequence isolated from Sorangium cellulosum which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1998;
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                     Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO
                                                          15-JAN-2002
                                                                                                                                        AA199683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37856 BP; 5655 A; 13666 C; 12913 G; 5622 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 20-33; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-294101/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 CCAGGCCGCGCGCGCCCCCCCCCCCCCCGCGCGGCGGCCGAGCCCCTCCAGGT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACTTGCTCCCGGTGCTCGCCGCCCCAGGAGTCCGCCGCGGCTGCTGCGGCCGCTGC 330
                                                                                                                                                                                                                                                            CGCGGCCGAGGCCGCCCCCCCGCCTCCGCCGCCACTATCGCCGCG
                                                                                                                                                                                                                                                                                                                  GGCCGCGCCTTCCGTGGCCGCGGAGTCGCCCGCGCCCTTCCGCGGCGGCGGCGCCTTCCGT 3009:
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                                                                                                                                        standard;
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                                                          (first entry)
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/product= "ORF14-transcription regulator"
/note= "GTG start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (35730..36242)
                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 183;
                                                                                                                                                                                                                                                                                                                                                       3938100 CCGCCGGTGCCGCCGTCGCCGCCGGATCCGCCGGGGGGTCGCCGAGGCCGCCGGTG 3938041
                    AAH26499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and macherical actions of M. tuberculosis strains CDC 1551 (AAI99683) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H37Rv (AAI99682). The method is useful for evaluating strain variation M. tuberculosis and has valuable application in the fields of M. tuberculosis genetics, epidemiology, patient treatment and epidemic restrictions.
                                                        AAH26499 standard; DNA; 1614 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann RD,
                                                                                                                                                            (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                   266 CAGGTGGACTTGCTCCCGGTGCTCG---CCGCCCCAGGAGTCCGCCCGGCTGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                               CATCGCCGCATTGCCGCCGCACCGCCGTGCCGCCGCCGCCGACCTCGCCGCCC 3937921
                                                                                                                                         TCGCCGCCGGTACCGCCGTTGCCGCCGTTGCCGCCATCGCCGCCAGTGTCGCCGCCAAGG 3937861
                                                                                                                                                                                                                                                                                   CCGCCGGTGCCGGTGCCGCCGCCGCCCCCGTCCCCGCCGGTGCCGGTGCCG 3937981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AAI99682).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 80.8; DB 22; Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112;
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polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the coding region of the human gene (see also AAB36494) encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the present sequence differs from that predicted from a cDNA clone (see AAB82803) in that it contains an additional 321 amino acids at its N-terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 7A; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000; 2000US-0517849
14-JUL-2000; 2000US-0616289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2001; 2001WO-US06356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human low density lipoprotein binding protein 2 (LBP-2) DNA
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                                                                                                                                                                                                                                                      217 CGCGCGGCGCCCCGCCCACGCCCCAGGCCCCAGGCCCGAGGCCCCTCCAGGTGGACTT 276
                                                                                                                                                   277 GCTCCCGGTGCTCGCCGCCGCCCAGGAGTCCGCCGCCGCCGCTGCTGCCGCCGCCGCCGC
                                                                                                                                                                                                                                TGCTGCCGCCGTCGCTGCCGCCCCGGCCCTGCCGCCTCTACGGTGGACACAGC 396
GCCCCCTCGCCTGGCCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGC
                                 GGCCCTGAAGCAGCCTCCGGCGCCCCTCCGCCACCCCGCCAGTGTCGGCGCCCGCGGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-565505/63.
                                                                                                                                                                                                                                                                                                          al Similarity
155; Conserv
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                           15.8%;
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                                                                                                                                                                                                                                                                                                                         Score 78.8; DB 22;
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                  Pred. No. v.vo
0; Mismatches
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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of
                                                                                                                                                New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                      exon
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                                                                                                                                                                                                                                                    (BOST-) BOSTON HEART FOUND INC.
                                                                                                                                                                                                                                                                                       02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
                                                                                                                           Example 4; Fig 23; 143pp; English.
                                                                                                                                                                                                                            Lees AM,
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DB; AAB82806.
                                                                                                                                                                                                                          Lees RS,
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                                                                                                                                                                                                                                                                           2000US-0517849.
2000US-0616289.
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2832..5153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "includes introns"
                                                                                                                                                                                                                                                                                                                                                                                                                                        ≖tag=
                                                                                                                                                                                                                            Law SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..4787
                                                                                                                                                                                                                                                                                                                                                                                                                           . . 4994
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..4899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4694
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                                                                                                                                                                                                                            Arjona AA;
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888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
RESULT 7
AAX53491/c
ID AAX53491 standard; DNA; 114955 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3125
                                                                                                                                                                                                                                                                                                                                                              acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-1999
                             WPI; 1999-229400/19.
                                                             Nyce JW;
                                                                                          (UYEC-) UNIV EAST CAROLINA
                                                                                                                           09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                         17-SEP-1998;
                                                                                                                                                                                                                                        WO9913886-A1
                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                     prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                      hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                  chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 CGCGCCGGCCCCCCCCCCACGCCCCAGGCCCCGGCCGAGCCCCTCCAGGTGGACTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 GCTCCCGGTGCTCGCCGCCCCAGGAGTCCGCCGCCGCTGCTGCCGCCGCCGCCGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGGCCGCGCCCCGCCTCCGCCGCCACTATCGCCGCGGC 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGCCGCCGCCGCCCAGCCGCTCCCCCGGCGGTGGCGCC 3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCCTGAAGCAGCCTCCGGCGCCCCCCCCCCCCCCGCCAGTGTCGGCGCCCCGCGGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                           97US-0059160
                                                                                                                                           98US-0093972
                                                                                                                                                                         98WO-US19419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78.8; DB 22
Pred. No. 0.00095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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New antisense oligonucleotides used in treatment of, e.g. pulmonary

vasoconstriction

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 108586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 108645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 108765 GCCNNHNNNSCGCCGCCCCCCCCNNHNNNSCCGCCGCCCCCCCCCNNHNNNSGCCGCCGCC 108706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 108885 CCCNNHNNNSGGGGCCCVAGGCGAGCCAGGCGCCGCCCCGNNHNNNSGGGGCCCVA 108826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 108945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, respiratory distress syndrome, pulmonary vasoconstriction, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target onligonucleotides (specifically AAX55180-271) can be used for the approach of the section of
AAZ17263 standard; cDNA; 1337 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CCTCAGGGTCACGCCCAGAACCCCCTGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CAGGCCCCGGCGGCCGAGCCCCTCCAGGTGGACTTGCTCCCGGTGCTCGCCGCCGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TTCCCCGTGCTGGGCCTGGACTCCCGGGGGGGGGGGGCGGCCTCATGAACTCCTTCCCGCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGCCCCTGCCGCCTCTA----CGGTGGACACAGCGGCCCTGAAGCAGCCTCCGGC
                                                                                                                                                                                                                                                                                                                                                       GCCCCCGCCNNHNNNSAGCCAGGCGCCGCCGCCCCCGCCNNHNNNSGAGCCAGGCGCCGC 108467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCCCCGCCNNHNNNSCCAGGCGCCGCCGCCCCGCCNNHNNNSGCCAGGCGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGCCGCCGCCCCCCCNNHNNNSA-GGCGCCGCCCCCCCCCCCNNHNNNSCAGGCGCC 108587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCCCCCCNNHNNNSCG 108448
                                                                                                                                                                                                                                                                          CGCCGCCACTATCGCCGCG 496
                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGAGCCAGGCGCCGCCCCCCCCCNNHNNNSCCGCCCCCCCNNHNNNSGCCGCCCCC 108766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGAGCCAGGCGCCGCCCCNNHNNNSGGGGCCCVAGGCGAGCCAGGCGCCGCCGCC 108886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77.4; DB 20; Length 114955; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.001;
Thes 265; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  رب
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                                                                                                                                                                                                                                                                                                                                                                                                                                   477
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В Qy

Matches 157;

Local

Similarity

15.4%;

Conservative

0; Mismatches 299; Score 77.2; DB 2 Pred. No. 0.0024;

Indels Length 1337;

0;

Gaps

0;

DB 20;

Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;

peptide analogues and antagonists.

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The present invention describes a library of human polynucleotides CC comprising the sequences given in AR212532 to AR217779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell csuspected of being cancerous, where the gene product is encoded by one CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and CC arrays for diagnostics (which may be used to determine function of a arrays for diagnostics (which may be used to determine function of a cenoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to CC identify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC and lung cancer. The polynucleotides can also be used to screen for contribute analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones WL, Kassa
Lamson G, Leshk
Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human genes and their expression products which differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1998;
28-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene expression product cDNA sequence SEQ ID NO:4735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kassam A, Ke
Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Dickson M, Drmanac R, Drmanac S
Garcia PD, Garcia V, Giese K, Inn
assam A, Kennedy GC, Kita D, Labat
eshkowitz D, Pot D, Randazzo F, Re
B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0075954
98US-0080114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0080666
98US-0072910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0080515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac R, Drman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Innis MA;
Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reinhard
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RESULT 9
AAX02974
AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-IR). may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemma, rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tango-77; human; IL-Ira; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-IR; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                              Example 5; Figure 3; 226pp; English.
                                                                                                                                                                                                                                                                                             WPI; 1999-153692/13.
                                                                                                                                                                                                                                                                                                                                  Pan
                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1998;
04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9906426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IL-1ra BAC contiguous DNA sequence 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX02974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808 CNNCNCCCCNCNCCNCCNNNNCNCNCCCCCCCC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTCCATTCCAGGCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid encoding the new human cytokine Tango-77 to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCGCCCCGGCCACGCCCAGGCCCCGGCGGCCGAGCCCCTCCAGGTGGACTTGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGCCCCCGCCTCCGCCGCCACTATCGCCGCGGC 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCAGCCTCCGGCGCCCCTCCGCCACCCCCGCCAGTGTCGGCGCCCGCGGCCGAGGC
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97US-0054646
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AAV55831/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; infiammation; nitro drug; resistance; protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3108 CCCCGCCGGCGCGCGCCCCCCCCCCCCCGACCGC 3152
                                                                                                                                                                                                                                                                                                               Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of the stabilising sequence-encoding insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV55831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV55831 standard; DNA; 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3198 BP; 807 A; 847 C; 681 G; 846 T; 17 other;
                            WPI; 1998-312463/27
                                                                Masucci MG;
                                                                                                                                          25-JUN-1997;
15-NOV-1996;
                                                                                                                                                                                                  17-NOV-1997;
                                                                                                                                                                                                                                       28-MAY-1998
                                                                                                                                                                                                                                                                            W09822577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2988 ccccaccecaacgeceecgeceecccccccccaageegaegeeeceeeeeeceee 3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MASU/) MASUCCI M G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTCCAGGCCGCGGCGCCCCCCCCCCCCCCAGGCCCCGGCGCCGAGCCCCAGCCCTCCA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGACTTGCTCCCGGTGCTCGCCGCCGCCAGGAGTCCGCCGCGGCTGCTGCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGGTGGGCGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCCCT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCC-----CCCCCGCCCCCCCCCCCCCCCCCCCCCACACCCCGGCCCACACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203;
                                                                                                                                                                                                                                                                                                                                                    pathological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                          96US-0030986
                                                                                                                                                                                                  97WO-IB01508
                                                                                                                                                                97US-0048945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%;
50.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75.6; DB 20; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195;
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Ş 밁 Q 밁 δÃ В δõ Дb Š 당 Š В

2934

2987 327 2874

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This is a nucleotide sequence of the stabilising sequence-encoding consert. The invention provides a method for increasing the resistance core protein to proteolytic degradation that comprises linking or conserving onto or into the core protein a stabilising polypeptide of coroula ((Glya)X(Glyb)Y(Glyc)ZIn where Glya, Glyb, Glyc are 1-6 coroula (Glya)X(Glyb)Y(Glyc)ZIn where Glya, Glyb, Glyc are 1-6 coroula (Glya)X(Glyb)Y(Glyc)ZIn where Glya, Glyb, Glyc are 1-6 coroula (Glya)X(Glyb)Y(Glyc)ZIn where Glya, Glyb, Glyc are 1-6 coroula (Glya)X(Glyb)X(Glyc)ZIn where Glya, Glyb, Glyc are 1-6 coroula (Glya)X(Glyb)X(Glyb)X(Glyc)ZIn where Glya, Glyb, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4B; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic methods such as in vivo imaging.
                                                                                                                    147 TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCCTGCGCCCCAGAGTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 AGGTGGACTTGCTCCCGGTGCTCGCCGCCGCCCAGGAGTCCGCCGCCGGCTGCTGCGGCCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 GGGGGGTGGGCGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCCCTTCCCCGTGCTGGGCCTGGACTCCC 86
                                                                                                                                                                                                                                         230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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48.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.4; DB 19; Length Pred. No. 0.0067; 0; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
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Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA
                                                                                                                                AAA50254 standard; DNA; 1926 BP
                                                                                                                                                                                                                                        314 CTCCTGCCCTCCTGCCCCCTCCTGCTGCCCCCTCCTGCTCCTGC
                                                                                                                                                                                                                                                                               447 CGCCGCGGGGCGAGGCCGCGCGCCCGCCGCCACTATCGCCGCGC 498
                                                                                                                                                                                                                                                                                                                          493 Tecccercerecrececcerc-crecrececcercerecrecrececcercerececc 435
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                                                                                                                                                                                                                                                                                                                                                CC (EBV) nuclear antigen protein 1 (EBNA), see AAY9556). EBNA1 is CC (EBV) nuclear antigen protein 1 (EBNA1, see AAY9556). EBNA1 is CC utilised in a novel method for obtaining a eukaryotic cell that is CC stably transfected with at least one episome. This method involves CC transfecting a eukaryotic cell with: (1) a first episome comprising CC is protein whose expression results in cell death and a selectable marker for eukaryotic cells; and (2) a second episome CC expression of the second protein prohibits the occurrence of cell CC death resulting from expression of the first protein to produce doubly transfected cells which also express an antigen that CC first and second proteins and the selective pressure specified by the marker are expressed, CC inst and second proteins and the selective pressure specified by the marker are expressed, CC and the selective pressure specified by the marker are expressed, CC inst and second proteins and the selective prossure specified by the marker are expressed, CC protein of interest from the other episome. Either or both episomes in which the selection desired to be expressed from 1 of the episomes, and the CC protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as CC a tag for the Cells. The method is applicable to cell culture or interest, using a novel method of selection, and complete acid encoding and reliably express CC a gene to finterest, using a novel method of selection, and complete acid encoding and complicable to cell culture or companions, for gene therapy. It allows the rapid complete acid encoding and complete compliance of that selection without the need for exogenous
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                              Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       selection factors, such as antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horlick RA, Chelsky D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-2000; 2000WO-US03547.
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  147 TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTC 206
                                                                                                                                                                                                             27 TCCCGGTGTTTCCTTGCACGCTGCTGGCCCCCCCCCTTCCCCGTGCTGGGCCTGGACTCCC 86
                                                                                                                                                                    nuclear antigen 1; EBNA1; episome; transfection; selection;
                                                                                                                           GGGGGGTGGGCGGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
                                                                                                                                                                                                                                                           230;
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                               14.98;
                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                               Score 74.4; DB 21; Pred. No. 0.0057;
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RESULT 11 AAA50254/

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Length 1926;

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AAA50254;

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The invention provides a composition comprising nucleic acid, histone HI protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus (EBV; latency-associated nuclear antigen; LANA; EBNA1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF82902 standard; DNA; 1926
                                                                                                                                                                                                                                                                                                                01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                          WO200125484-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EBV tethering protein EBNAl encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2001
                                                                                                                                                                                                                                                                                                                                       29-SEP-2000; 2000WO-US26908
                                                                                                                                                                                                                                                              Robertson
                                                                                                                                                                                                                                                                                    (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                         P-PSDB; AAB62332.
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                                                                                                                                                                              composition for use in gene therapy comprises an expression vector hat includes a nucleic acid sequence encoding a nucleic acid bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-281736/29.
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                                                                                                                                                                                                                                                              ES,
                                                                                                                                           Fig 9C; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                              Cotter MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                      RESULT 13
AAA75454/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease, Huntington disease and sequence represents the nucleotide sequence (EBV) tethering protein ENNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1926 BP; 487 A; 352 C; 872 G;
                                                                                                                                                                                  two-hybrid system;
                                                                                                                                                                                           Origin of replication; protein protein interaction; replication;
                                                                                                                                                                                                                Nucleotide sequence of the Epstein Barr nuclear antigen
                                                                                                                                                                                                                                     15-JAN-2001
                                                                                                                                                                                                                                                                            AAA75454 standard; DNA; 2580 BP
                   WPI; 2000-593546/56.
                                                                              30-MAR-1998;
                                                                                                 30-MAR-1998;
                                                                                                                      05-SEP-2000
                                                                                                                                           US6114111-A
                                                                                                                                                               Epstein-barr virus
                                                          (RIGE-) RIGEL PHARM INC
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                                                                                                  98US-0050863
                                      Huang
                                                                                                                                                                                   nuclear antigen; ss
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48.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes. The present of the Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Composition for detecting protein-protein interactions

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the Epstein Barr nuclear antigen. It is used to produce bait vectors of the invention. The specification describes a compositions and methods for a genetic system of detecting protein-protein interactions in a mammalian host cell. The system comprises bait and test, both containing selection genes, and viral origin of replications which require bound viral replication proteins to effect replication. The compositions is useful for detecting an interaction between a bait protein and a test protein. It is useful in
                           multiple gene expression; receptor; transporter protein; gene transcription factor; adhesion molecule; antisense therapy;
                                                Anti-sense strand; plasmid pCMVEBNA; EBNA 1; episome; transfection; Epstein Barr Virus Nuclear Antigen 1; origin of replication; EBV orip; eucaryotic host cell; recombinant cell line; ion channel;
                                                                                                                  17-JAN-2000
                                                                                                                                                          AAX90923 standard;
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                                                                                           Anti-sense strand of pCMVEBNA plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2580 BP; 632 A; 512 C; 1054 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 17-20; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          two hybrid system comprises bait and test vector which selection gene, vector viral origin of replication and
                                                                                                                                                                                                                                                                                                                                                                                                                                                147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian two-hybrid system for detecting protein-protein interactions
                                                                                                                                                                                                             CTCCTGCCCTCCTGCCTCCTCCTGCTGCTGCTCCTGCTCCTGCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian host cell.
                   amplification;
                                                                                                                                                                                                                                CGCCCGCGGCCGAGGCCGCGCCCCCCCGCCGCCGCCACTATCGCCGCGGC
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                                                                                                                (first entry)
                                                                                                                                                          DNA; 5452 BP
                   cell immortalisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%;
48.7%;
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Pred. No. 0.0054;
0; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 2580;
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                                      therapy;
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Epstein-barr virus

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Matches
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Best Local
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1746
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Synthetic.
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AGGTGGACTTGCTCCCGGTGCTCGCCGCCCCAGGAGTCCGCCGCCGCTGCTGCGGCCG
                                                                                                                                                                             TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCCAGAGTC
                                                                                                                                                                                                                                                                                                                                                             GGGGGGTGGGCGGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
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98US-0130114.
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/product= "EBNA 1 protein"
/note= "Epstein Barr Virus Nuclear Antigen 1"
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48.78;
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Pred. No. 0.
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1805
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RESULT 15
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the invention.
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                                                          7432
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06-NOV-1998;
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  TGCAGGTCGGGGCTGAGCTCCAGTCCCGCTTCTTTGCCTCCCAGGGCTGCGCCCAGAGTC 206
                                                                                                                                                                                                                      GGGGGGTGGGCCTCATGAACTCCTTCCCGCCACCTCAGGGTCACGCCCAGAACCCCC 146
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Search completed: October 10, 2002, 15:12:59
Job time: 1204 secs

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Patent No. 5215881
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Title:
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Maximum Match 100%
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is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

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6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-745-880-3
US-08-486-343A-1
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PCT-US-95-07349-1
US-08-98-136-1
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US-08-362-495-4
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GENERAL INFORMATION:
                              TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1309 base pairs
TYPE: nucleic acid
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APPLICANT: Suda, Xikuo
APPLICANT: No. 6087171nes, Howard O.
TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS
TITLE OF INVENTION: NEURONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                          NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/14614
FILING DATE: 19-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3315
                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/301,416
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,522
FILING DATE: 15-DEC-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 18-NOV-1996
                 STRANDEDNESS:
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US-08-246-489-1
US-09-105-537-9
US-09-105-537-9
US-09-105-537-3
US-09-105-537-3
US-09-369-0-473-1
US-09-869-0-473-1
US-09-869-102-1
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Farabow, Garrett

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                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOV-1990
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOV-1990
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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o. 5460950
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Mang, Polly A.
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Kaufman, Rnadal J.
Tekamp-Olson, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barr, Philip J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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US 07/621,457
                                                                                                                                                                                                                                                                                                                                                                                                                                          US/07/885,972A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corporate Center, P.O. Box 457
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Pred. No. 1.1e-16;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5965425
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INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
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LENGTH: 4405 base pairs
TYPE: NUCLEIC ACID
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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            APPLICATION NUMBER: US 01 ETILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 01 ETILING DATE: 20-MAY-1992
                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                        STREET: Spring House Corporate Center, P.O. Box CITY: Spring House STREE: Pennsylvania
                                                                                                             FILING DATE:
                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                             COUNTRY:
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APPLICATION NUMBER:
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Brake, Anthony J.
Kaufman, Rnadal J.
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                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US 07/621,092
                               us 07/885,972
                                                             US 08/480,382
                                                                                                                             US/08/745,880
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                                                                                                                                                              Version #1.25
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US-08-480-382-3/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 4405 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08480382 Patent No. 5986079
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REFERENCE/DOCKET NUMBER: GIE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9266
TELEPAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kaufman, Rnadal J.
APPLICANT: Tekamp-Olson, Patricia
APPLICANT: Wasley, Louise
APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
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APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
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LOCATION:
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                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 19477
                                                                                                                                                                                                                                                                                               ADDRESSEE: Howson & Howson
STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCGGTCCCCGCCCGGCGGCAGCGTCACGGCGCGGAGGCGGGAGGCGCGGCGGCGCGC 90
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                                                                                                                                                                                                                                           Pennsylvania
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29-NOV-1990
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56.7%;
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08486343A
Patent NO. 6071695
GENERAL INFORMATION:
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPPERMANN, HERMANN
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Best Local :
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INFORMATION FOR SEQ ID NO: 3:
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APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING TITLE OF INVENTION: MORPHOGENIC PROTEIN EXPRESSION NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES ADDRESSEE: INC.
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APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOV-1990
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PRIOR APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                 COUNTRY: U
ZIP: 07148
                                                                                                                         CITY: HOPKINTON
STATE: MA
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                                                                                                                                                                             STREET:
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45 SOUTH STREET
                                                                                           USA
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APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/620,859
APPLICATION NUMBER: 29-NOV-1990
          Score 43.4; DB 2; Length 4405; Pred. No. 0.32;
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REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)-248-7000
TELEPAX: (617)-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ME
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, Edmund R
REGISTRATION NUMBER: 27,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2493 CCCACCGCGTCCGCAGCCCACCCGTCCTGCTCGGGCCGCCTTCCTGGTCCGGACCGCGA 2552
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                                                                                                                                                                                         CITY: HOPKINTON
                                                                                                                                                                                                              STREET:
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APPLICATION NUMBER:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/486,343A
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ilarity 48.6%;
Conservative
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)N: 435
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PCT/US95/07349
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             EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: GIP OF 08/846,247
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
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US-09-320-878-21/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO:
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LENGTH: 17415 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US 07/938,021
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2553 GTGCCGAGAGGGCAGGGCCGGCTCCGATTCCTCCAGCCGCATCCCGCGACGTCCCGCCA 2612
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REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (508)-435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRP-091PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0;

0; Mismatches 108;

Indels

0; Gaps

0

Score 43.2; DB 3; Length 14060; Pred. No. 0.37;

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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-658-136-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08658136 Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                    TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 5970
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: EHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5733 TGAGGTCCCGGTGTCCCCAGCGGTCCCTGGCGTCCCGGTGGTCCCGGCGGTCCTGGCGT 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5793 TCCCGGCGGTCTGGTGTCCCCGGGCGCACCGGGTGCAACTCGGGCGGTCCCGGCGGTCCC 5734
                            SEQUENCE CHARACTERISTICS:
LENGTH: 14060 base pai
                                                                                                             REFERENCE/DOCKET NUMBER: GE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5553 GTCGTCGCACGGGGACACCGGGGGTGGCTCAG 5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5673 CTCCGGGTGCCGCACCGGGCGCCTCGGGCGCTCGGGCGGTCACGGAGGTCCCCATGGCA 5614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 GGCCGAGCACGGCCACAGCCTGGGTGGCTCCG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 CAGCGGGTTCGCTCGCGTAGAGCGCAGGGCGCGCGATGAAGGCGGTGAGCCCGGTGCG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: UNE PUCCE.
CITY: FRAMINGHAM
                                                                                                                                                                                                                           NAME: LASSEN, ELIZABETH REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 0170:
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 47.4
es 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGCGCGCCCCGTGTCGCACCGGCGTGTCCCGGCGGGCCCGGTGGCCCCGTGCGGCGG 5554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCTCGGGCCGCAAGGCGCCGTCGGGCTGCCGCGGCGGCGGGGAGCTGGCGTGCCGTGCCT 458
: 14060 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLINGER, KATHERINE W
LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DACKOWSKI, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREGORY
                                                                                                                                                                                                                                                                                                                                                                        us/08/658,136
                                                                                                                                                                                                                           31,845
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                                                                                                                                                                                                  GEN4-17.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43.2; DB 3; Length 5970; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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US-08-804-227C-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: DeHoff, Bradley S.

APPLICANT: Kuhstoss, Stuart A.

APPLICANT: ROSteck, Paul R., Jr.

APPLICANT: Sutton, Kimberly L.

APPLICANT: TOTALE STATE CONTROLLED STATE 
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Plant, Thomas, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYKETIDE SYN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CONA
FEATURE:
                                                                                       FEATURE:
                                                                                                             TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 CTGCGGCCCAGCGCCCGGCGCCCGCCTCAA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 CGGCGGCGGGAGCTGGCGCTGCGTGCCTGGCCGA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 GCTCGGGGCGCTGGCGGGGCCCCGGGCCGCGCCCCGGGCCCCTGCCCTGCCT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCAAGGCGCCGTCGGGCTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 CCTAACGATGCCGCCCGCCGCCCGCCCGCCTGGCCCTGGCCCTGGGCCTGGGCCTGTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 CGGTGCCCCGAGCGCGCGGGCGCGGAGCCAAAGGGAGCCGGAGCCGGCCGGACGGGCC 308
                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPONERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Plant, Thomas, G. REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 8.6%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7, Application US/08804227C b. 5876991
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                                                                                                                                                                                           nucleic acid
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                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                            CDS
350..14002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 21,
                                                                                                             DNA (genomic)
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                                                                                                                                                                  single
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US-08-804-198-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08804198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43062 CCGGGGCGGCCAGCGC 43047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43182 GGGCGACCTCGCCGACAAGGTCGAACCCGGCGTCACCGGTGGGCAGCAGGCGGCCGAGCA 43123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43122 CTCTGCGGGCGGTGGTGCGCCGCGCGCGGGGCCCTGGGCCGGGGCGTACCGGCTGAGCA 43063
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LOCATION:
FEATURE:
             REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
                                                                                                                                                                           OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1:
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burgett, Stanley G. APPLICANT: Kuhstoss, Stuart A. APPLICANT: Rao, Nagaraja R.
                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 GCTCCGCAGCCGCGC 500
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                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 46285
                                                                                                                                            APPLICATION NUMBER: US/08/804,198 FILING DATE:
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nes 123; Conser
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36155..41830
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20110..31284
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14046..20036
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                                                                                                  EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09428517 Patent No. 6251636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER APPLICATION NUMBER: 60/106,100
                                                                                                                                                                                                                                                                                      APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
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OTHER INFORMATION: Description of Artifical Sequence: Recombinant DNA
                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                  ENGTH: 50937
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LENGTH: 44377 base pairs
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STRANDEDNESS: single
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350..14002
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48.0%;
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Pred. No. 0.4;
0; Mismatches 133; Indels
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                                                               ; TOPOLOGY: 11; MOLECULE TYPE: US-08-658-136-2
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US-08-658-136-2
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Query Match 8.6
Best Local Similarity 50.0
Matches 108; Conservative
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APPLICANT:
APPLICANT:
                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 53526 base pairs
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                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                            TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                          H: 53526 base pairs nucleic acid
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LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
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QIAN, FE
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                                                                                                linear
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                                                                               DNA (genomic)
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               8.6%;
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 Score 43.2; DB 3; pred. No. 0.4; 0; Mismatches 108;
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Pred. No. 0.4;
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                               Length 53526;
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                Qγ
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                                                                                                                                                                        ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-658-136-1
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                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
Patent No.
                                                                                                             Matches
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 53577 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: QIAN, FENG
TITLE OF INVENTION: PO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3761 CTGCGGCCCAGCGCCCGGCGCGCGCGTCAA 3796
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                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 CGGCGGCGGGAGCTGGCGCTGCCTGGCCGA 464
309 CCGGAGCTTGCCTTGCCTCGCTCGCCCCAGCGGGTTCGCCTCGCGTAGAGCGCAGGGC 368
                                                                             249 CGGTGCCCGAGCGCGGGCGGGGCGAGGCAAAGGGAGCGGAGCCGGCCGGACGGGCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                               108;
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                                                                                                                                                                                                                                                                                                      508-872-5415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLINGER, KATHERINE
LANDES, GREGORY M
BURN, TIMOTHY C
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNORS, TIMOTHY D
                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                        single
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                                                                                                                           8.6%;
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                                                                                                               0,:
                                                                                                                           Score 43.2; DI Pred. No. 0.4;
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                                                                                                               Mismatches 108;
                                                                                                                                          DB 3;
                                                                                                                                            Length 53577;
                                                                                                               Indels
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RESULT 14
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
                                                                                                                                             US-08-034-650-9
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TITLE OF INVENTION: NOVEL MOLECULES OF TANGO
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILLING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
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LENGTH: 152331
                                                                                      Sequence 9, Application US/08034650 Patent No. 5641671 GENERAL INFORMATION:
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APPLICANT: Pan, Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                      21931 GCGCGGCCCGCNCGGGGCGG 21912
                                                                                                                                                                                                                                                                                           LOCATION: (1)...(152331)
OTHER INFORMATION: n = A, T, C or
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LOCATION: (1)...(15233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                               APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3761 CTGCGGCCCAGCGCCCGGCGCGCCTGCCGCGTCAA 3796
APPLICANT: VISSER, Christiaan TITLE OF INVENTION: PRODUCTIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                       GGGTGGCTCCGCAGCCGCGG 499
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                                                                                                                                                                                                                                                                                                                                                                                                   GCGCAGGGCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCAAGGCGCC 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124;
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47.7%;
PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.47;
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Search completed: October 10,
Job time: 165.733 secs
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ZIP: 20036-5601
ZIP: 20036-5601
COMPUTER READABLE FORM:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
Compatible
PC-DOS/MS-DOS
Palease #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
                                                                                                                                                                                                                                                                 1621
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                                                                 1801 CGCGCTGGCTCGCATGCGCCG 1825
                                                                                                                                                                                                 FEATURE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 07/727,235
FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                 414
                                                                                                                                                                                                                                                                                              294 GGCCGCGGACGGGGCCCGGAGCTTGCCTGCCTCGCTCGCCCCAGCGGGTTCGCTCG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                            234 GGCTCGGGAGTGTCGCGGTGCCCCGAGCGCGCCGGGCGGAGGCAAAGGGAGCGGAGCC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KOKULIS, Paul N. REGISTRATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                 CAGCCTGGGTGGCTCCGCAGCCGCG 498
                                                                                                                                                              GGCGCCGTCGGGCTGCGGCGGCGGGGAGCTGCCGCTGCCTGGCCGAGCACGGCCA 473
                                                                                                                                                                                                                                 CGTAGAGCGCAGGGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCCCAA 413
                                                                                                                                                                                                                                                                 GTTCGCCCTGGCCGGGCTCGTCGCGTGTGCCGCCTGTGCCGCGGTCGTGCTTGGCTTCG
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                                                                                                                                                                                                                                                                                                                                                                                            126;
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1559..2617
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202) 822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                                                                                                                                                                                                          8.5%;
47.5%;
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                 2002, 17:54:40
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Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2900;
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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
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   0000000
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DB
   408
368.4
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299.2
293.2
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length: 2000000000
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                                                                                                                                                                       Match
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Gapop 10.0 , Gapext 1.0
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BI398600
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B1546228 603188614
B2327284 hw10a02.x
B1598458 603246959
AW028893 wv97c12.x
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AI791586 oj38h08.y
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BG337080 602434352
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11720 row: j column: 16
High quality sequence stop: 739.
Location/Qualifiers BI544702 843 bp mRNA linear EST 05-SEP-2001 603242661F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5285103 5', mRNA sequence. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Falkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 843)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. /organism="Homo sapiens"
/db_xcef="taxon:9606"
/db_xcef="taxon:9606"
/clone="Ithe"NIH_MGC.95"
/clone_lib="NIH_MGC.95"
/tissue_type="hippocampus"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_l: BamHI; Site_2: Sall-XhoI (gtcga:); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS
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                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), iconshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 570)
                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                      BI552992.1 GI:15440304
                                                                                                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                   603193628F1 NIH_MGC_95 Homo sapiens
               DNA Sequencing by: Incyte Genomics, Inc
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distribution: MGC clone distribution information can be
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                                                            (NHGRI), Shiraki
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            EST.
                                                                                          BG337080
BG337080.1
                                                                                                                              mRNA sequence.
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Plate: LLAM11667 row: h
High quality sequence sto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sal1-XhO1 (gtcg); Oligo-dT primed using primer S·TTTTTTTTTTTTTTVN-3; size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.

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/clone_lib="NIH_MGC_95"
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/lab_host="DH10B"
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Pred. No. 3.3e-65;
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cDNA clone IMAGE:4552357
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                  CCGCAGCCGCGGC 500
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                                                 GCGGCGGCGGGAGCTGGCGCTGCCTGGCCGAGCACGG-CACAGCCTGGGTGGCT
1 (bases 1 to 911)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/Clone_libe*NuH_MCC_46"
/tissue_type="leiomyosarcoma cell line"
/tissue_type="leiomyosarcoma cell line"
/lab_host="0H10B (phage resistant)"
/lab_host="0rgan: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
/clone="IMAGE:4552357"
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Query Match
Best Local 9
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63 GCGATCGGGCTTAGTCGGAGCTCCGAAGGGAGTGACTAGGACACCCGGGTGGGCTACTTT 122
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                                             68 CCGATCGGGCTTAGTCGGAGCTCCGAAGGGAGTGACTAGGACACCCGGGTGGGCTACTTT 127
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512 bp mRNA linear EST 09-NOV-1999 au91g11.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783684 5' similar to SW:ID4_MOUSE P41139 DNA-BINDING PROTEIN INHIBITOR ID-4. [1] ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 309.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Other_ESTs: au91g11.x1
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WashU-NCI human_EST Project
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                            /note-"Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SStI; Site_2: XhOI; Double-Stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2783684"
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Primates;
                                                                                                                                                                                                         Score 408; DB 9;
Pred. No. 3.5e-59;
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                                                                                                                                                                                                      Insert Length: 590 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 280.
                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 590 Std Error: 0.00
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1 (bases 1 to 531)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                       Ph.D.
                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1685699"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398;
                                                                                                                                                                                                                                                                                                                                                                                      AIT91586 522 bp mRNA linear EST 13-DEC-1999 oj38h08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1500639 5' similar to SW:ID4_HUMAN P47928 DNA-BINDING PROTEIN INHIBITOR ID-4.; contains MER22.b3 TAR1 repetitive element; mRNA sequence.
CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                         Unpublished (1997)
Other_ESTs: oj38h08.x5
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 522)
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603188614F1 NIH_MGC_95 Homo sapiens
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 826)
                                                                                                                          mRNA sequence.
BI546228
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                                                                     human.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1500639"
/clone_lib="NCI_CGAP_Kid3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
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200 c 172 g
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             644
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Best Local (
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GGGTGGCTCCGCAGCCGCGGC
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), S
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC lone distribution: MG
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5260155"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI: XhOI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI: XhOI (gtcgag p); Oligo-dT primed using primer 5. TTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NuMP/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 261 c 307 g 130 t
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Pred. No. 1.7e
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TITLE
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GATTCCCTCGTAAAACCCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCG
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hw10a02.x1 :
similar to
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                     Conservative
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/db_xref="taxon:9606"
/clone="IMAGE:3182474"
/clone_lbb="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000
                                                                                                                                                                                                                                                                                                                                                                   clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Scares and M. Fatima Bonaldo. " 158 \ c 186 \ g 72 \ t
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99.7%;
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                                                                                                                                                                                                                                                                                Score 358; DB 10;
Pred. No. 8.2e-51;
0; Mismatches 0;
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NGE:3182474 3'
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TITLE
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1 (bases 1 to 817)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAMI1745 row: i column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                  /note-"Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalITxhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 223 c 316 g 120 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5294681"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hypothalamus"
/lab_host="DH10B"
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92.3%;
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                     306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 298 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Location/Qualifiers
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                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring_cell_features"
                                                                                                                                                                                                         Average insert size 1.69 kb. Life Technologies 11549-011"
                                                                                                                                                                                                                                                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2542102"
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98.4%;
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455 bp mRNA linear EST of MI-P-AY1-nrc-h-10-0-UI.sl MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrc-h-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cktuggle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message. cDNA Library Preparation: M.I.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
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201 Kildee Hall, Ames,
Tel: 5152944252
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Mammalia;
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Normalization and subtraction:
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/clone="MI-P-AVI nrc-h-10-0-UI"
/clone_1b="MI-P-AVI"
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Eutheria; Cetartiodactyla; Suina; Suidae;
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               Seq prime POLYA=No.
                                        Email: cktuggle@lastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
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Sus scrofa
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BI398642.1 GI:15177703
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398 bp mRNA linear EST:
MI-P-AY1-npv-c-01-0-UI.sl MI-P-AY1 Sus scrofa cDNA clone
MI-P-AY1-npv-c-01-0-UI 3', mRNA sequence.
                                                                                                                                                                          Iowa State University
201 Kildee Hall, Ames,
                                                                                                                                                                                                         Molecular Genetics Laboratory, Department of Animal
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Bonaldo, M.F., Lennor
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                                              Genome Res. 6 (9),
                                                                                                                                                              Sus scrofa
                                                                                                                                                                                           EST
               Contact: Tuggle CK
                                                                discovery
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Similarity 83.3%;
Molecular Genetics Laboratory, Department of Animal Science
                                                                                Normalization and subtraction: two
                                                                                                                              Mammalia;
                                                                                                                                           Eukaryota;
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153 c 139 g 45 t
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECORI; The MI-P-AY1
library is normalized library derived from the MI-P-AY0
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI.P-AY1-npv-c-01-0-UI"
/clone_lib="MI.P-AY1"
                                                                                                                              Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                             Lennon, G. and Soares, M.B.
                                                 791-806 (1996)
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Pred. No. 1e-
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RESULT 14
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                                                                                                                     TGGGCGGCTCGGCGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo-dT track not found, Not I site shown in beginning of seque is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
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Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cktuggle@iastate.edu
BI398600 385 bp mRNA linear to: MI-P-AY1-npu-e-10-0-UI.s1 MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-npu-e-10-0-UI 3', mRNA sequence.
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/lab_host="DHIOB (Life Technologies)"
/lab_host="Nector: pT/T3D-Pac (Pharmacia) with a modified
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AYO
| library is derived from placenta. For a detailed
/description of the library from which this clone was
/derived, please visit our web site at
/ttp://plgest.genome.lastate.edu/. The procedure used to
/create this library has been previously described (Bonaldo
/Lennon and Soares, Genome Research 6:791-806, 1996)
/TAG_SEQ=None found"

TAG_SEQ=None found"

65 t
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Pred. No. 1.8e-32;
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Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab University of Iowa Clone distribution: clones will be availal through Research Genetics (www.resgen.com)
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Fax: 5152942401
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201 Kildee Hall, Ames,
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mmalia; Eutheria; Cetartiodactyla; Suina; Suidae;
(bases 1 to 385)
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/db_xref="taxon:9823"
/clone=Ib="MI-P-AYI"
/clone_lib="MI-P-AYI"
/clone_work
/clone="MI-P-AYI"
/clone=lib="MI-P-AYI"
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Pred. No. 5.8e-32;
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RESULT 15
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                                                                                                                                                                                                       Query Match
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324
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                                                                                                                                                                                 Local Similarity
                     CCCTCGTAAAACCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCG----
CCCTCGCAAAACGCAGAGCGACCCTCCCGTCAATTGTTGGGCGCGGGATCGCCGGGAGCT 265
                                                                             GTGCTTTTGCTTTTTTTTTTTCCTTTGGGCTCGGGCTGAGTGTCGCCCACTGAGCAAAGATT 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI399954 BI399954 374 bp mRNA linear EST : MI-P-AY1-nrh-f-11-0-UI.sl MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrh-f-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq prime POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 374) Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. CoMA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOWA State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13 Forward
                                                                                                                                                                                                                                                                   53
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                         /note="vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoR; The MI-P-AX1 library is normalized library derived from the MI-P-AX0 library, ultimately derived from placenta tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://plyest.genome.lastate.edu/. The procedure used to create this library has been previously described (Bonaldo Lennon and Soares, Genome Research 6: 791-806, 1996) TAG_SEQ=None found"

145 c 132 g 43 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="crossbreed"
/db_xref="taxon:982"
/clone="MI-P-AXI-nrh-f-11-0-UI"
/clone_lib="MI-P-AXI"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
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                                                                                                                                                                             47.6%;
83.1%;
                                                                                                                                                              0;
                                                                                                                                                           Score 238.2; DB 10;
pred. No. 9.3e-31;
0; Mismatches 34;
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                                                                                                                                                      354 CGTAGAGCGCAGGGCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCAA 413
                             474 CAGCCTGGGTGGCTCCGCAGCCGC 497
                                                                                                                                                                                     295 GCCGC-GGACGGGCCCGGAGCTTGCCTGCCTCGCTCGCCCCAGCGGGTTCGCTCG
                                                                                                                                                                                                                                                 264 TCGCGGTGCCCCGAGCGCTGACCGAGCGCACCGGGCGGGAGGCAAGGGGAGCGGAGCCG
                                                             84 GGCGCCGTCGGGCTGCGGCGGCGGGGGAGCTGGCCTGCCCTGGCCTGGCCGAGCACGGCCA 25
                                                                           CAGCCTGGGCGGCTCGGCGGCCGC
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Search completed: October 10, 2002, 20:27:28
Job time: 701.733 secs

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Minimum DB seg length: 0
Maximum DB seg length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                               184.4
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1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*

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8: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:*

9: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:*

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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
100.0 1322
36.9 225
23.4 1309
10.3 154746
10.3 154746
10.1 114955
9.8 2561
9.8 114955
                                                                                                                                                                                                                                                       Match Length
                                                                                                                                                                                                                                                                                                                                                                                                      is the number of results predicted by chance to have a ter than or equal to the score of the result being printed.
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Listing first 45 summaries
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  Human herpesvirus
Human adenosine Al
Human immune/haema
Rabbit low density
Human adenosine Al
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                                                                                                                                                      Human secreted pro
Regulator of neuro
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14169	14148	14139	14060	14060	5970	5970	3957	17415	17415	17415	10877	4405	4405	4405	4405	77536	1227	12425	1614	1888	1887	125401	125401	53789	4672	9252	3399	2207	790	421	375	798	117213	48	3787
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AAS81252	AAT13821	AAH98954	AAA28423	AAT94102	AA256003	AAA75635	AAA09686	AAA59897	AAV80733	AAT11639	AA255620	AAZ38795	AA225275	AAT05556	AAQ25444	AAA14651	AAS72464	AAH26495	AAH26499	AAV24113	AAV24114	AAD17186	AAD17186	AAV21187	AAS73772	AAK68601	AAL26787	AAX77135	AAF27264	AAA31440	AAI84136	AAF30757	AAV62176	AAS20000	AAH81775
DNA encoding novel	Polycystic kidney	Human EST-derived	Human polycistin c	Human PKD1 cDNA.	Contig 002 from co	tide	HSV-2 immediate ea	a	Human osteogenic p	Human osteogenic p	Human BMP-7 gene 5	Human PACE encodin	Human PACE-like pr	Human PACE coding	PACE composite seq	Nucleotide sequenc	DNA encoding novel	Human low density	Human low density	LH-2 protein codin			Streptomyces nours	Amycolatopsis medi	DNA encoding novel	Human immune/haema	Human breast cance	Human nerve mutati	Chicken atonal hom	Plant microsatelli	Human polynucleoti	Micromonospora meg		DNA encoding pyrid	

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ALIGNMENTS

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Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; ID4; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; helix-loop-helix; HLH; cytostatic; ds AAD11113 standard; DNA; 1322 BP Stockert E, (LUDW-) LUDWIG INST CANCER RES. (SLOK) SLOAN KETTERING INST CA (CORR) CORNELL RES FOUND INC. 21-JAN-2000; 2000US-0489101. 19-JAN-2001; 2001WO-US02015 26-JUL-2001. Human small cell lung cancer associated gene, 24-SEP-2001 AAD11113; WO200153349-A2 2001-457597/49 Scanlan MJ, (first entry) Jager D, CANCER RES 01d LJ, Gure AO, ID4. Chen

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RESULT 2
AAC10488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leamyosarcoma or synovial sarcoma. The present sequence is a DNA encoding human ID4 protein. This small cell lung cancer associated gene is designated as NY-SCIC-4. ID4 protein is a member of dominant negative helix-loop-helix (HLH)
06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                      AAC10488;
                                                                       AAC10488 standard; cDNA; 225 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 57; Page 91-92; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1322 BP; 267 A; 376 C; 417 G; 262 T; 0 other;
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                                 AAQ94779
ID AAQ9
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AC AAQ9
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Best Local
 07-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 14563
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                       AAQ94779 standard; DNA; 1309 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225 BP; 36 A; 55 C; 80 G; 53 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 14563; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                      188 AAAGATTCCCTCGTAAAACCCAGAGCGACCCT 219
                                                                                                                                                                                                                                                                                                                                                          194 AAAGATTCCCTCGTAAAACCCAGAGCGACCCT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GCGATCGGGCTTAGTCGGAGCTCCGAA-GGAGTGACTAGGACACCCGGGTGGGCTACTTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCCGGTGCTTTTGCTTTTTTTTCCTTTGGGCTCGGGCTGAGTGTCGCCCACTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCCGGTGCTTTTGCTTTTTTTTTCCTTTTGGGCTCGGGCTGAGTGTCGCCCACTGAGC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGATCGGGCTTAGTCGGAGCTCCGAAGGGAGTGACTAGGACACCCGGGTGGGCTACTTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGCGGTTGTGAGTAGTACCGGGAGTGGGGTGATCCCGGGCTAGGGGGAGCGCGGCG--C 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.9%;
98.1%;
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Pred. No. 1.4e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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Regulator of neuronal proliferation RNP-1 partial DNA.

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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1309 BP; 305 A; 339 C; 381 G; 284 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A vector contg. a nucleic acid encoding an EXP and/or ElA regulator - is used to induce DNA synthesis in differentiated neurons and replace neurons after injury or neuro:degenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1994;
17-DEC-1993;
Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide;
antibacterial; fungicide; protozoacide; antirheumatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence corresponds to RNP-1 which has no significant homologyg to other characterized sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 30; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-231568/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuman T, Nornes HO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SPIN-) SPINAL CORD SOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulator of neuronal proliferation; neuron; RNP-1; ss.
                              Human herpesvirus 2 complete DNA genome.
                                                26-MAR-2002 (first entry)
                                                                     AAD25519;
                                                                                      AAD25519 standard; DNA; 154746 BP
                                                                                                                                                                                                                                                                                                                                              145 TITTITITCCTTTGGGCTCGGGCTGAGTGTCGCCCACTGAGCAAAGATTCCCTGGTAAA 204
                                                                                                                                                                                                                                                        118
                                                                                                                                       238 GYGAGCCCGGTGCG-CCCTCGGGCGTCAAGGCGCCGTCGGGCTGCGGCGGGGGAGCTG
                                                                                                                                                                                                385
                                                                                                                                                                                                                  178 GCGGGGGACCGAGCTCGCTCTGCTTGTCGCGGGTCCTCTCCAGAAGCGCGCGATGAAGGCG 237
                                                                                                                                                                                                                                     265
                                                                                                                                                                                                                                                                                                                205 ACCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCGGTGCCCCGAGCGCG 264
                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                    GTGAGCCCGGTGCGCCCCTCGGGCCGCCAAGGCGCCGTCGGGCTGCGGCGGCGGGGAGCTG 444
                                                                                                                                                                                                                                                        CTCGGAGCCGCCGGGTGCTGCCGAGCGCCGGACGCAGAGGAGGGGAGCAAAGCAAATTGCG 177
                                                                                                                                                                                                                                                                          ACAAAAACCTGAGCTACCCTTTCCAAAACCCCGAGCAGCTCTCGTCGATTTCTG----GAG 117
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0301416
93US-0169522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US14614.
                                                                                                                                                                                                                                                                                                                                                                          23.4%; Score 116.8; DB 16; Length 61.8%; Pred. No. 1.4e-15; ative 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suda K;
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antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosis; immune response; vasotropic; vaccine; gene therapy; autoimmune disease;
vasculitis; ds.
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Human herpesvirus 2.

WO200176643-A1

07-APR-2000; 2000US-195680P.

(BAYU) BAYLOR COLLEGE MEDICINE.

Orson FM, Kinsey BM, Bhogal BS;

WPI; 2002-066308/09.

Composition for oral delivery of vaccines, comprises expression vector containing antigenic genomic sequence, bound to aggregated protein polycationic polymer conjugate or suspension

Disclosure; Page 90-132; 145pp; English.

The invention relates to a composition comprising an expression vector CC bound to an aggregated protein-polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide configen which is a fragment of a gene or genome associated with an CC antigen which is a fragment of a gene or genome associated with an CC antigen which is a fragment of a gene or genome associated with an CC arthitis, vasculitis, and multiple sclerosis, pathogenic genomes CC consisting of bacterium, fungus, protozoa and virus such as human CC immunodeficiency virus (HTV), herpes simplex virus (HSV), hepatitis CC virus (HCV), influenza and respiratory syncytial virus (RSV), and CC cytokine expression vector), is useful for inducing an immune response CC (systemic and/or mucosal) in an organism. The cytokine appression vector CC contains a sequence for granulocyte macrophage-colony stimulating factor CC contains a sequence for granulocyte macrophage-colony stimulating factor CC contains a sequence for granulocyte macrophage-colony sciumlating factor CC different promoter polymucleotide sequences. The expression vector, as a CDMA vaccine is useful for treating a condition in an organism. The CC to the vice useful for treating a condition in an organism. to the invention.

Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 other;

Query Match Best Local : al Similarity 155; Conserv Conservative 10.3%; Score 51.6; DB 24; Length 154746; 50.3%; Pred. No. 0.051; tive 0; Mismatches 149; Indels 4; 4; Gaps

1184 CGACCGCGACCGGTTCCGGCGCGCGTGGCGGCGGCCGACGCGGTCATCGGACCGTGCCT 1243

371 GCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCAAGGCGCCGTCGGGCTGCG 430

Qy

491 CAGCCGCG 498

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Db 126126 GGTGGCCTGGGAGACGGCCGCGCGCCTGGCCCGACGGGGGTCCTGGGCGCGCGAGCGGGC 126067
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AAD25519/c
AAD25519 standard; DNA; 154746 BP.
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                                                                                                                                                                                                                                       The invention relates to a composition comprising an expression vector co bound to an aggregated protein polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide co suspension. The expression vector contains a promoter polynucleotide and carbinitis, useful is a fragment of a gene or genome associated with an expression vector, and multiple sclerosis, pathogenic genomes consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium, fungus, protozoa and virus such as human consisting of bacterium (HrV), herpes simplex virus (HSV), heaptitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and optionally comprising a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response contains a sequence for granulocyte macrophage-colony stimulating factor (systemic and/or mucosal) in an organism. The cytokine expression vector contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interpleukin-12 (II-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or characteristic suseful for treating a condition in an organism. The cytokine are under transcriptional control of the action is suseful for treating a condition in an organism.
                                                                                             Matches 155;
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide; antibacterial; fungicide; protozoacide; antinemmatic; antiinflammatory; antiarthritic; rheumatoid arthritis; neuroprotective; multiple solerossis; immune response; vasotropic; vaccine; gene therapy; autoimmune disease;
                                                                                                                                                                             Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 90-132; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for oral delivery of vaccines, comprises expression vector containing antigenic genomic sequence, bound to aggregated protein polycationic polymer conjugate or suspension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1420 GAGCTCCG 1427
                                            191 GATTCCCTCGTAAAACCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-195680P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-US11372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasculitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human herpesvirus 2 complete DNA genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
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                                                                                                                   Local
                                                                                                                                                                                                                               the invention
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinsey BM,
                                                                                             Conservative
                                                                                                              10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhogal BS;
                                                                                             0
                                                                                                                 Score 51.6; DB 24; Length 154746; Pred. No. 0.051;
                                                                                             Mismatches
                                                                                             149; Indels
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                                                                                     Gaps
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RESULT 6
AAX53491
ID AAX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 125886 CCGTCGGG----CGGTCTAGGGTTGAACCGGCGAGGGCGGCGGCGGCGGCGGCGGAGCCCCG 125831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 125946 CGCGGAGGAGGAGGAGGCGGCGGCGGCGGCGCGGGTCCTCCGCCGCCGCCGGGCCCGGG 125387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126006 GGAGCCCGAGCCCGAGCTCGGGCCCGAGCCCGAGCCCCACGAAGACGGCGGACC 125947
The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiration; respiration; pulmonary hypertension; pulmonary vasoconstriction; emphysema; pulmonary hypertension; pulmonary vasoconstriction; emphysema; colon cancer; breast cancer; lung cancer; lunghoma; lumphoma; carcinoma; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                              New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction  \begin{tabular}{ll} \end{tabular} \label{table_equation} 
                                                                                                                                                                                     Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                            WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                              (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9913886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 GCGGCGGGAGCTGGCGCTGCCTGCCTGGCCAGGCACGGCCACAGCCTGGGTGGCTCCG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 CAGCCGCG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 GCGCGATGAAGGCGGTGAGCCCCGGTGCGCCCCTCGGGCCGCAAGGCGCCGTCGGGCTGCG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 GTGCCCCGAGCGCGGGCGCGGGCGCGGGGCGGGGCCCGCGGGGCCCC 310
                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0093972
97US-0059160
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RESULT 7
AAK813737c
ID AAK813
XX
AC AAK813
XX
DT 07-NOV
XX
DE Human:
KW Cytost
XX
WO2001
XX
WO2001
XX
O9-AUG
XX
O9-AUG
XX
PR 11-JAN
PR 24-FEB
PR 16-MAR
PR 119-MAY
PR 119-MAY
PR 119-MAY
PR 119-MAY
PR 28-JUN
PR 30-JUN
PR 30-JUN
PR 30-JUN
PR 30-JUN
PR 31-JUN
PR 30-JUN
PR 31-JUN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 104646 GGGCGCCCGSNNNDNNCCGCBGGCCBGGCCGCCSNNNDNNCCGCBGGCCBGGCGCG 104705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 104586 CCBGGGGGGCGCCSNNNDNNCCGCBGGCCBGGCGCGCGCSNNNDNNCCGCBGGCCB 104645
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104766 GGCCBGGGCGSNNNDNNCCGCBGGCCBGGGCSNNNDNNCCGCBGGCCBGGCSNNNDNNCC 104825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases pulmonary vasoconstriction, including lung diseases pulmonary vasoconstriction, inflammation, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary diseases (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
04-FEB-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

10-MAR-2000

17-MAR-2000

17-MAR-2000

18-APR-2000

19-MAY-2000

07-JUN-2000

07-JUN-2000

07-JUN-2000

07-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 CCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCGGTGCCCCGAGCGCGCC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 GCTGCGCTGCCTGGCCGAGCACGGCC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 GAGCCCGGTGCGCCCCTCGGGCCGCAAGGCGCCGTCGGGCTGCGGCGGCGGGGAGCTGGC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
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Similarity 33.8%;
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                                          2000US-0179065
2000US-0180628
2000US-0184664
2000US-0189350
2000US-0189874
2000US-0199874
2000US-0198123
2000US-0198123
2000US-0205515
2000US-0205816
     2000US-0215135
2000US-0216647
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        07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
  14 - SEP - 2000
21 - SEP - 2000
21 - SEP - 2000
25 - SEP - 2000
25 - SEP - 2000
26 - SEP - 2000
27 - SEP - 2000
27 - SEP - 2000
29 - SEP - 2000
20 - OCT - 2000
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2000US-0217487.
2000US-0217496.
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20000S-0232397
20000S-0232399
20000S-0232399
20000S-0232400
20000S-0232400
20000S-0232405
20000S-0233063
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20000S-0229509.
20000S-0229513.
20000S-0230437.
20000S-0230438.
20000S-0231242.
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2000US-02342723.
2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
          2000US-0241808
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAK82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)
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20-OCT-2000;
01-NOV-2000;
                                                                                                                                                                                                                             08-DEC
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17-NOV-
17-NOV-
                                                                                                       Disclosure; SEQ ID NO 36185; 3071pp + Sequence Listing; English.
                                                                                                                                         WPI; 2001-483426/52.
                                                                                                                                                          Rosen CA,
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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VON-
VON-
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2000US-0251856.
2000US-0251868.
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2000US-0241826.
2000US-0244617.
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2000US-0256719.
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2000US-0246523.
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RESULT B
ANALZ6500/c
ID AAH265
AXX 12-NOV
XX 12-NOV
XX 12-NOV
XX RABbit
XX Low de
KW Low de
KW Vaccin
XX VOTCLC
XX VACCIN
XX VOTCLC
XX COPYCLC
XX COPYCL
XX COPYCLC
XX COPYCLC
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ğ
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Best Local Similarity 49.6%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                    WPI; 2001-565505/63.
P-PSDB; AAB82807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                    02-MAR-2000; 2000US-0517849
14-JUL-2000; 2000US-0616289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH26500 standard; cDNA; 2561 BP.
                                                                                                                                                                                                                                                   (BOST-) BOSTON HEART FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001WO-US06356
                                                                                                                                                                              Lees AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 ACAGCCTGGGTGGC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CCGCCCCCACGGCTTCCTGCAGCAGCGCCCCGAGCCGGCTCAGCATGATGGCGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 AGGCGCCGTCGGGCTGCGGCGGCGGGGAGCTGGCGCTGCCTGGCCGAGCACGGCC 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 GCGTAGAGCGCAGGGCGCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCA 412
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                                                                                                                                                                              Lees RS, Law SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                              Arjona AA;
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New isolated low density lipoprotein binding polypeptide for treating,

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FX SX COCCOCCOCCOCCOCC
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AAX53491/c
ID AAX534
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PD XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein (LEP-2, see AAB82807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides of termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2561 BP;
                                                                                                                          impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                             Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                              AAX53491 standard; DNA; 114955
                                                                                                                                                                                                                                              Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               863
                                WO9913886-A1
                                                                                                prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 GGGCTCGGGAGTGTCGCGGTGCCCCGAGCGCGCGGGCGCGGAGGCAAAGGGAGCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293
                                                                                                              nepatocellular carcinoma; kidney cancer; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTAGAGCGCAGGGCGCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCCGCA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGGCGGCGGCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAGCCTGGGTGGCTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCGCCGTCGGGCTGCGCGGCGGCGGGGGGCTGCCCTGGCCCGAGCACCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2A; 143pp;
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 A; 937 C; 879 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%;
54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB:
Pred. No. 0.16,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2561;
                                                                                                                  hepatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    804
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AAH81775/c
ID AAH81775 standard; I
XX
AC AAH81775;
XX
DT 21-SEP-2001 (first
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC directed against at least 2 minumes selected rion cording regions of RNAs corresponding to target genes, gene (CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC end, the 3'-end and the juxta-section between coding and non-coding CC regions and all segments of RNAs encoding proteins associated with one CC or more diseases, conditions or mixtures. The antisense oligonucleotides (specifically AXX55272-74. These multiple target CC oligonucleotides (specifically AXX55180-271) can be used for the CC antisense treatment of diseases and conditions. Typical diseases and CC conditions are those associated with impaired respiration and CC conditions are those associated with impaired respiration and CC condition, including lung diseases, pulmonary vasoconstriction, cystic fibrosis, CC respiration, respiratory diseases, pulmonary vasoconstriction, emphysema, chronic CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, CC pancreatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                         δã
                                                                                                                                                                                                                                                                                                                                                                                                                Db 110675
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                                                                                                                                 RESULT 10
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Best Local S
                                                                                                                                                                                      110495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 CCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGAGTGTCGCGGTGCCCCGAGCGCGC 265
                                                                                                                                                                                                                           444
                                                                                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification describes antisense oligonucleotides (AAX52869-X55271)
                                                                                                                                                                                                                    GGCGCTGCGTGCCTGGCCGAGCACGGCCACAGCCTGGGTGGCTCCGCAGCCGGGC 500
                                                                                                                                                                                                                                                                                                GCGCGNNHNNNSGGCGGCGCGCGCNNHNNNSGGCGGGCGCGGCGGGNNHNNNSGGCGG
                                                                                                                                                                                                                                                                                                                                                                       CGGGCGGCNNHNNNSGGCGGGCGCGNNHNNNSGGCGGGCGCCCCNNHNNNSGGCGGGCG 110616
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNHNNNSGGCGGGGCGCGCGGGGCCCNNHNNNSGCGCGCGGGGCCCCNNHNNNSGGCGC
                                                                                                                                                                                                                                                             GCGGCGCGGGGNNHNNNSGGCGGGCGCGCGGGGCNNHNNNSGGCGGGGGGCGCGGGGCC 110496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against at least 2 mRNAs selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0093972
97US-0059160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US19419
                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%;
37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48.8; DB 20; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from target genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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(first entry)

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RESULT 11
AAS20000
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AAH81492-AAH82376 represent the human and rat derived nucleic acid of fragments described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 438-439; 579pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000; 2000DE-1004102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3787 BP; 898 A; 1210 C; 1073 G; 606 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483415/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2001; 2001WO-EP01003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human differential transcription-associated cDNA SEQ ID 284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                           444
                                                                                                                           155
                                                                                                                                                        385
                                                                                                                                                                                                         326 CCCTCGCCCCAGCGGGTTCGCCTCGCGTAGAGGCC-GCGCGCGCGCGATGAAGGCG
                                                                                                                                                                                                                                                                               266
                                                                                                                                                                                                                                                                                                              334
                                                                                                                                                                                                                                                  274
                                                                                                                                                                                                                                                                                                                                         206 CCCAGAGCGACCCTCCCGTCAATTGTTGGGCTCGGGGAGTGTCGCGGTGCCCCGAGCGCGC 265
                                                               95
                                                                                         GCCCTCCCCTC 455
                                                                                                                         CCGCGCCGGGAGCCGCCCGCGGGCCGGGGCGGGGGGGCCCAGGGGCTGAGAGTGCGCGGGGGGGCCCC 96
                                                                                                                                                        GGCCCGCGCGCGCTCGCGGCCGGGCGTCCACAATGCCGGCGGGCTGCTGGGG
                                                                                                                                                                                                                                                CGGGCGCGAGGCAAAGGGAGCGGAGCCGGCCGGACGGGGCCCGGAGCTTGCCTT 325
                                                                                                                                                                                                                                                                                                            GGCCGCGCGCGG 84
                                                                                                                                                                                                                                                                                                                                                                       144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chal A, Hinzmann B, M, Hellriegel M, S
                                                                                                                                                                                                                                                                                                                                                                                    h 9.6%;
Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmitz A, Sers C;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 22; Length 3787; Pred. No. 0.26; O; Mismatches 105; Indels
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    exon
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                 variation
                                                                                                            exon
                                                                                                                                                                                                                                                  exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding pyridoxal (pyridoxine, vitamin B6) kinase (PDXK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS20000 standard; DNA; 44861 BP
                                                             variation
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                                                                 /number= 6
                                                                                                                                                                                               /number= 5
30924..33792
/standard_name= "Single nucleotide polymorphism" replace(33831,G) /*tag= s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number = 2
2646=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Pyridoxal (pyridoxine, vitamin B6) kinase, specifically claimed in claim 27" 4093..4179
                                                                                           /standard_name= "Single nucleotide polymorphism"
33793..33880
/*tag= q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
replace(3930,G)
                                                replace(33801,A)
/*tag= r
                                                                                                                                                                                                                                                                                          /standard_name= "Single nucleotide polymorphism"
replace(28683,A)
                                                                                                                                                                                                                                                                                                                                                                                                  /number= 1
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                                                                                                                                                     replace(33776,C)
                                                                                                                                                                                                                                              /standard_name= "Single nucleotide polymorphism"
30877..30923
                                                                                                                                                                                                                                                                                                                                        replace(28631,G)
                                                                                                                                                                                                                                                                                                                                                        /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(4252,T)
                                                                                                                                                                         /number=
                                                                                                                                                                                                                                                                                                                                                                                    28606..30876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18922..26464
/*tag= g
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/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product= "PDXK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'standard_name= "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 'number= 3
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'number= 3
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                                                                                                                                                                                                                                                                                                                                 /standard_name= "Single nucleotide polymorphism"
40496..40562
/*tag= aj_
                    /standard_name= "Single nucleotide polymorphism" replace(40875,C) /*tag= ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name= "Single nucleotide polymorphism"
38518..40495
                                                                     replace(40841,A)
/*tag= ao
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replace(37287,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cons_splice=(5'site:NO,3'site:NO)
replace(33922,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33881..35300
/standard_name= "Single nucleotide polymorphism"
                                                                                                        /number= 11
                                                                                                                                                                                                                                             replace(40521,T)
                                                                                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                               replace(40516,C)
                                                                                                                                                                                                                                                                                                                                                                                        replace(38622,C)
/*tag= ai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(38397,T)
/*tag= aq
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replace(37545,A)
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37316..37427
/*tag= ac
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replace(33840,A)
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated human pyridoxal (pyridoxine, vitamin B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in studying the expression and function of PDXK, and in expressing PDXK protein for use in screening for candidate drugs to treat PDXK related diseases and for therapeutic purposes. A transgenic animal is useful for studying expression of the PDXK isogenes in vivo, for in vivo screening and testing of drugs targeted against PDXK protein, and for testing the efficacy of therapeutic agents and compounds for autoimmune polyglandular disease type 1. The polypeptide is useful for studying the effect of the variation on the biological activity of PDXK and the binding affinity of candidate drugs targeting PDXK for the treatment of autoimmune polyglandular disease type 1. Genotyping and haplotyping is useful for improving the efficacy and reliability of several steps in the discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and development of drugs for treating diseases associated with PDXK activity, e.g., autoimmune polygiandular disease type 1, to validate PDXK as a candidate agent for treating a specific condition or disease predicted to be associated with PDXK activity, and in the design of clinical trials of candidate drugs. This sequence (located on chromosome clinical trials of candidate drugs. This sequence (located on chromosome 21922.3) encodes human pyridoxal (pyridoxine, vitamin B6) kinase (PDXK) and forms the reference sequence on which the isoforms AAU11952 and
13-JAN-1999
                                                                          AAV62176;
                                                                                                                                             AAV62176 standard; DNA; 117213
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P-PSDB; AAU11951.
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/note= "encoded protein shown
61241..62071
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/note= "encoded protein shown
complement (58970..60760)
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/note= "encoded protein shown
complement (51701..53575)
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/note= "encoded protein shown
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complement (44853..47297)
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/note= "encoded protein shown
complement (50035..51666)
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/note= "encoded protein shown
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/product= "ORF#27 protein"
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/note= "encoded protein shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Micromonospora megalomicea subsp. nigra.
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/gene= negDV"
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/note= "eryVIV, dnmV homolgoue; encodes AAB82208"
complement (8228..9220)
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/note= "eryCVI homologue; encodes AAB82206"
6592..7197
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complement (9226..10479)
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/_^+>= "ervBVIII, dnmU homologue, encodes AAB82207"
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/gene= "megDII"
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/*raduct= "TDP-3-k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene= "megy"
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/note= encodes AAB82204"
4651..5775
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928..2061
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2,3-dehydratase"
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/note= "encodes AAB82202"
2072..3382
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/product= "TDP-megosamine /
/note= "eryCIII homologue;
3462..4634
                                                                                                                            /gene= "megBV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "eryCI, DnrJ homologue, encodes
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; encodes AAB802203"
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17947..18207
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22957..24237
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                                                                                          26998
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'function= "ACP1"
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|tion= "AT3"
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Best Local Similarity
Matches 105; Conserv
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         418 CCGTCGGGCTGCGGCGGGGGAG 441
                                                                                         298
                                                                               GCGGACGGGGCCCGGAGCTTGCCTGCCTCGCTCGCCCCAGCGGGTTCGCTGCGTA 357
                             GCCCGTTCGATGCGGTCACCGGTGAGGGTCTCGACGGTGCCGTCGTCGAGCGTCGCGGCG
                                                GAGCGCAGGGCGCGCGATGAAGGCGGTGAGCCCGGTGCGCCCCTCGGGCCGCAAGGCG
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Conservative
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26998..27258
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24544..25581
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32257..32799
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29953..30477
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22957..24237
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                                                                                                                                                                                                                                                    /gene= "megAIII"
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/function= "AT5"
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/function= "KR4"
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                                                                                                                                                           9.1%;
51.5%;
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                                                                                                                                                 Score 45.6; DB: pred. No. 0.87; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                       activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; haematopoiesis; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4196; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                             Sequence 375 BP; 54 A; 138 C; 113 G; 41 T; 29 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAO04205
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AAGGCGCCGTCGGGCTGCGGCGGGGGGGGGGCTGGCGTGCCTGGCCTGGCCAGCACGCC 471
                                                 CGCGTAGAGCGCAGGGCGCGCGATGAAGGCGGTGAGCCCCGGTGCGCCCCTCGGGCCGC 411
                                                                                                                 Similarity
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Pred. No. 0.
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0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant microsatellite sequence; core repeat sequence; detection; pro DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant microsatellite marker #401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 195; 392pp; English.
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399 CGGCGGCAGCAGCGGGCTGTTCGGGCCGGGCGGGCGGCCGGC	TACT TATT GGGA	Query Match Query Match Query Match Query Match Best Local Similarity 63.3%; pred. No. 1.4e-13; Matches 219; Conservative 0; Mismatches 103; Indels 24; Garaches 219; Indels 24; Garaches 24; Garaches 219; Indels 24; Garaches	RESULT 1 US-09-234-332-5 US-09-234-332-5 ; Sequence 5, Application US/09234332A ; patent No. 6087168 ; GENERAL INFORMATION: APPLICANT: Cedars-Sinal Medical Center APPLICANT: Michel F. Levesque, M.D. APPLICANT: Toomas Neuman, Ph.D. TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF ITLE REFERENCE: P07 41494 CURRENT APPLICATION NEURONS; TRANSDIFFERENTIATION OF EPJ FILE REFERENCE: P07 4194 CURRENT FILING DATE: 1999-01-20 NUMBER: FastSEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 5 ; LENGTH: 3138 TYPE: DNA ORGANISM: Human FEATURE: NAME/KEY: gene LOCATION: (0) COTHER INFORMATION: Zic 1 Protein gene; Genbank Accession US-09-234-332-5	28 48.6 9.7 4848 4 US-08-955-957A-4 29 48.6 9.7 4848 4 US-08-955-957A-6 c 30 48.4 9.7 1578 1 US-08-681129-1 c 31 48.2 9.6 2721 6 5215881-2 c 32 48 9.6 1203 4 US-09-086-010-1 34 48 9.6 4257 2 US-08-690-473-1 35 48 9.6 4257 4 US-09-259-821A-1 c 37 48 9.6 4257 4 US-09-259-821A-1 c 38 47.8 9.6 12001 1 US-08-483-568A-11 c 39 47.8 9.6 12001 1 US-08-483-688-11 c 39 47.8 9.6 15079 4 US-09-385-028-1 d 47.6 9.5 1153 4 US-09-385-028-1 42 47.6 9.5 3181 4 US-09-135-021-1 43 47.6 9.5 3181 4 US-09-135-020-1 45 47.6 9.5 3181 4 US-09-135-020-1 45 47.6 9.5 3181 4 US-09-135-020-1
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US-09-103-840A-2/c
: Sequence 2, Application US/09103840A
: Patent No. 6294328
                                                                                                                                                                         Sequence 7, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3940557 CTGGTCGGCGTCGGCGCCGGCCCGGCTCCGCCGTCACCGCCTTGGCCGCCGCCCC 3940498
                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   3940437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHMAN, APPLICANT: WHITE, OWER
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 150
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                   APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GCGCACATGGGAGCCTTCAAGCTCAACCCGGGCGCGCGCACGAGCTGTCCCCGGGCCAGAGC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 GCCGCAGCGCTCGGGCCCACGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ATGCAGGACCGTGAACTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCC 162
                                                                                                                                                                                                                                                                                                                                                                                                                             223 TCGGCGTTCACGTCGCAGGGCCCGGGCGGCCTACCCCGGCTCCGGCTGCGGCTGCG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GCCAGCTTCGCGCGCCACCATCACCACTCCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                             GGTGGGGTTATCGGCGCCCGGC---CAGCACCCCCATCCCGCCTTGTCCGCCGGC 3940321
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                                                                                                                                           DeHoff, Bradley S.
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Best Local (
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NAME/KEY:
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ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                  24041 CGGCCCAGGGCGTACGCGGCGCCAGCGCGCACCTCGACGCGCTGGCCGAACGCGCCC 24100
                                                                                                                                                                                                                                                                       23801 GCTGCGACGTCACCGACCGCGCGCGCACTGGCCGCGCTCGACGAGCACGCGCCCACCG
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431 CGGGCGGCCTGCACCACGCGCACTCGGACGCGCAGGGCCAC
                                                                                                                                                                                                                                                                                                  191 CGGCCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCCCGGCG
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OPERATING SYSTEM: MS-
OPERATING ASCI(DOS) 7
OPERATING ASCI(DOS) 7
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                                                                                                                 CGGCCGCGGGCCTCGACGCGCTGGTGCTGTTCTCCTCGGTCTCCGGAGTGTGGGGCGGCG
                                                                         CGCGGCTTCCGGGGACTTCGGCGCCGGCCGGCCGGCCAGCACGGGCTGTTCGGGCCGGGCG 430
                                                                                                                                                      ACGTTGGCTCCTACTCTGGGCCGCCCTTCAACTCCACCCGGGACTTCCTGTTCCGCAGCG
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20110..31284
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46.1%;
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Pred. No. 0
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0.0071;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgett, St
APPLICANT: Kuhstoss,
APPLICANT: Rao, Nagas;
APPLICANT: Richardson
APPLICANT: Rosteck, P.
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                                                         23741 CCGACGCCCCGCACAGGCCGCCGCCGCCGACTGACCGGCCGTCTCCCTCGTCCCCTGC 23800
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SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pai
 23801 GCTGCGACGTCACCGACCGCGCCGCACTGGCCGCGCTGCTCGACGAGCACGCGCCCCACCG 23860
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NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 99
REFERENCE/DOCKET NUMBER: P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
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                             131
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                                                                                                                               Local
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OPERATING SYSTEM:
                                                                                      71 CCGCCGCGGCGGCGGCGGCTGCCGCCGAGATGCAGGACCGTGAACTGAGCCTGGCGG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                           CGGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCAAGCTCAACC 190
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1. 5945320
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LILLY CORPORATE CENTER
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ROSteck, Paul R., Jr.
VENTION: PLATENOLIDE SYNTHASE GENE
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Kuhstoss, Stuart A.
Rao, Nagaraja R.
                                                                                                                    Conservative
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350..14002
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36155..41830
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20110..31284
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31329..36071
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                                                                                                                               11.18;
46.18;
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                                                                                                                 Score 55.4; DB 2; Length 4
Pred. No. 0.0071;
0; Mismatches 216; Indels
                                                                                                                                              Length 44377;
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1252 GTCAGAGCCGCCCAGCTCGGCTACCAGCCCTCGGCCGCCTCGGGCGAGGACGCGGCCGCC 1311

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                                                                                                                        Matches
                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1910 base pair
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                                                1192 CTGACGGCCGTCGGCACCGGCCGCCGCGACGGCCGCGGCGCCCCAGGAGCCG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 CGGGCGGCCTGCACCACGCGCACTCGGACGCGCAGGGCCAC 471
178 TTCAAGCTCAACCCGGGCGCGCACGAGCTGTCCCCCGGGCCAGAGCTCGCGTTCACGTCG 237
                                                                                    118 CTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCC 177
                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 6.0.4
SOFTWARE: Microsoft Word Version 4.0b
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
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                                                                                                                        al Similarity
172; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      1910 base pairs
                                                                                                                                                                                                             DNA sequence encoding
Streptomyces lividans Protease X
SRMATION: bp 12 to 1910 comprises
SRMATION: S. lividans DNA sequence, incl
DRMATION: bp 1 to 11 represents cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lichenstein, Henri
                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                               Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                 double stranded
                                                                                                                                        10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Streptomyces Lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US92/05532
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                                                                                                                      Score 51.4; DB 5;
Pred. No. 0.044;
0; Mismatches 201;
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                                                                                                                                                                                                                                   including Protease X.
                                                                                                                                                        Length 1910;
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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Oleski, Nancy
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
1312 AACCGCGCGTTCTTCGAGGCGGTCGTCAAGTCCGTCGCCGAGAAGCGCGCCGCCCAACCCG 1371
                                                                          1252 GTCAGAGCCGCCCAGCTCGGCTACCAGCCCTCGGCCGGCTCGGGCGAGGACGCGGCCGCC 1311
                                                                                                                                                    1192 CTGACGGCCGTGCTCGGCACCGGCCCCGCGACGGCCGCGGCGCCCCAGGAGCCG 1251
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1
MOLECULE TYPE:
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LENGTH: 2261 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                178 TTCAAGCTCAACCCGGGCGCGCGCGAGCTGTCCCCGGGGCCAGAGCTCGGCGTTCACGTCG 237
                                                                                                                                                                                       118 CTGAGCCTGGCGGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCC 177
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                                     238 CAGGGCCCCGGCGTACCCCGGCTCCGCTGCGGCTGCCGCTGCGGCCGCAGCGCTCGGG 297
                                                                                                                                                                                                                              Local Similarity nes 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2261 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                Conservative
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46.1%;
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                                                                                                                                                                                                                                              Score 51.4; DB 1; Length 2261; Pred. No. 0.043;
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                              201; Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MOTIOKA, Sinji
APPLICANT: Scheirlinck, Trees
APPLICANT: Scheirlinck, Trees
APPLICANT: Komari, Tosihiko
TITLE OF INVENTION: Stamen-spec
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                           INFORMATION FOR SEQ ID NO: 7:
                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pair
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 91402590.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                    STRANDEDNESS:
                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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ORGANISM:
                                                      TOPOLOGY:
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                                                                                                        2370 base pairs
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                                                                                                                                                                612-332-9081
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Oryza sativa
                                                     linear
                                                                                                                                                                                612-332-5300
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                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-351-413-8
; Sequence 8, Application US/08351413
; Patent No. 5750867
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                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile
NUMBER OF SEQUENCES: 17
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                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/351,41
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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nes 167; Conserv
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CITY: Falls Church
STATE: Virginia
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                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                ADDRESSEE: BIRCH, STEWART, KO
FILING DATE:
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promoter"
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T42"
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initiation"
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Best Local Similarity
Matches 167; Conserv
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pairs
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ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
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STRAIN: Akihikari
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STRANDEDNESS: doub
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OTHER INFORMATION:
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CGTCTGCAACTGCGTCAAGGACGCCGCCGCCGGCTTCCCCGCCGTCGACTTCTCCCGCGC
                            CGGCGCCTACCCCGGCTCCGCTGCGGCTGCGGCCGCAGCGCTCGGGGCCCACGC
                                                            CTGCTGCGACAGCCTCGGCGTGCTCAACCGGATGGCCCCGGGCCCCGCCGACCGCGTCGC
                                                                                         CAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCC 245
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/note= "ATG
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site determined by primer extension"
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/note= "TATA Box"
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Pred. No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                    FEATURE:
                                                                                                              FEATURE:
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MEDIUM TYPE: Floppy disk
                                                                                                                            LOCATION: 1..1808
OTHER INFORMATION:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Maintenance of male-sterile
TITLE OF SPOUENCES: 17
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                                                                               LOCATION:
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                 NAME/KEY:
                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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REGISTRATION NUMBER: 30,3
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DEDNESS: double
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    Oryza sativa
Akihikari

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                                                                                                                            /label= PT42
/note= "sequence comprising anther specific
promoter PT42"
                                              /note= "TATA Box"
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RESULT 10
US-08-242-677-1/c
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Patent No. 5
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Best Local Similarity
Matches 167; Conserv
INFORMATION FOR
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APPLICANT: Wu, Foon W
TITLE OF INVENTION: C
TITLE OF INVENTION: 7
TITLE OF INVENTION: 7
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                        REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L
                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                      CITY: Houston
STATE: TX
                                                                        REGISTRATION NUMBER:
                TELEFAX:
                                                                                                                       CLASSIFICATION: 435
                                                                                                                                     FILING DATE:
                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1809
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CTGGACGCGGGTCCGCAGTTCCCGGCCATCGGGGTGGGCAGCTTCGCGCGCCACCATCAC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCAAGCT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/08242677
5677143
                                                                                                                                                                                                                                                                                                                       P.O. Box 4433
              713-789-2679
                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                              Cellular Nucleic Acid Binding Protein
and Uses Thereof in regulating Gene E
Treatment of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Richard B
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                                                                                                                                                                                                                                                                                                                                     White & Durkee
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/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "transcription initiation
site determined by primer extension"
                                                                                                                                                  US/08/242,677
                                                                     33,732
                                                          UTSD: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 0.051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
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                                                                                                                                                                                                                                                                                                                                                                                              Expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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the

SEQUENCE CHARACTERISTICS: LENGTH: 5173 base pair

pairs

TYPE: nucleic acid STRANDEDNESS: single

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; NAME/KEY:
; LOCATION:
US-08-242-677-1
                                                                                                                  FILE OF INVENTION: ANTAGONISTS

FILE REFERENCE: 28600-20210.00

CURRENT APPLICATION NUMBER: US/09/773,816

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/243,458

PRIOR FILING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 60/179,305

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1
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US-09-773-816-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09773816 Patent No. 6340774
                                                                               SEQ ID NO 1
LENGTH: 23673
                                                                                                                                                                                                                                           TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR FILE REFERENCE: ANTAGONISTS
                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
                                             ORGANISM: Human
NAME/KEY: misc_feature LOCATION: (1)...(23623)
                                 FEATURE:
                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTTCTCGGCCAGGGCGCTCAGGACCAGCTTCTCCTCTACGCGGCCGGACCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGCCAGCGCGGCC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCTTCCCGGGCC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCACGGCAGCCTCGGCGCCAGGCGCGCGCGCGAGCAGATCGCGCAGCGCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TCCAGTAGCGGCCCGTCCTCGCGGGGCCGCAAACATGGCCCGACGGCTGCTAGCACT
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Pred. No. 0.05;
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; OTHER INFORMATION: n = A,T,C
US-09-773-816-1
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US-08-592-874-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19496
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/37.
FILING DATE: 24-AN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19610
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA SEGMENTS AND METHODS TITLE OF INVENTION: POLYSACCHARIDE PRODUCTION NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 GGCGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCCCGGCGCC 252
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         STREET: 261 MAD
CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 177; Conserv
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: JULES E. GOLDBE. STREET: 261 MADISON AVENUE
                                                                                                                                            APPLICATION NUMBER:
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCCCGGCTCCGCTGCGGCTGCCGCTGCGGCCGCACGCCCCACGCCGCGCAC
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MIKOLAJCZAK, MARCIA
ARMENTROUT, RICHARD W.
ARMENTROUT, RICHARD W.
VENTION: DNA SEGMENTS AND METHODS FOR INCREASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAMAZAKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLOCK, THOMAS J.
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48.2%;
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                                                                                                                                                                   US/08/592,874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 23673;
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TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

TYPE: nucleion strandedness:

unknown

nucleic acid

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g
                                                                                                                                                           ; ORGANISM: Sphingomonas sp. S88 US-09-096-942-2
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                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 28804
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                                                                                             Query Match
Best Local Similarity
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                                                                              Matches 147;
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Production of xanthan Gum by Sphingomonas Bacteria TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris FILE REFERENCE: seq list for appl filed from pro. appl CURRENT APPLICATION NUMBER: US/09/096,942
CURRENT FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yamazaki, Motohide
APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-06-12 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pollock, Thomas J APPLICANT: Mikolajczak, Marc
                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/049,428
                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
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14456 ATCTCGATACGCAGAAGCTCGCACAGCTCCAGGGCGCGAGCGCGATACCGTCGGCACCGG 14515
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                                      182 AGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGG 241
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                                                                                Conservative
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N-terminal
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                                                                                             Pred. No. 0.061;
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                                                                              Mismatches
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                                                                                                                  Length 28804;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Pollock, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09096867 Patent No. 6030817
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APPLICANT: Thorne, Linda
APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,867
CURRENT APPLICATION NUMBER: US/09/096,867
CURRENT FILING DATE: 1998-06-11
EARLIER APPLICATION UNBER: 60/049,428
EARLIER FILING DATE: 1997-06-12
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14756 ACCGCCAG 14763
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                                                  CGGGCCTG 489
                                                                                                GGCCGGGCGGCGGCCTGCACCACGCGCACTCGGACGCGCAGGGCCACCTCCTTCTCC 481
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Sequence 5. Application US/09144085

Sequence 5. Application US/09144085

Patent No. 6280999

GENERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Betlach, Mary C.

APPLICANT: Ziermann, Rainer

TITLE OF INVENTION: SORARGIUM POLYKETIDE SYNTHASES AND ENCODING DNA

TITLE OF INVENTION: STARRGIUM POLYKETIDE SYNTHASES AND ENCODING DNA

TITLE OF INVENTION: SUMBER: US/09/144,085

CURRENT APPLICATION NUMBER: US/09/144,085

CURRENT APPLICATION NUMBER: 09/010,809

EARLLER APPLICATION NUMBER: 09/010,809

EARLLER FILING DATE: 1998-01-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 423

TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence: DNA fragment

OTHER INFORMATION: corresponding to a KS domain of Sorangium

OTHER INFORMATION: cellosporum SMP44 gene

US-09-144-085-5
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Best Local S
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Maximum DB seq length: 2000000000
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URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AG080435 Pan trog1
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AG060267 Pan trog1
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                                                                                                      CACGCCGCACACGTTGGCTCCTATTCGGNGCCTACCTTTAATCCACCCGG 642
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Conservative

0; Mismatches Score 224.2; DB 9 Pred. No. 1.7e-23;

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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) This clone is also available
through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov).
IMAGE ID-1768598
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UI-R-C3-sf-a-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-sf-a-03-0-UI 3', mRNA sequence.
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Program for Rat Gene Discovery and Mapping
University of Iowa
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/Nev_stayer adult
//lab_bost="Delta" full (Life Technologies)"
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CATCACCACTCCGCCGCGGCGGCGGCGGCGGCTGCCGGAGATGCAGGACCGTGAACTG 120
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1 (bases 1 to 503)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP from Gibco High quality sequence stop: 4
                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1692 Std Error: 0.00
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 488.
Location/Qualifiers
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                                                                                                                                        /clone="IMAGE:2013410"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                         T 3']; double-stranded CNNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento
                                         Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE097311 496 bp mRNA
UI-R-BO1-apv-h-02-0-UI.sl UI-R-BO1 Rattus
UI-R-BO1-apv-h-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE097311.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE097311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 496)
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                    // Clone_lib="UI-R-BO1"
/clone_lib="UI-R-BO1"
/clone_lib="UI-R-BO1"
/clone_lib="UI-R-BO1"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="BH10B (Life Technologies)
/lab_host="bH10B (Life Technol
                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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97.3%;
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in (Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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Sciurognathi; Muridae;
  Lennon and
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BASE COUNT
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257879 MARC
BF441548
BF441548.1
                                                                                                                                                                                                      Seq
                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
 Similarity
                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG Plate: 86 row: G column: 7
                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                           PCR PRimers
                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0186, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ummalia; Eutheria; Cetartiodactyla; Suina; Suidae; (bases 1 to 487)
                                                                                                                                                                                                     primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MARC
                                                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

192 c 152 g 74 t
                                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                       Location/Qualifiers
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TAG_SEQ=None fou
179 c 140
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 22.6%;
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Sus scrofa cDNA 5', mR
Score 113.2; DB 10; Pred. No. 1.4e-07;
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Pred. No. 7.3e-14;
D; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                    tissue normalized
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         Length 487;
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Laegreid, W.W.
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                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other_ESTs: mg08e03.x1
Contact: Marra M/WashU-NCI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i This read is a RESEQUENCE of a previously sequenced This read has been verified (found to hit its origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1894008 441 bp mRNA linear EST 15-MAR mg08e03.yl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:423196 5' similar to gb:D32167 Mouse mRNA for zic
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                      MGI:257748
                                                                                                                                                                                                                                     correct orientation)
                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
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Location/Qualifiers
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                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:423196"
                                                   /clone_lib="Soares mouse
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc
                                     /sex="unknown"
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Rodentia;
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mg08e03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:423196 5' similar to gb:D32167 Mouse mRNA for zic profess (Mousee m NA)
                                                             WashIngton University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 455)
                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                              Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
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mouseest@watson.wustl.edu
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Best Local :
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               fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Art
                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCACCATCACCACCCGGCCACGTCGGCTCCTACTCCAGCGCTGCTTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5":14.5dpc total fetus"
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/clone="IMAGE:423196"
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera;
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survey sequence T7 end of BAC #
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0.0003;
ches 116; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 CCCGGGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCCCGG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPGI-98 and was constructed by partial EcoRI dispestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the Ibrary and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be constructed to the DGP's found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                    GGGCGCGGCCGGCCTGCACC 445
                                                                                                                                                                                                                                                                  GSASGCGCGCGMGCRAGSGKMGSAGSSGRCGGACSGSGGSBSSSKRKGGASGCASCSSAY 516
                                                                                                                                                                                                                                                                                                                                                                     GCCCSCGCGCGCGCGCCGCCGGCAGCSCASGCSSGMAGYAGSGASRSVYSGGSSSS
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CNS00720 932 bp DNA linear GSS 03-JUN Drosophila melanogaster genome survey sequence T7 end of BAC #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14M09"
/note="end : T7"
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                          243
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                                                                                                                                                                                                                                                                                                                                                                                               183 GCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 CCTGGCGGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCAA 182
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                                                                                                                                                                                       CGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAACTCCACCCGGGACTTCCTGTT 362
                                                                                                                                                                                                                                        CSCSGGCSSCGCSCCCSCCCCSCCCCSSCGCSSSSGCGGSGGCSSGCGSCGCGSCGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    fly), gen
AL066742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 932)
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/db_xref="taxon:7227"
/clone_llb="RPCI-98"
/clone="BACR14809"
/note="end: T7"
1 202 c 241 g 91 t 243
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Best Local Similarity
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                                                                                                                                                                                                                                                              865
                                                                                                                                                                                                                                                                                                                                              925 CSBSCSCSCSSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSS
                                                                                                                                                                                                                                                                                                                                                                                        83 CGGCGGCGGCTGCCGCCGAGATGCAGGACCGTGAACTGAGCCTGGCGGCGGCGCAGAACG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                   GCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCAAGCTCAACCCGGGCGCGCACG
                                         ACTCTGGGCCGCCCTTCAACTCCACCCGGGACTTCCTGTTCCGCAGCGCGCGGCTTCCGG 382
                                                                                                                           CCGCTGCGGCTGCCGCTGCGCCCACGCCCCACGCCGCGCACGTTGGCTCCT 322
                                                                                                                                                                       AGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCCCCGGCGTACCCCGGCT
                                                                                                                                                                                                                                                            SSGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGS
  ASAGSYVSSASSSSSSSSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSSSSSSSSSSCSCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome sur BACR19D16 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey so AL053013 AL053013.1 GI:4934461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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1 (bases 1 to 925)
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/clone="BACR19D16"
/note="end : TET3"
a 61 c 61 g
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.48;
14.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82.2; DB 12; Pred. No. 0.0037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 925;
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RESULT 11
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70 TCCGCCGCGGCGGCGGCGGCGGCCGCCGAGATGCAGGACCGTGAACTGAGCCTGGCG 129
                                                                                                                                                                                                                                                                                       10 GACGCGGGTCCGCAGTTCCCGGCCATCGGGGTGGGCAGCTTCGCGCGCCACCATCACCAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and malanogaster BAC library end of Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                        GCGGCGCAGAACGGCTTCGTTGATTCCGCCGCGCGCACATGGGAGCCTTCAAGCTCAAC 189
                                                                                                                                                          SCSSYCCSSSBSSSKCSSTSBSCSCCCSSKSVCGTSCSSSSSSCSSSSSTSSSSTSSSTS
                                                                                                                                                                                                                                               SMCGKKCGSTTBGSTTTTTTSSGSGYGKGCSSGSGBSCSCCSSCSCSCSCSCCBCCCCC
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1 (bases 1 to 925)
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
/clone="BACR19D16"
/note="end: TET3"
1 61 c 61 g 172 t 511
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                                                                                                                                                                                                                                                                                                                                                              16.1%; Score 80.4; DB 1 16.0%; Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                           195;
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survey sequence TET3 end of BAC #
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                                                                                                                                                                                                                                                                                                                                              133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 others
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251
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                                                                                                                                                      Local Similarity
                                                                                     GACGCGGGTCCGCAGTTCCCCGGCCATCGGGGTGGGCAGCTTCGCCGCGCCACCACCACCAC 69
                               TCCGCCGCGGCGGCGGCGGCGGCCGCCGAGATGCAGGACCGTGAACTGAGCCTGGCG
                                                                 GSSGVSSNSSSASKSSSSGSVSSGSGSGSGSVSG 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes DNA, clone: PTB-051K02.R, AG063084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 821)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS (genome survey sequence). troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-051K02.R.
                                                                                                                                        Conservative
                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                             Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tracking errors.
                                                                                                                                                                                                                 /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
404 c 352 g 8 t 38 others
                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                        /clone="PTB-051K02.R"
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                             1. .821
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                      15.7%;
                                                                                                                                    Score 78.4; DB
Pred. No. 0.013;
0; Mismatches 2
                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor, T.D., Yada, T.,
                                                                                                                                      218;
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Query Match
Best Local Similarity
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AG081191. GI:16632993
GSS; GSS (genome survey sequence).
Pan troglodytes male lymnhohlant nor control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC endwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,\underline{Y}., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC end sequences
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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troglodytes male lymphoblast DNA, clone_lib:PTB
Library clone:PTB-077J08.F.
troglodytes
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R.Site 2
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                                                                                                            /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
382 c 553 g 32 t 3
                                                                                                                                                                                                                                           /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-077J08.F"
                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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   15.4%;
47.2%;
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genomic
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                                                                                                     AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library or and the conformation of the library and the conformation of the library and the conformation of the library and both to Order individual BCORI lance the entire library or
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ALORGYA2
                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL066742.1 GI:4945205
                                                     and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
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                               Location/Qualifiers
/organism="Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilidae; Drosophila.
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12 CGCGGGTCCGCAGTTCCCGGCCATCGGGGTGGGCAGCTTCGCGCGCCACCATCACCACTC 71
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         Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ence are derived from the chimpanzee BAC library PTB This BAC ence are generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-018L17.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGU41117 976 bp DNA Pan troglodytes DNA, clone: PTB-018L17.F,
                                                                                                                                                                                                                                                                                                 Fujiyama, A., Hattori, M.,
Totoki, Y., Watanabe, H. a)
                                                                                                                                                                                    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T. Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini;
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/clone_lib="RPCI-98"
/clone="BACR14809"
/note="end: T7"
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nd Sakaki, Y
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Search completed: October 10, 2002, 20:27:22 Job time: 701.733 secs
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                                                  ccccccccccccc 353
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LIBRARY
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R.Site 2
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1.976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/287 c 495 g 51 t 84 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-018L17.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                        Score
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105.2
68.2
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3: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:*
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AAS61863
AAA62683
AB199239
AAX53491
AAX53491
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        AAL36353
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Human Zicl gene.
Mouse ischaemic co
Human adenosine Al
Human adenosine Al
Eucalyptus grandis
Eucalyptus grandis
Human musculoskele
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Lung small cell ca
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50.2	50.2	50.2	50.4	50.4	50.4	50.4	50.4	50.4	50.6	50.8	51	51	51.2	51.4	51.8	51.8	52.4	52.4	52.4	53	53.4	54.6	54.6	55	55.4	55.4	55.4	55.6	56	56.4	56.4	56.4	56.6	56.6	
10.0	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.3	10.4	10.4	10.5	10.5	10.5	10.6	10.7	10.9	10.9	11.0	11.1	11.1	11.1	11.1	11.2	11.3	11.3	11.3	11.3	11.3	
4563	1065	1053	109519	28804	28804	28804	28804	2561	1382	3303	5173	2370	2061	1910	4566	3717	3372	1902	1791	2561	58857	2049	1698	1811	44377	44377	37856	3431	4403765	154746	154746	3957	125401	0	
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AAA3/093 AAS46080	AAH78255	AAH44045	AAS08693	AAV81474	AAV99812	AAT92474	AAT37329	AAH26500	AAQ64890	AAS54127	AAT89783	AAQ53880	AAF86409	AAQ34549	AAC74710	AAA64660	AAH48729	AAD22003	AAV82460	AAH26500	AAA58471	AAS76210	AAS84408	AAS91924	AAT80414	AAT78508		Þ		AAD25519					
Human PRO148/ (UND Human DNA encoding	Nucleotide sequenc	Streptomyces sp. C	Micromonospora DNA	ragn	Sphingomonas S88 s	Sphingomonas genus	Sphingan biosynthe	Rabbit low density	Human derived adre	Pseudomonas aerugi	Human Immunodefici	Sequence comprisin	4-amino-4-deoxycho	Streptomyces livid	Human ORFX ORF265	DNA encoding centr	Human HCN2 cDNA.	Human transporters	Triticum sp. cyste	Rabbit low density	Nucleotide sequenc	DNA encoding novel	DNA encoding novel	DNA encoding novel	Platenolide syntha	Platenolide syntha	S. cellulosum DNA	Human EST-derived	Mycobacterium tube	Human herpesvirus	Human herpesvirus	HSV-2 immediate ea	Streptomyces nours	Streptomyces nours	

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ALIGNMENTS

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RESULT 1
AAD11112
ID AAD1
  PAARX TRANSPORT
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                                                                                                                                                                                                                                                                          Human small cell lung cancer associated gene, ZIC2
                                                                                                                                                                                                                                                                                               24-SEP-2001
                                                                                                                                                                                                                                                                                                                        AAD11112;
                                                                                                                                                                                                                                                                                                                                               AAD11112 standard; DNA; 1602 BP
                                                                                                                    WO200153349-A2.
(LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                              21-JAN-2000; 2000US-0489101.
                                                                   19-JAN-2001; 2001WO-US02015.
                                                                                                                                                                                                    Homo sapiens
                                                                                            26-JUL-2001.
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                                                                                                                                                                 Location/Qualifiers
1..1602
                                                                                                                                          /*tag= a
/product= "Human ZIC2 protein"
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RESULT 2
AAS61863
ID AAS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAPP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecula. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-3 encoding human ZIC2 protein.
                 AAS61863 standard; cDNA; 1602 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 57; Page 90-91; 152pp; English.
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                                                                                                                                CCGGGCCTGCCAGAGCAGCA 500
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Pred. No. 3e-75;
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                                                                                                                                                                                                                                                                 The invention relates to novel isolated lung small cell cancer antigen copynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen presenting cells expressing (II) is useful for stimulating and/or expanding T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating and/or expansion of the cells. A composition comprising (I) is useful for stimulating and/or expansion of the cells in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An AASG1460-AASG1874 represent novel human lung small cell appatient. AASG1460-AASG1874 represent novel human lung small cell
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Best Local
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21-JUN-2000;
01-SEP-2000;
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14-SEP-2000;
19-DEC-2000;
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                                                                                                                                                                                                                                                              Sequence 1602 BP; 275 A; 578 C; 536 G; 213 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 274; 295pp; English.
                                                                                                                                                                                                                                                                                               cancer antigen coding sequences of the invention.
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                               121 AGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTC
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AGCCTGGCGGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTC
                                                                                                                               2002-010896/01.
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2000US-232565P.
2000US-257037P.
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                                                                      Converting epidermal cells into neurons, useful for isolating nerve growth factors or for gene therapy, comprises dedifferentiating cell and transfecting with vectors with a cDNA coding neurogenic transcription factors
The present sequence is the human Zicl gene from Genbank. It was used to provide sequence information for the cloning of Zicl cDNA, which was used to transfect cultured epidermal cells. This was
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Zicl gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002
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                                                                                                                                                                                                                                                                                             vasospastic
                                                                                                                                                                                                                                                                                                                                                 Mouse ischaemic condition related cDNA sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABI99239 standard; cDNA; 2947 BP
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                              WPI; 2002-034733/04
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                                                                                                                               18-MAY-2000; 2000JP-0145977.
                                                                                                                                                               18-MAY-2001;
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                                                                                                                                                                                                                                                                                                                 Mouse; ischaemia;
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                                                               Asai S,
                                                                                                                                                                                                                                                                                                                 compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701 A; 898 C; 840 G; 699 T; 0 other;
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Best Local
                                Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence.
                                                                                                                                                                                                                                                   Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                          AAX53491 standard; DNA; 114955 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2947 BP; 659 A; 818 C; 787 G; 683 T; 0 other;
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               hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 CGCCGCGCACATGGGAGCCTTCAAGCTCAACCCGGGCGCACGAGCTGTCCCCGGGCCA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGGACGCGCAGGCCACCTCCTCTTCCCGGGCCTGCCAGAGCAG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGCGCCCAGCAGTCTTCGCTGCTTCGGCCGGCGGCTTTGGGGGGCCCACACGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 191-194; 2690pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 37; 120pp;
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                                                                                                                                                                                                                                            195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                       135 GCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCAAGCTCAACCCCGGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGGTCCGCAGTTCCCGGCCATCGGGGTGGGCAGCTTCGCGCGCCACCATCACCACCTCCGC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
TGGCTCCTACTCTGGGCCGCCCTTCAACTCCACC-CGGGACTTCCTGTTCCGCAGCGCGC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGSNNNDNNGCCBGGGCGCCGCCGGCCGGCCGGCCGSNNNDNNCCBGGGCGCCGCCGCCGGC 105124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BGGCCBGGGCGCCGCCGGCCGGGCCGSNNNDNNGGCCBGGCGCGCCGCCGGCCGGCCGGCC
                                                           CCCCGGCTCCGCTGCGGCTGCCGCTGCGGCCCAGCGCTCGGGCCCCACGCGCACGT 314
                                                                                                                                                                                   CCGGGCCGSNNNDNNGGGCGCGCCGCCGGCCGGCCGSNNNDNNGGCGCGCCGCCGCCGCCG
                                                                                                                                                                                                                                            CGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGGGCCCCGGCGCCTA 254
                                                                                                                                                                                                                                                                                                           CGGGCCGSNNNDNNCBGGGCGCGCCGGCCGGCCGGCCGSNNNDNNBGGGCGCGCCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGGCGGCGGCGGCTGCCGCCAGATGCAGGACCGTGAACTGAGCCTGGCGGCGGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0093972
97US-0059160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.6%; Score 68.2; DB 20; 36.8%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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DЪ

Db 105365 GGCCGGGCCGSNNNDNNCCGCCGGCCGGGCCGGNNNDNNCGCCGGCCGGGCCGSNNNDNN 105424

GGCTTCCGGGGACTTCGGCGCCGGCCGGCGGCAGCACGGGCTGTTCGGGCCGGGCGCGG 433

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The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and con-coding regions of RNAs corresponding to target genes, gene coding and concoding regions, intron-exon borders, the committation codons, genomic flanking regions, intron-exon borders, the committee of the juxta-section between coding and non-coding coding and intron-exon borders, the committee of the juxta-section between coding and non-coding coding and intron-exon borders. The antisense oligonucleotides conditions or mixtures. The antisense oligonucleotides coding and conditions. Typical diseases and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration, allergic rhinitis, acute asthma, allergies, asthma, impeded confilammation, including lung diseases, pulmonary vasoconstriction, conditions including lung diseases, pulmonary vasoconstriction, conditions, respiration, pulmonary vasoconstriction, pulmonary vasoconstriction, methysema, chronic constructive pulmonary disease (COPD), and cancer, bung cancer, lung cancer, nepatocellular carcinoma, kidney cancer, melanoma, correspiration of the helpotocellular carcinoma, kidney cancer, melanoma, correspiration of the helpotocellular carcinoma, without metastasize cancer, becast and recersive cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; paln; cystic fibrosis; pulmonary distress syndrome; paln; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; brast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenosine A1 receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX53491 standard; DNA; 114955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides used in treatment of, e.g. pulmonary
have metastasized to the lungs, including breast and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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97US-0059160
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 Db 105203 GCCCNNHNNNSCGGCCCGGCCGGCGCGCCCVNNHNNNSCGGCCCGGCCGGCGGCGCG 105144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 105563 GCCGGGCGGGCAAGCCGGGCCGGGGCCGAGCCAGGGGCCCNNHNNNSVGCGGAGCCVG 105504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 105143 CCCVGNNHNNNSCGGCCCGGCC 105122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                        Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; basic; box binding factor; basic helix-loop-helix zipper; homeofic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC56076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC56076 standard; DNA; 438 BP
WPI; 2000-579369/54
                              Wood M,
                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis transcription factor DNA sequence #207.
                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001
                                                                                                             11-MAR-1999;
18-AUG-1999;
                                                                                                                                                            09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                              14-SEP-2000
                                                                                                                                                                                                                            WO200053724-A2.
                                                                                                                                                                                                                                                           Eucalyptus grandis.
                                                                (FLET-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 ACATGGGAGCC--TTCAAGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTC
                                                                             (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 GGGCCACCTCCTCTTCCCGGGC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 CACCCGGGACTTCCTGTTCCGCAGCGCGCGCGCCTTCCGGGGACTTCGGCGCGGCGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 GCTTCGCGCGCCACCATCACCACTCCGCCGCGGCGGCGGCGGCGGCTGCCGAGATGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOCS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCAGCGCTCGGGCCCACGCCGCGCACGTTGGCCTCCTACTCTGGGCCGCCCTTCAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGACCGTGAACTGAGCCTGGCGGCGCGCGCAGAACGGCTTCGTTGATTCCGGCCGCCGCGC
                                                              FLETCHER CHALLENGE FORESTS LTD.
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                              McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                             99US-0266513.
99US-0149485.
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                                  Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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                                  Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247;
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RESULT 8
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AC AAC5
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Best Local
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   11-MAR-1999;
                                                                  09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                                    WO200053724-A2
                                                                                                                                                                                                                                                                                       Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                         Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogamy; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain; zipper; LIM domain; AP2; EREBS; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC56714 standard; DNA; 438 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis transcription factor DNA sequence #585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 438 BP; 66 A; 196 C; 111 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 100; 747pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGGCCACAAGGCCAGCCACCGCAAGCACGCCTCCTCCGCCGCCGCCGCCGCCGCCGGGGG 189
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                                                                                                                                                                                                                                                                                                                                                                 Cys2His2;
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                                                                                                                                                                                                                                                                                                                                                                 box element; MYB; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 438;
0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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RESULT 9
AAL36157
ID AAL3
XX AAL3
AC AAL3
XX O8-J
Y
XY O8-J
XY O8-J
XY O8-J
XY O8-J
XY OUIn
KW Card
KW Oard
KW Oard
KW Oneur
KW musc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; undigrary; anticonvulsant; antibacterial; antifungal; antiparasitic; undigrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                     08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-halix zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
                                       cardiant; gene therapy; cancer; immune disorder; cardiova neurological disease; infection; human; secreted protein;
                                                                                                                                                                        Human musculoskeletal system related polynucleotide SEQ ID NO 2718
                                                                                                                                                                                                                                                               AAL36353;
                                                                                                                                                                                                                                                                                                       AAL36353 standard; DNA; 9968 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 438 BP; 65 A; 195 C; 111 G; 65 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel plant transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 498; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood M, McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                   370 CGCCGCCGCCCCCGCCCAGCGGGGTGAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 TGCGGCCGCAGCGCTCGGGCCCCACGCGCGCGCACGT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACAAGCGGTGCCACTACGAGGCCCCCCCCCCCCATCCCGCCCTCCTTCTCCGCCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTCGGCGTTCACGTCGCAGGGCCCCGGCCTACCCCGGCTCCGCCTGCCGCTGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGGTCCACGAGTGCTCGATCTGCCACAAGAGCTTCCCCACCGGCCAGGCGCTCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACGACCAGCCGACCTCGAGCACCTCCGCGGCGACCTCCTCCGGCGTCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGATGCAGGACCGTGAACTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGGCAGCTTCGCGCGCCACCATCACCACTCCGCCGCGGCGGCGGCGGCGGCGGCGCCGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9905-0149485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenk MA, Glenn

    Mismatches

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Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors
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0;

249

musculoskeletal system; ds.

26-SEP-2000	PR 21-SEP-2000; 2000US-0234474. PR 25-SEP-2000; 2000US-0234997.	14-SEP-2000	14-SEP-2000	14-SEP-2000	14-SEP-2000	14-SEP-2000	12-SEP-2000	08-SEP-2000	08-85-800	08-SEP-2000	08-SEP-2000	08-SEP-2000	08-SEP-2000	06-SEP-2000;	05-SEP-2000;	05-SEP-2000	01-SEP-2000	01-SEP-2000;	01-SEP-2000;	30-AUG-2000;	.0002-2000	22-AUG-2000;	22-AUG-2000;	18-AUG-2000;	14 - AUG - 2000;	14 - AUG - 2000;	14-AUG-2000;	14 - AUG - 2000;	14-AUG-2000;	14-AUG-2000;	14 - AUG - 2000;	14 - AUG - 2000;	14 - AUG - 2000;	26-JUL-2000;	14 -JUL - 2000;	11-JUL-2000;	11-JUL-2000;	07-JUL-2000;	30-JUN-2000;	28 - JUN - 2000;	19-MAY-2000;	18-APR-2000;	17-MAR-2000;	02-MAR-2000;	24-FEB-2000;	31-JAN-2000;		AX PF 17-JAN-2001: 2001WO-US01338.	PD 02-AUG-2001.	YX MOZOO153307-K1.	20000155267	OS Homo sapiens.	
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PA	PR	PR ?	o p	א א א	PR	א ק א ק	PR	PR	בי גע גע	PR	PR	PR	בי ג	PR	РR	PR.	ב ל ל	PR	PR	PR	DR 7	2 P. C.	PR	PR	אק אק	PR	PR	P R	PR	PR	P X	PR	PR	PR	PR PR	PR	א ^י ם אים	PR	PR	קי געק	PR R	PR	קים אים	PR	PR	N. C.	PR	לי א	PR	PR	PR	PR	
(HUMA-) HUMAN	11-DEC-2000; 05-JAN-2001;			DEC	DEC		E	BEC			VON-	VON-	17-NOV-2000	VON-	VON-	NOV-	17-NOV-2000	VON-	17-NOV-2000	-NOV		17-NOV-2000	17-NOV-2000;	08-NOV-2000;	08-NOV-2000	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	08-NOV-2000;	01-NOV-2000;	20-OCT-2000;	20-OCT-2000;	20-OCT-2000;	20-0CT-2000;	20-OCT-2000;	20-OCT-2000;	13-0CT-2000;	02-OCT-2000;	02-OCT-2000;	02-0CT-2000;	02-OCT-2000;	29-SEP-2000;	29-SEP-2000;	29-SEP-2000;	27-SEP-2000;	27-SEP-2000;	
AN GENOME SCI INC.	; 2000US-0254097. ; 2001US-0259678.	20000	20000	20000	20000	20000	20000	20000	20000	20000	20000	20000	20000	20000	2000u	20000	20000	20000	2000U	20000	20000	20000	20000	20000	20000	20000	2000U	20000	20000	20000	20000	20000	2000U	20000	20000	2000U	20000	20000	2000U	20000	20000	20000	20000	20000	20000	20000	2000u	20000	20000	20000	20000	20000	

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parasitic infections.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9968 BP; 2324 A; 2302 C; 2695 G; 2647 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 2718; 781pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                      GCCGCCCGCCTGCGCCCGGGCCGCCGCCGC
                                                                                                      G-GGCCACCTCCTTCCCGGGCCTGCCAGAGC 496
                                                                                                                                          GCAGCACGGGCTGTTCGGGGCCGGGCGGGCGGCCTGCACCACGCGCACTCGGACGCGCA 464
                                                                                                                                                                                                         CACCCGGGACTTCCTGTTCCGCAGCGCGCGGCGTTCCCGGGGACTTCGGCGCCGGGCGGCGG
                                                                                                                                                                                                                                                                            CCGGGCCCTCGCTCCCGCCCGCCCGACGTCTTCTCCGCCGCGCCCCGCCTTAG 185
                                                                                                                                                                                                                                                                                                                                                                                                               GCAGGACCGTGAACTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTTCGCGCGCCACCATCACCACTCCGCCGCGGCGGCGGCGGCGGCGGCGCGAGAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-451937/48.
                                                                                                                                                                                                                                                                                                            CGCAGCGCTCGGGCCCCACGCCGCCACGTTCGCTCCTACTCTGGGCCGCCCTTCAACTC
                                                                                                                                                                                                                                                                                                                                              GCCGTCGGGTCCAGCCGCAGCCGCAGCCGCCCCCCCCTCCTTGGCGGCGCCGTCGGC
                                                                                                                                                                                                                                                                                                                                                                              GGCGTTCACGTCGCAGGGCCCCGGCCTACCCCGGCTCCGCTGCGGCTGCCGCTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACATGGGAGCCTTCAAGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%;
46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 2
Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 9968;
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                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                               284
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   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster; antifungal; antibiotic; nysl; ds.
 (ALPH-)
                                 (UYNO-)
                                                                                                    08-FEB-2000;
10-APR-2000;
                                                                                                                                                         08-FEB-2001;
                                                                                                                                                                                        16-AUG-2001.
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                                                                                                                                                                                                                          WO200159126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD17184 standard; DNA; 65140
                                                                                     14-APR-2000;
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UNIV NORGES TEKNISK NATURVITENSKAPELIGE
SINTEF STIFTELSEN IND TEK FORSK.
ALPHARMA AS.
SINVENT AS.
                                                                                                    2000GB-0002840.
2000GB-0008786.
                                                                                                                                                         2001WO-GB00509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noursei nysl DNA of nystatin PKS gene cluster
                                                                                     2000GB-0009387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                           63765..64961
/*tag= m
                                                                                                                                                                                                                                                                                                                                                     /product= "NysR5 protein"
/note= "CDS does not include
complement (62551..63615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers complement (1..1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/product= "NysR1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1056..2576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NysD2 partial protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                           /product= "ORF2 protein"
                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "NysR4 (short) protein"
/note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "NysR2 protein"
/note= "CDS does not incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "NysC
50260..51015
                                                                                                                                                                                                                                                          /product= "ORF1 protein"
                                                                                                                                                                                                                                                                                                            /note= "CDS does not include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "NysR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "NysE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product= "NysB protein"
6550..49840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/product= "NysA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "NysD1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06..6906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..16530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..61047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..57190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..54305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   include
                                                                                                                                                                                                                                                                                                            start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     start codon"
                                                                                                                                                                                                                                                                                                                                                                              start codon"
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RESULT 10 AAD17184

밁 QΥ Вþ 20 В δÃ Вр δõ 밁 δÃ 밁 Ωy В δõ 밁 δÃ

64

465 124 184 345 244 285 304 364 165 424 105 484

45

(DZIE/)

SEKU/)

(BRAU/)

(STRO/)

AAE10131,

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18987 TGCTGTCCGCCATGGCCCAGGAATCCCTGCCGGACGGCGCCGCCGCCGCCGCCGCTGCTGC 19046
                                                                                                         19467 TGGTGCTGCCCGAGC 19481
                                                                                                                                                                                                                                                                                                                                              19227 TCACCGCCGGGGACTGGGCGCCGCCGACCACCCGTCGGCGCGCCACCGTCGAACTCG
                                                                                                                                                                                                                                                                                                                                                                                                        19047 GCAAGGACCGCCCGAGGAGCTCTCCGCCGTCACCGGCCTGGCCCGCGCCCACGTCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zotchev SB, Senue: TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is a Streptomyces noursei nys1 DNA of nystatin PKS gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 116-151; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals -
                                AAD17186 standard; DNA; 125401 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGGAGCCTTCA 181
                                                                                                                                                                                                                                                                                                                 302 ACGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAACTCCACCCGGGACTTCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TGCTCCTGGACGCGGGTCCGCAGTTCCCGGCCATCGGGGTGGGCAGCTTCGCGCGCCCACC 61
                                                                                                                                                                                              GGCCGGGCGGCGGCCTGCACCACGCGCACTCGGACGCGCAGGGGCCACCTCCTTCC
                                                                                                                                                                                                                                                       TCCGCAGCGCGCGCTTCCGGGGACTTCGGCGCCGGGCGGCGGGCAGCACGGGCTGTTCG
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                                                                                                                                      CGGGCCTGCCAGAGC
                                                                                                                                                                  TCCGCGCCGGCGACGACGGCCGGCTGCGACCGTCGAGGAACTGACCCTGGCCGCCCCCC
                                                                                                                                                                                                                           CCGACCACGGGGTCCAGGGCCCGGGCCTGCCGGCCACCGCCTTCGTCGAACTGGCCG
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ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE10125, AAE10126, AAE10127, AZ
1, AAE10132, AAE10133, AAE10134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STROM A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fjaervik E, Brautaset T,
letta H, Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 274; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56.6; DB Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE10128, AAE10129, AAE10130,
4, AAE10135, AAE10136, AAE101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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    08-FEB-2000;
10-APR-2000;
14-APR-2000;
The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme \,
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(SZIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200159126-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyketide synthase; antifungal; antibiot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces noursei nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001.
                                                                                                                                    WPI; 2001-557614/62
P-PSDB; AAE10143, A/
                                                                                                                       AAE10149,
                                                                                                                                                                                                Zotchev SB,
                                                                                                                                                                                                                                                           (ZOTC/)
(SEKU/)
(FJAE/)
                                                                                                                                                                                                                             (STRO/)
                                                                           nystatin polyketide synthase polynucleotides ful as antibiotics and antifungals -
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                                                                                                                                                                                                                                                       ) DZIEGLEWSKA H.
) ZOTCHEV S B.
) SEKUROVA O N.
) FJAERVIK E.
                                                                                                                                                                                                                             STROM A R.
                                                                                                                                                                                                                                                                                                                   ALPHARMA AS.
SINVENT AS.
                                                                                                                                                                                                                                                                                                                                                             UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
                                                                                                                                                                                                                                          BRAUTASET T.
                                               Page 188-254; 266pp; English
                                                                                                                         AAE10150
                                                                                                                                                                               Ellingsen TE,
                                                                                                                                                                                                                                                                                                                                                                                         ; 2000GB-0002840.
; 2000GB-0008786.
; 2000GB-0009387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-GB00509
                                                                                                                                                                                                 Sekurova
                                                                                                                                                                                                                                                                                                                                                STIFTELSEN
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/product= "NysI complete protein"
34792..51099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "CDS does not include start codon"
complement (59045..60241)
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/product= "NysK protein"
57503.58687
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51155..57355
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/product= "NysD2 complete protein"
120628..121308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (60238..61296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "NysL protein" complement (58786..58980)
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/note= "CDS does not inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "NysM protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "NysR4 (long) protein"
                                                                                                                                    AAE10144, AAE10145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                ON,
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                                                                                                                                                                                 Sletta H,
                                                                                                                                                                                                                                                                                                                                                  IND TEK FORSK.
                                                                                                                                                                                  Fjaervik E, Braut
letta H, Gulliksen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not
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                                                                                                                                        AAE10146,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79248 TGCTGTCCGCCATGGCCCAGGAATCCCTGCCGGACGGCGCCGCCGCCGCCGCTGCTGC 79307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79728 TGGTGCTGCCCGAGC 79742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79668 TCCGCGCCGGCGACGAGGCCGGCTGCGACCGCGTCGAGGAACTGACCCTGGCCGCCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursel nystatin PKS gene cluster DNA.
   Pala P,
                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                 14-DEC-1993;
                                                                                                 13-DEC-1994;
                                                                                                                                                                                                  Herpes simplex virus type 2.
                                                                                                                                                                                                                                 Herpes-simplex-virus type 2; vaccine; infection; ds.
                                                                                                                                                                                                                                                                                 HSV-2 immediate early protein ICP4 DNA sequence.
                                                                                                                                                                                                                                                                                                                   31-JAN-2001
                                                                                                                                                                                                                                                                                                                                                   AAA09686;
                                                                                                                                                                                                                                                                                                                                                                                  AAA09686 standard;
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                                                                                                                                  22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 CGGGCCTGCCAGAGC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 GGCCGGGCGGGCGGCCTGCACCACGCGCACTCGGACGCGCACGGCCACCTCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGCCAGAGCTCGGCGTTCACGTCGCAGG
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21; Conservative
Gheysen DR,
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                 93GB-0025496.
                                                                                                 94WO-EP04138
                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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Slaoui MM,
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                                                                                                                                                                                                                                                HSV-2; infected cell protein 4;
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Pred. No. 0.11;
 Koutsoukos MC;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      2427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 16; 28pp; English.
                                                                                                                                                    AAD25519;
                                                                                                                                                                                                                                                                            2547 GCCCGCCGAGGGCC
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                                                                                                                                                                                       AAD25519 standard; DNA; 154746 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding ICP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  severity and duration of episodes. The present sequence represents HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immediate early herpes-simplex-virus type 2 (HSV-2) ICP4 protein is used in vaccines for therapeutically or prophylactically treating H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 TGAACTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGG 173
                                                                                                                                                                                                                                                                                                           474 CCTCTTCCCGGGCC 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCTGCGCGGGGACCTGCGCGTGGCCGGCGGCAGCCGAGCCGCCGTGGCCGTGCG 2186
                                                                                                                                                                                                                                                                                                                                                GCCCCCCGCCCGACGCCGCCGCCGCCGCGCGCCGCCGCGCGCGCGCTGACCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGCCCCACGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAACTCCACCCGGGA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCTCCGCCGCCGCCGCCGCCGCGGACCTGCTTCCAGAACCAGAGCCTGCGCCCCCT 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCTTCAAGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGGCCAGAGCTCGGCGTTCAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGTGAGCCTGGTCGCCGGGGCCCTGGGCCCCGGCGCTGCCGGAGCCCGCGCCTGCT 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCCACCATCACCACTCCGCCGCGGCGGCGGCGGCGGCTGCCGAGATGCAGGACCG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-024142/03.
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Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide; antibacterial; fungicide; protozoacide; antiheumatic; antiinflammatory antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosii

immune response; vasotropic; vaccine; gene therapy; autoimmune disease;

Human herpesvirus 2 complete DNA genome.

26-MAR-2002

(first entry)

vasculitis; ds

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for oral delivery of vaccines, comprises expression containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a composition comprising an expression to an aggregated protein-polycationic polymer conjugate.
CTTCCTGTTCCGCAGCGCGCGCTTCCCGGGGACTTCCGCCCCGGGCGGCGGGCAGCACGG 413
                                                                     GAGCTCCGCCGCCGCCGCCGCGGGACCTGCTCCTTCCAGAACCAGAGCCTGCGCCCCCT
                                                                                                                                                                                                                                                                                                                                                                      CGCCGTGAGCCTGGTCGCCGGGGCCCTGGGCCCGGGCGCTGCCGGGGCCTGCT 151955
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                                                                                                                                                                                                                                                                                                                  AGCCTTCAAGCTCAACCCGGGCGCGCACGAGCTGTCCCCGGGGCCAGAGCTCGGCGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                         TGAACTGAGCCTGGCGGCGCGCAGAACGGCTTCGTTGATTCCGCCGCCGCGCACATGGG 173
                                                                                                                                                                       GTCGCAGGGCCCCGGCCTACCCCGGCTCCGCTGCCGCCTGCCGCTGCCGCCAGCGCT
                                                                                                                   CGGGCCCCACGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAACTCCACCCGGGA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 90-132; 145pp; English.
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Pred. No. 0.11;
0; Mismatches
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                                                                                                                                                        The invention relates to a composition comprising an expression vector bound to an aggregated protein-polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide sequence operatively linked to a polynucleotide sequence encoding an infectious disease, cancer and autoimmune disease such as rheumatoid arthritis, vasculitis, and multiple sclerosis, pathogenic genomes consisting of bacterium, fungus, protozoa and virus such as human immunodeficiency virus (HTV), herpes simplex virus (HSV), and optionally comprising a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response (systemic and/or mucosal) in an organism. The cytokine expression vector
                                             different promoter polynucleotide sequences. The expression vector, DNA vaccine is useful for treating a condition in an organism. The present sequence is human herpesvirus 2 complete DNA genome related
                                                                                                    contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for oral delivery of vaccines, comprises expression containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus 2; cytostatic; cancer; immunosuppressive; vir antibacterial; fungicide; protozoacide; antirheumatic; antiinfl antiarthritic; rheumatoid arthritis; neuroprotective; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 90-132; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000;
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                                 the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inritic; rheumatoid arthritis; neuroprotective; multiple sclerosis; response; vasotropic; vaccine; gene therapy; autoimmune disease;
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Query Match

Sequence

154746 BP;

23003 A;

54701 G; 22824 T; 0 other;

Score 56.4; 54218 C;

DB 24;

Length 154746;

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RESULT 15
AAI99683/c
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                                                          Evaluating strain variation of Mycobacterium tuberculosis, compute determining the nucleotide sequence of the strain at positions genome corresponding to positions where M. tuberculosis strains
                                                                                                              WPI;
                                                                                                                                                                                                                                                                   US6294328-B1
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                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; d
                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis strain H37Rv genome
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                                                                                                                                                                                                                                                                                                                                                                                                          AAI99683;
                       Claim 4;
                                                                                                                                      Fleischmann RD,
                                                                                                                                                                                                                 24-JUN-1998;
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                                                                                                                                                                 INST GENOMIC RES.
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3940320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                                                                                                                                163 GCGCACATGGGAGCCTTCAAGCTCAACCCGGGCGCCACGAGCTGTCCCCGGGCCAGAGC 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GGCAGCTTCGCGCGCCACCATCACCACTCCGCCGCCGCCGCCGCCGCCGCCGCCGAG 102
                                        GCCGCAGCGCTCGGGCCCCACGCCGCGCACGTTGGCTCCTACTCTGGGCCGCCCTTCAAC 342
                                                                                                                                                                                                                TCGGCGTTCACGTCGCAGGGCCCCGGCGCCTACCCCGGCTCCGGCTGCGGCTGCCGCTGCG 282
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Pred. No. 0.086;
0; Mismatches 1
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Search completed: October Job time: 1424 secs 10, 2002, 14:50:58

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Minimum DB seq length: 0
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3546	3546	3468	3468	3468	3468	3468	3468	3468	3468	3468	3468	3468	3468	3468	3468	1393	1393
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Sequence 14, Appr		4.4	Sequence 2, Appli	, U	`	4.		4,0		4 (4		.		٠,	٦,

ALIGNMENTS

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Patent No. 6143878
                                                                                                                                                                                       APPLICATION NUMBER: AU PM9714
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/00799
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 10981
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATING
OPERATING SYSTEM: DOS
OPERATING FASTSED Versi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3923 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Koopman, Peter
APPLICANT: Goodfellow, Peter
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 29-MAY-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Scully, Scott, Murphy & Presser
T: 400 Garden City Plaza
Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08860635A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Applicat Patent No. 6316597 GENERAL INFORMATION:
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Best Local Similarity
Matches 202; Conserv
                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GOODIELOW, PETER AND PROTEIN AND TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
SEQUENCE CHARACTERISTICS:
LENGTH: 3923 base pairs
                                                                                      TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                   FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   088
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                                                                                                                NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                     APPLICATION NUMBER: AU PFILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/281,476
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGGTCCCGCGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGTCAACGGCTCCAGCAAGAACAAGCCGCACGTCAAGCGGCCCATGAACGCCTTCATGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCGGGGGCGCCAAGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCAGCCGCGGCGGAGGAAGTCGGTGAAGAACGGGCAGGCGGAGGCCAGAGGAGGCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGGCCGCCGCAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGGAGGAGGCGGAGCGCTGCGCGTGCAGCAAGAAGAAGGACCACCCGGATTACAAGT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATCGACGAGGCCAAGCGGCTGCGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTCAGCAAGACGCTGGGCAAGCTCTGGAGACTTCTGAACGAGAGCGAGAAGCCGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATCAGCAAGCGCCTGGGGGCCGAGTGGAAGGTCATGTCCGAGGCCGAGAAGCCGCCCGT 358
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                                                                    516-742-4366
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                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                      UMBER: PCT/AU95/00799
29-NOV-1995
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                                                                                                                      10981
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Pred. No. 7.9e-18;
0; Mismatches 101;
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            FILING DATE: 29-NOV-1994
APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/007:
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10981
                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOODMAN, Peter
APPLICANT: GOODIELOW, Peter
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
 TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                 APPLICATION NUMBER: AU P.
                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/860,635A FILING DATE: 29-MAY-1997
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                         COMPUTER:
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400 Garden City Plaza
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179 GCGGCGGGGGCGCCAAGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                          640 GCGTCAACGGCTCCAGCAAGAACAAGCCGCACGTCAAGCGGCCCATGAACGCCTTCATGG
                                              419 ACCGGCCGCGCCAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCG 478
                                                                                                    820 TCGTGGAGGAGGCGGAGCGGCTGCGCGTGCAGCAAGAAGGACCACCCGGATTACAAGT
                                                                                                                                                                                                                                                       299 AGATCAGCAAGCGCCTGGGGGCCGAGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGT
                                                                                                                                                                                                                                                                                                                                                      239 TGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGG
                                                                                                                             TCATCGACGACGACGCCAAGCGCGCGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGT
ACCAGCCGCGGCGGAGGAAGTCGGTGAAGAACGGGCAGGCGGAGGCAGAGGCCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09281476 Patent No. 6316597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2249 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KOODMAN, Peter
APPLICANT: GOODICALIOW, PETER
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/281,476
           FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 CATGGTGTGGTCCCGCGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCAAGATGCACAA 293
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STATE: NY
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CITY: G
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TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                   APPLICATION NUMBER: PCT/AU95/00799 FILING DATE: 29-NOV-1995
                                                                                        APPLICATION NUMBER: FILING DATE: 05-DE
                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                             11530
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                                                                                                                                                                                                                                                                                      IBM Compatible
NUMBER:
                                                                                      05-DEC-1994
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69.2%;
                                                                                                         AU PM9835
                                                                                                                                             08/860,635
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Pred. No. 2.1e-16;
0; Mismatches 81;
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; MOLECULE TYPE: CDNA US-09-281-476-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 182;
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COPERATION SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,016A
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: JACKSON, DAYIG A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 2249 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HOUDE, A TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 CGGCGGCGGCGGGGGCCAAGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 CAAGTACCGGCCGCCGCAAGA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 CATGGTGTGGGCGCAGGCTGCGCAGGAAGCTGGCAGACCAGTACCCGCATCTGCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 GCCGTTCATCGACGAGGCCAAGCGGCTGCGCGCGCTGCACATGAAGGAGCACCCGGATTA 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 CATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAA
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
STATE: N.J.
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: KLAUBER & JACKSON STREET: Continental Plaza, 411 Hackensack Avenue
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                                                                                             JACKSON, David A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SILVERSIDES, David W. DANEAU, Isabelle M.F. HOUDE, Alain
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Pred. No. 2.1e-16;
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RESULT 6
US-08-196-016A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08196016A Patent No. 5596089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1667 base pairs
TYPE: nucleic acid
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                                                                                                                    APPLICATION NUMBER: US/00 FILING DATE: 14-FEB-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: Continental Plaza, 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DANEAU, Isabe APPLICANT: HOUDE, Alain
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1032 GAGG 1035
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                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SRY GENOMIC SEQUENCES AND USE IN TISSUE TITLE OF INVENTION: SEXING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         852 AAAAGTGGCTCTAGAGAACCCTCAAATGCAAAACTCAGAGATCAGCAAGTGGCTGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CAAGATGGCCCAGGAGAACCCCAAGATGCACACTCGGAGATCAGCAAGCGCCTGGGGGC 320
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                                                                                                                                                                                                                  MEDIUM TYPE: FIOPPY ... COMPUTER: IBM PC compatible COMPUTER: YSTEM: PC-DOS/MS-DOS
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                                                                                      NAME: JACKSON, David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: Y-chromosome, SRY gene
                   TELEFAX: 201-343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
               APPLICATION NUMBER: US 0' FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                             APPLICATION NUMBER: US 0 FILING DATE: 14-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                              APPLICATION NUMBER: US 07 FILING DATE: O8-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                 APPLICATION NUMBER: 1
FILING DATE: 05-MAY-1
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1294 GAGCCAAGAGGCCACAGAA 1312
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LENGTH: 1661 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1234 AGAGACTACTAGCCATACACCGAGACAAATACCCGGGCTATAAATATCGACCTCGTCGGA 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGC 253
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                                                                                                                                                                                                                                                                                                                                                                                           STREET: 660 WILL
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                STATE:
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nes 175; Conserv
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                E: Sprung Kramer Schaefer & Briscoe 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                  US 07/441,703
                                                                                                                                                      US 07/872,646
                                                                                                 US 07/715,181
US 07/312,543
                                                                                                                                                                                                                        us/08/239,276
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Pred. No. 8e-15;
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                                                                                                                                                                                                                                                                                                              1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: WOrdPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                       ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 19
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ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 530
PRIOR APPLICATION UMBER: US 08/239,276
PFILING DATE: 05-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1190 AGCCGGCAGCATCGGAGAAGTATCCTGACTACAAGTACAAGCCGCGCGCCCAAGCGCA 1247
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CITY: Tarrytown
STATE: New York
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
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                                                                                                       US/08/468,579B
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                                                                                                                                                                                                                                           Sequence 6, Application US/08468577B Patent No. 6001804
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                       STREET: 000
STREET: New York
STATE: New York
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                1190 AGCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGCCCAAGCGCA 1247
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FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
COMPUTER READABLE FORM:
                                                                                                                                                                           TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 19
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/872,646
                                                                                                                                                       CORRESPONDENCE ADDRESS
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TYPE: nucleic acid
STRANDEDNESS: single
                      COUNTRY: USA
ZIP: 10591-5144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/715,181
                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208;
                                                                                                          E: Sprung Kramer Schaefer & Briscoe 660 White Plains Road
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US-08-239-276-5; Sequence 5, Application US/08239276; Patent No. 5840836
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                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 3243 nucleotides
                                                                                                                                                         1190 AGCCGGCAGACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGCGCCCAAGCGCA 1247
                                                                                                                                                                                                                                                                                                                    1070 AAGATCCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCTTGGATCT 1129
                                                                                                                                                                                                                                                                                                                                                                                                1010 AGCAGCCACATCAAGAGGCCCCATGAACGCCTTCATGGTGTGGGCCCAAGGATGAGCGGAGG 1069
    APPLICANT:
                                                                                                                                                                                                                                      1130 CGCTGGAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAGGAACAGGCGGCGCTG 1189
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                  382 CGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCGCAAGACCA 439
                                                                                                                                                                                                                                                                             322 GAGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCCAAGCGGCTG 381
                                                                                                                                                                                                                                                                                                                                                           262 AAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGGCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                    202 CAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US U
FTT.ING DATE: 17-FEB-1989
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  Rabin, Daniel
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 1570 nucleotides
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APPLICATION NUMBER: US/01
FILING DATE: 05-MAY-1994
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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338 ATCG-TCATCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGC 385
                                  382 CGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCC 430
                                                                           278 CGCTGGAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAGGAACAGGCTCTGCTG
                                                                                                   322 GAGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTG
                                                                                                                                                           218 AAGATCCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCTTGGATCT
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                                                                                                                                                                                                                                                                                                                  98 GAGGAAGCCATGCTGAGCTGCGACATGGATGGCTCCCGCCACTTCCCCGAGTCCCGAAAC
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OPERATING SYSTEM: System 7.5
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                                                                                                                                                                                                                                      Matches 198;
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                                                                                                                                                                                                                                                         Best Local Similarity
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APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 5:
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STREET: but
CITY: Tarrytown
TMATE: New York
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LENGTH: 1570 nucleotic
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APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
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158 AGCAGCCACATCAAGAGGCCCCATGAACGCCTTCATGGTGTGGGCCCAAGGATGAGCGGAGG 217
                                   202 CAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGC 261
                                                                                                               APPLICATION NUMBER: FILING DATE: 14-JUN
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OPERATING SYSTEM: System
SOFTERAN
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                                                                             98 GAGGAAGCCATGCTGAGCTGCGACATGGATGGCTCCCGCACTTCCCCGAGTCCCCGAAAC 157
                                                                                                                                                       38 ATCAGCCTGGACTCATCCCCAGCCAAGGAGCGGCTGGAGGACGGCTGTGTGCACCCACTG
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                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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10591-5144
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660 White Plains Road
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56.78;
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Pred. No. 7.1e-10;
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                                                                  TOPOLOGY: US-08-468-577B-5
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                                                                                                                                                                  TELEFAX: (914) 332-1844 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MD TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
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                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 1
FILING DATE: 05-MAY-
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APPLICATION NUMBER:
FILING DATE: 08-JUN-
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 514
                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                 LENGTH:
 198;
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5. 6001804
                Similarity
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                                                                                                                                                                                                                                                                   Kurt G. Briscoe
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                                                                                                                              1570 nucleotides
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660 White Plains Road
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 Conservative
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                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette, 3.50 inch, 1.4 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              System 7.5
                                                                                                                                                                                                                                                                                                                        US 07/312,543
                                                                                                                                                                                                                                                                                                                                                                         US 07/441,703
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                                                                                                                                                                                                                                                   33,141
0; Mismatches 150; Indels
              Score 97; DB 3;
Pred. No. 7.1e-10;
                                                                                                                                                                                                                                     MDI 251.8-KGB
                              Length 1570;
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Gaps
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Patent No. 5840836
GENERAL INFORMATION:
                                                                              NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 07/872,646
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 14-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 08-JUN-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1397 nucleotides
                                                                                                                                    REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.4-KGB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US,
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OPERATING SYSTEM: System
SOFTWARE: WordPerfect
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Tarrytown
  STRANDEDNESS:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                    TELEPHONE:
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                     nucleic acid
                                                                                                                                                                                               Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                 (914) 332-1844
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single
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                                                                                                                                                                                                                                                        US 07/312,543
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US-08-239-276-1
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                    INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-UUN-1992
PRIOR APPLICATION NUMBER: US 07/715,181
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA: APPLICATION NUMBER: US
SEQUENCE CHARACTERISTICS:
                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               FILING DATE: 14-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-MAY-PRIOR APPLICATION DATA:
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OPERATING SYSTEM: System
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STATE: New York
                                                                                             REFERENCE/DOCKET NUMBER: 33
                                                                                                                                                                    APPLICATION NUMBER: US 07/312,543 FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                        TELEPHONE:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                 Kurt G. Briscoe
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                                  (914) 332-1700
(914) 332-1844
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04-DEC-1989
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                                                                                                             33,141
                                                                                               MDI
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Pred. No. 1.1e-07;
                                                                                               251.5-KGB
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LENGTH: 1397 nucleotides

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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                 FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
TITTUG DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
EILING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 05-MAY-1994
                                                      FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 14-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 GGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGGGGGGCAAGATGGCCCAGGAGA 277
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REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.8-KGB
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/468,577B FILING DATE: O6-JUN-1995 CLASSIFICATION: 514
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CITY: Tarrytown
STATE: New York
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Local Similarity 65.3%;
                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 04-DEC
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ZIP: 10591-5144
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                                                                                                                                                      NUMBER: US 07/441,703
04-DEC-1989
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Matches 139; Conserv
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1397 nucleotides
TYPE: nucleic acid
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                                                                            278 ACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCGAGTGGAAGGTCATGT 337
                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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AGAAGTATCCTGACTACAAGTACAAGCCGCGGC 212
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Search completed: October 10, 2002, 17:33:14 Job time: 31.7333 secs

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A1052267 oy58e06. x
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A1292258 qm76c01. x
AW005568 wz85h12. x
A1199308 gy41a10. x
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A1146406 qa06b04 x
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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ALIGNMENTS

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Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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BE119829.1
EST.
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                                                                                                                                                                                                    Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 76-194, >(CGG
                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                     )n#Simple_repeat
Seq primer: M13
POLYA=No.
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                                                                                                                                                        primer: M13 Forward
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CAO-ban-e-05-0-UI"
                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            norvegicus cDNA clone
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RESULT 2
BF305922
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 CCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGGGGGCAGCCGGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGGCTGCTGGCGGCCGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCGCAAGACCAA
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                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM1007 row: 1 column: 02 High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web from which this clone was derived, please visit our web the library minus description of the library from which this clone was derived, please visit our web the library minus description of the library from which this clone was derived, please visit our web the library minus description and Soares,
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/clone="IMAGE:4123153"
/clone_lib="NIH_MGC_17"
                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                             Location/Qualifiers
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96.0%;
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Pred. No. 1.6e-28;
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Best Local
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hes 298; Conserv
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                       Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be consortium/LLNL at:
                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 965)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                              Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             965 bp mRNA linear EST 15-FEB-1999 qy22a10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2012730 3′ similar to gb:X71136 SOX-10 PROTEIN (HUMAN);, mRNA sequence.
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                                                                                                                                                                       Tissue Procurement:
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AI356682.1
                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D.,
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/lab.host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: porB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the prime of the constructed by clowing 5; adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 231 c 249 g 99 t
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84.7%;
                                                                                                                                                                 David N. Louis, M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGGAAACTTTTGTCGGAGACGGAGAGCCGGCCGTTCATCGACGACGCTAAGCCGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299;
                                                                                                                                                                                                                      qz02q05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2020376 3' similar to qb:X71136 SOX-10 PROTEIN (HUMAN); contains MER22.tl TAR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
Ph.D.
                                                                                                                                                                                                 EST
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                             AI373018.1 GI:4152884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 480.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI Sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

1 329 c 308 g 125 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 265.4;
Pred. No. 1.7
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hes 56;
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             M.D.,
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             Myrna
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               R. Rosenfeld M.D.,
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   REFERENCE
                                                       SOURCE
                                                                      KEYWORDS
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Best Local
                                          ORGANISM
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443 CGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGGCTCCTGGCGGCGGCG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGGTGCTCCCGCGGGCAGCGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA
                                                                                                                                                                                                                                                                                                                                                                                     CGCTCATGAAGAAGAAGAATAAGTACACGCTGCCCGGCGGCTGCTGCCCCCCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oy58e06.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1670050 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN); contains MER22.tl TAR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1163 Std Error: 0.00
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 429.
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                                                                     Homo sapiens
                                                                                                                                             AI052267.1 GI:3308258
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135 c 154 g 49 t 1 others
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/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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Pred. No. 2.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 443;
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                                                                                                GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA
                                                                                                                                                          GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCCGCAGAGACCAAGA 442
                                                                                                                                                                                 AGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGC
                                                                                                                                                                                                          AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC
                                                                                                                                                                                                                                                       AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCG
                                                                                                                                                                                                                                                                                                    AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                                                                                                            CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCTGCTGGCCCCCCGGCG 426
                                                                                                                                                                                                                                AGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCC
AI631443 452 bp mRNA linear EST 16-DEC-1999 wa89a09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2303320 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN); contains MER22.t1 TAR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1670050"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="9410blastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCCTGCTGGCCCCCCGGCG
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                                                       CGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGCGGCTCCTGGCGGCGGCGGCG 496
                                                                                                               GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAAACCAAGA
                                                                                                                                                                       GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCCGCCGCAAGACCAAGA 442
                                                                                                                                                                                                                                 AGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
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Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 452)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PGR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475992-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 138 c 160 g 51 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE: 2303320"
/clone_lib="NCI_CGAP_GC6"
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/lab_host="DH10B"
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Pred. No. 2.3e-26;
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366 CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCTGCTGGCCCCCGGCG 419

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REFERENCE
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AI292258
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hes 298;
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GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCCAAGA
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                                                                                                                                        AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC 382
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                                                                             GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCGCAAGACCAAGA 442
                                                                                                                                                                          AGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCG
                                                                                                           AGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGC
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clone IMAGE:1894656 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN
):contains MER22.tl TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1171 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 460)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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Pred. No. 2.3e-26;
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Query Match
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                                                                                                                                                                            203 AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                               66 CGGGGGGCGGCGGCGACTCCACCGCGGCGGCGGCGGCGGCAACCAGAAAAAACAGCC
AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Tnsert Length: 1157
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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Pred. No. 2.3e-26;
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                                                                           143
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                                                                                                                                 Local
                                     CGGGGGGCGGCGGCAACTCCACCGCGGCGGCGGCCGGCGGCAACCAGAAAAACAGCC 150
                                                                       GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA
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1 (bases 1 to 463)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI199308 463 bp mRNA linear EST 01-DEC-1998 gi41a10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859034 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN); contains MER22.tl TAR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1191 Std Error: 0.00
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                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -40UP from Gibco
                                                                                                                                                                                                           104
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                         adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed
                                                                                                                                                                                                       Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                   Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:1859034"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                             52.9%;
                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into I and Eco RI sites of the modified pT73 vector. is normalized, and was constructed by Bento
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                                                                                                       Pred. No. 2.3e
0; Mismatches
                                                                                                                               Pred. No. 2.3e-26;
                                                                                                               56;
                                                                                                                                                 Length 463;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1141 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 463.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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     104
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clor the Not I and Eco RI sites of the modified pT7T3 v. Library is normalized, and was constructed by Bent Soares and M.Fatima Bonaldo."

142 c 167 g 52 t
                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:1702774"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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EST.
                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length; 1157 Std Error: 0.00
                                                                                                                                                     Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 462.
                                                                                                                                                                                                                                                                      Bonaldo, Ph.D.
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/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1702724"
/clone_lib="NCI_CGAP_Brn23"
                                                                                                                                        Location/Qualifiers
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84.2%;
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Pred. No. 2.3e-26;
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                                                                                         FEATURES
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                                                                          source
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AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE: 3070109
BF513177
                                                                                                        Email: cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message. cDNA Library Preparation: M.E.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LLNL
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 1-37,
>GC_rich#Low_complexity 90-133, >GC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF513177.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF513177 478 bp mRNA
UI-H-BW1-amj-d-03-0-UI.sl NCI_CGAP_Sub7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 478)
                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                           primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fattha Bonaldo."

143 c 164 g 51 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.9%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 264.4; Lb .,
Pred. No. 2.3e-26;
Pred. No. 2.5e-26;
                                                                                                                                                                                                                                                                                                                        Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                               of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/clone="IMAGE:3070109" /clone_lib="NCI_CGAP_Su

/lab_host="DH10B (Life Technologies)"

Sub7

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263 AGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGCTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 CGGGGGGCGGCGGCAACTCCACCGCGGCGGCGGCGGCGACCAGAAAAAACAGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCCGCCAAGACCAAGA 442
                                                                                                                                                                                                                                                                                                                                              CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCGGCTGCTGGCCCCCCGGCG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA
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        qa06b04.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1685935 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN); contains MER22.tl TAR1 repetitive element; mRNA sequence.
AI146406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6. The

NCI_CGAP_Sub6 Iibrary derived from NCI_CGAP_Sub6. The

NCI_CGAP_Sub7 Iibrary had I2 million recombinants. A

single-stranded DNA preparation of NCI_CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver

comprising: the IMAGE pool (NCI_CGAP_Kd3 pool 1 LLAM

334-337, 3682-3683, 3798-3803 (IMAGE CloneIDs

1322376-1323911, 1456008-145675,1500552-1502855);

NCI_CGAP_Kd3 pool 1 LLAM

3383-3342,3722-3725, 376-3778

(IMAGE CloneIDs 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI_CGAP_Ld5 pool 1 LLAM

3575-3882,

1492104-1493255); NCI_CGAP_Ld5 pool 1 LLAM

3575-382,

1492104-1493255); NCI_CGAP_Ld5 pool 1 LLAM

3575-382,

3851-3854 (IMAGE CloneIDs 1414920-1147991, 1320904-1522439);

NCI_CGAP_GC4 pool 1 LLAM

3164-3167, 3716-3720,

3733-3735 (IMAGE CloneIDs 1257096-125831, 149964-1470983);

1101192-1101959, 1217928-1220615); NCI_CGAP_CD001 pool 1

LLAM

2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-106125

1144584-1145351), (6% of the driver population) plus a

pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE

CloneIDs 2708616-2712535) and NCI_CGAP_Sub2 (IMAGE

CloneIDs 2708616-2712535) and NCI_CGAP_Sub2 (IMAGE

CloneIDs 2710536-2712455) (4% of the driver population),

plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE

CloneIDs 2712456-2723391) (10% of the driver population),

plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE

CloneIDs 2712456-2723391) (10% of the driver population),

plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE

CloneIDs 2723969-2733190) (40% of the driver population),

plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE

CloneIDs 2723969-2733190) (40% of the driver population),

plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE

CloneIDs 2723969-2733190) (40% of the driver population),

plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE

CloneIDs 2726969-273391) (10% of the driver population),

plus a pool of 5,472 clones 
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84.2%;
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Pred. No. 2.3e-26;
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ORIGIN

Matches

BASE COUNT

RESULT 13 AI146406

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DEFINITION

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                    151 CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGTGCCCGCGGGCAGCGGCGCA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                       203 AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGCTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                                                                                                                                                                                  91
                 CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGGCTGCTGGCCCCCGGCG 444
                                                                            GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA
                                                                                                                  GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCCGCAAGACCAAGA 442
                                                                                                                                                           AGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGC
                                                                                                                                                                                               AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC
                                                                                                                                                                                                                                       AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute / National Institute of Neuroli
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 480)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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EST.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1685935"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                        323
                                                                                                                                                     151
                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                      AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC 382
                                                               AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCCG 270
                                                                                                        AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGGCCG 322
                                                                                                                                                 CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGGCAGCGGCGCA 210
                                                                                                                                                                       AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                     CGGGGGGGGGCGCCAACTCCACCGCGGCGGCGGCGGCAACCAGAAAAAACAGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 483)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (CGAP/BTGAP), Tumor Gene Index (Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 480.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1154 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1421743.1 GI:4267674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 104
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                               adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

152 c 175 g 51 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                    Score 264.4; DB 9;
Pred. No. 2.3e-26;
0; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the modified pT7T3 vector. constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
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                                                                                                                                                                                                                                                                                                                                                             Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. Fatima
                                                                                                                                                                                                                                                                                                                      0;
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KEYWORDS
SOURCE
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AW028031
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                                                                                                              331 GAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGA 390
                     203 AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGCTCCCGCGGGCAGCGGCGCA 262
                                                                  45 CGGGGGGCGCCGGCAACTCCACCGCGGCGGCGGCGGCGGCAACCAGAAAAACAGCC 104
                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCGGCTGCTGGCCCCCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGGAAACTTTTGTCGGAGACGGAGAAGCCGGCCGTTCATCGACGAGGCCTAAGCGGCTGC 330
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 485)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1189 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo,
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                   109
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                               T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

145 c 176 g 54 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2501832"
/clone_1ib="NCI_CGAP_Brn23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                            52.9%;
                                                                                                                                                       0;
                                                                                                                                                    Score 264.4; DB 9; Length 485; Pred. No. 2.3e-26; O; Mismatches 56; Indels 0
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                                                                                                                                                       Gaps
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Qу	Qу Db	Qy	Qу Db	Db
443 CGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGGCG	383 GCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCGCGCG	323 AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCCAAGCGGCTGC 382 	263 AGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAGCGCCTGGGGGCCC 322	105 CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGGGGGCAGCGGCGCA 164

Search completed: October 10, 2002, 20:27:16 Job time: 698.733 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
          987654
                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     488
463.2
328
292.2
264.4
264.4
264.4
                                                                                                                                                                                                                                                    Score
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
4: /SIDS1/gcgdata/h
5: /SIDS1/gcgdata/h
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     100.0
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Gapop 10.0 , Gapext 1.0
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     4091
1542
2376
2312
1161
1085
1087
1116
     ij
                           AAD11111
AAX16151
AAX16153
AAX16152
AAX16154
AAD11110
AAK52388
AAK53268
     AAK52284
                   Chicken Sox1 cDNA.
Degenerate human S
Human small cell 1
Human polynucleoti
Human polynucleoti
Human polynucleoti
                                                                                                                                                                                                                                                 Description
                                                                                                                                               Human small cell 1
Human Soxl encodin
Mouse Soxl cDNA.
polynucleoti
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Islet cell antibod	AAV63557	20	3243	23.6	118	45	
Human islet cell a	AAZ09919	20	3243	23.6	118	44	
Human pancreatic i	AAZ32338	20	3243	23.6	118	43	
Islets of Langerha	AAQ05686	11	3243	23.6	118	42	
Mouse ischaemic co	ABI99688	24	2215	23.8	118.8	41	
Drosophila melanog	ABL05610	23	7108	23.8	119	40	
Drosophila melanog	ABL05611	23	2310	23.8	119	39	
VGT24 of	AAC61724	21	2033	24.2	. 121	38	
Fish protamine gen	AAQ87042	16	2762	24.2	121.2	37	
Mouse Sox-18 gene.	AAT51617	18	1588	24.8	123.8	36	
Bovine SRY-related	AAT33008	17	2840	24.9	4	35	
	AAQ94813	16	1661	24.9	•	34	
Bovine sex-determi	AAQ94811	16	1661	24.9	4	ω	
Bovine sex-determi	AAQ94814	16	1661	24.9	_	32	
SOX4 coding sequen	AAT59844	18	1422	25.7	128.4	31	
Human cervical can	AAH72650	22	4467	26.0	130.2	30	
Porcine sex-determ	AAQ94812	16	1667	26.1	130.4	29	
S	AAS61805	24	441	26.8	134	28	
	ABI99491	24	2069	27.1	135.4	27	
Sox-9 cf	AAT30308	17	2514	28.3	141.4	26	
Human gastric canc	AAF22715	22	744	28.3	141.4	25	
pY53.3 (NCIMB 4030	AAQ20684	13	2151	28.3	141.6	24	
Rabbit mt-box. Or	AAQ20680	13	996	28.4	141.8	23	
Human SOX-9 cDNA.	AAT30309	17	3934	•	•	22	
=	AAS87736	23	434		156.6	21	
Human cDNA sequence	AAH16401	22	1788			c 20	
	ABL18480	23	4298	38.7	193.4		
Drosophila melanog	ABL18481	23	2298			18	
encoding no	AAS87779	23	1969	•	•	17	
small cell	AAS61666	24	395	•	٠	16	
Lung small cell ca	AAS61625	24	412		•	15	
Human small cell l	AAD11119	22	8372			14	
DNA encoding novel	AAS87738	23	2378		•	13	
	111	22	2509		258.4	12	
Mouse ischaemic co	931	24	2283	•	٠	11	
Human polynucleoti	AAK53372	22	1501		•	10	

Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; SOX1; ds. Human small cell lung cancer associated gene, SOX1 24-SEP-2001 AAD11111; AAD11111 standard; DNA; 4091 BP (first entry)

RESULT 1 AAD11111 ID AAD1

ALIGNMENTS

PAARX TRANSCARA TO THE TRANSCARA THE TRANSCARA TO THE TRA (LUDW-) LUDWIG INST CANCER RES (SLOK) SLOAN KETTERING INST CANCELL RES FOUND INC. 21-JAN-2000; 2000US-0489101. Homo sapiens 19-JAN-2001; 2001WO-US02015 26-JUL-2001. WO200153349-A2 Location/Qualifiers 61..1224 /*tag= a /product= "Human SOX1 protein" /*tag= CANCER RES

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AAX16151
ID AAX161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-2, encoding human SOX1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded isolated nucleic acid comprising an NA Group 3 or 4 molecule -
              AAX16151 standard; cDNA to mRNA; 1542 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4091 BP; 924 A; 1109 C; 1110 G; 943 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 57; Page 88-90; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTGGCGGCCGCGCGGG 500
                                                                                                                                   CGGCCGCCGCAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGG 480
                                                                                                                                                                                                                  ATCAGCAAGCGCCTGGGGGCCGAGTGGAAGGTCATGTCCGAGGCCGAGAAAGCGGCCGTTC
                                                                                                                                                                                                                                                                                                              CTCCTGGCGGCCGGCGGG 500
                                                                                                                        CGGCCGCCGCAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGG
                                                                                                                                                                     ATCGACGAGGCCAAGCGGCTGCGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTAC
                                                                                                                                                                                             ATCGACGAGGCCAAGCGGCTGCGCGCCTGCACATGAAGGAGCACCCGGATTACAAGTAC
                                                                                                                                                                                                                                         ATCAGCAAGCGCCTGGGGGCCGAGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTC 360
                                                                                                                                                                                                                                                                 TGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGGAG
                                                                                                                                                                                                                                                                                        TGGTCCCGCGGGCAGCGCCAAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAG
                                                                                                                                                                                                                                                                                                                                    GGCGGGGGGCGCCAAGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTG 240
                                                                                                                                                                                                                                                                                                                                                             ATGTACAGCATGATGATGGAGACCGACCTGCACTCGCCCGGCGCGCCCCAGGCCCCCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCCCGTCTATGCTCCAGGCCCTCTCCTCGCGGTGCCGGTGAACCCGCCAGCCGCCCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 500; DB 22;
Pred. No. 9.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4091;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     population. The method comprises: (a) detecting Sox1 gene expression in the cells; and (b) isolating those cells expressing Sox1. Also described is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Sox1 expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence encodes human Sox1. Detection of Sox1 expressing cells important in diagnosing and treating cancers of the neurological disorders, especially for repair of accidentally induced trauma in the CNS or for correction of congenital or pathological diseases of the CNS. A patient with a neurological disorder can act as self-donor. Cells may be isolated from the patient and either sorted to extract neuroblasts, or treated in order to differentiate neuroblasts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolating neuroblastic cells from a population - by detecting the expression of the Soxl gene in the cells and sorting the cells to isolate those cells expressing Soxl
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1542 BP; 238 A; 565 C; 560 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method has been developed for isolating neuroblastic cells from a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 45-47; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       from specific or general precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lovell-Badge R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDICAL RES COUNCIL.
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Local
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                                                                                                                                    ATGTACAGCATGATGATGGAGACCGACCTGCACTCGCCCGGCGCGCCCCAGGCCCCCACG
                                                                                                                                                                                       1999-095759/08.
                                                                                                                                                                                                                                                                                               499;
                                                                                                                                                                                                                                                                                                                        Similarity
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60..1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Sox1"
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                                                                                                                                                                                                                                                                                                                        Score 488; DB 20;
Pred. No. 7.8e-68;
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                                                                                                                                                                                                                                                                                                                                               Length 1542;
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A method has been developed for isolating neuroblastic cells from a cell population. The method comprises: (a) detecting Soxl gene expression in the cells; and (b) isolating those cells expressing Soxl. Also described is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Soxl expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence represents mouse Soxl cDNA. Detection of Soxl expressing cells is important in diagnosing and treating cancers of the nervous system. Neural stem cells are useful for the treatment of neurological disorders, especially for repair of accidentally induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                             Disclosure; Page 43-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2376 BP; 439 A; 772 C; 745 G;
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                                                                                                                                                                                                                                              Sox1; neuronal stem cell gene; neuroblastic cell; system; neurological disorder; ss.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   population. The method comprises: (a) detecting Sox1 gene expression in the cells; and (b) isolating those cells expressing Sox1. Also described is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Sox1 expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence represents chicken Sox1 cDNA. Detection of Sox1 expressing cells is important in diagnosing and treating cancers of the nervous system. Neural stem cells are useful for the treatment of neurological disorders, especially for repair of accidentally induced trauma in the CNS or for correction of congenital or pathological diseases of the CNS. A patient with a neurological disorder can act as self-donor. Cells may be isolated from the patient and either sorted to extract neuroblasts, or treated in order to differentiate neuroblasts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolating neuroblastic cells from a population - by detecting the expression of the Soxl gene in the cells and sorting the cells to isolate those cells expressing Soxl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2312 BP; 421 A; 739 C; 714 G; 438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method has been developed for isolating neuroblastic cells from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 41-43; 60pp; English
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                                                                         GCGG 499
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                                                 CCGG 638
                                                                                                                                                               CGGCTGCGCGCGCTGCACATGAAGGAGCACCCGGATTACAAGTACCGGCCGCCGCCCAAG
                                                                                                                                                                                                                GGGGCCGAGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGACGACGAAG
                                                                                                                                                                                                                                                  CGGCGGAAGATGCCCCAGGAGAATCCCAAGATGCACAACTCGGAGATCAGCAAGCGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCCCCGCCGCCGGCGGAGGGAAGTGAGGAAGCCCCGTGAATGTACAGCATGATG
                                                                                                GGCGCCGAGTGGAAGGTGATGTCGGAGGCCGAGAAGCGGCCTTTCATCGACGAGGCGAAG
                                                                                                                                                                                                                                                                           CGGCGCAAGATGGCCCCAAGAACCCCCAAGATGCACCAACTCGGAGATCAGCAAGCGCCTG
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                                                                                                                                                 CGGCTGCGGGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCCGGCGAAG
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81.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 328; DB 20;
Pred. No. 5.1e-43;
0; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Degenerate human Sox1 coding sequence RNA
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67..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "replace(34..36, "agy")"
64..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
34..36
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            322..324
                                                319..321
                                                                                     316..318
                    /*tag= s
/note= "replace(319..321, "cun")"
                                                        /*tag= r
/note= "replace(316..318,
                                                                                                                                                                                                   253..255
                                                                                                                                                                                                                                                                                                     /*tag= k
/note= "replace(199..201, "cgn")"
235..237
/*tag=
                                                                                                /*tag= q
/note= "replace(291..294,
                                                                                                            /*tag=
                                                                                                                         291..294
                                                                                                                                    /*tag= p
/note= "replace(277..279,
                                                                                                                                                                        /*tag= o
/note= "replace(253..255, "cun")"
                                                                                                                                                                                                          /*tag= n
/note=_"replace(250..252,
                                                                                                                                                                                                                                                                           244..246
                                                                                                                                                                                                                                                                                                                                                     199..201
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/note= "replace(196..198, "cgn")"
                                                                                                                                                                                                                                                                                                                                                                                                                                    '*tag= h
'note= "replace(184..186, "agy")"
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'note= "replace(157..159, "cgn")"
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/note= "replace(148..150, "cgn")"
L57..159
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/note=_"replace(67..69, "agy")"
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note= "replace(187..189, "cgn")"
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                                                                                                                                                                                                                                               note= "replace(244..246, "agy")"
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/*tag* aq /note= "replace(805807, "agy")" 811813 /*tag* ar /note= "replace(811813, "agy")"	9, 01,	778780 /*tag= an /note= "replace(778780, "agy")" 784786 /*tra=	<pre>/note= "replace(760762, "cun")" 769771 /*tag= am /*tag= am /note= "replace(769771, "agy")"</pre>	/*tag= ak /*tag= ak /note= "replace(742744, "cgn")" 760762 /*tag= al		/note= "replace(583585, "agy")" 631632 /*taq= ai	ω m ≖	55.2	/*tag= ae /note= "replace(505507, "cgn")" 508510	424426 /*tag= ad /note= "replace(424426, "cun")" 505507	/note= "replace(409411, "cun")" 421423 /*tag= ac /*tote= "replace(421423, "cun")"	eplace(406408, "agy"	/*tag= z /note= "replace(388390, "cun")" 406408	<pre>/*tag= y /note= "replace(385387, "cun")" 388390</pre>	/*tag= x /note= "replace(370372, "cgn")" 385387	/*tag= "replace(367369, "cgn")" /note= "replace(367369, "cgn")" 370372	/*tag= v /note= "replace(361363, "cgn")" 367369	/*tag= u /note= replace(328330, "cun")" 361363	/note= "replace(322324, "cgn")" 328330
Db 121 GGNGGNGGNGCNAAYCARGAYAAG Oy 241 TGGTCCCGCGGGCAGCGCCAAGATGGCC	Qy 121 AACCTCTCGGGCCCGGCGGGGGGGGGGGGGGGGGGGGGG	OY 61 ATGTACAGCATGATGATGAGAGACCGACCT : : : : : : : : Db 1 AUGUAYUCNAUGAUGAUGARACNGAYUU	Query Match Best Local Similarity 53.9%; Pred. Matches 237; Conservative 103; Mi	/note= ' /note= ' /note= ' /*tag= / /note= '	FT variation 10211023 FT /*tag= bh FT /note= "replace(1021 FT variation 10301032 FT /*tag= bi	variation 10091 /*tag= /note=	FT variation 1006.1008 FT variation /*tag= bf FT /note= "replace(1006	/note= variation 985.99 /*tag= /note=	variation 98298 /*tag=	variation	variation variation	variation	FT variation 934936 FT variation 94936 FT /*tag= ay /*occor= **replace(928	variation	FT variation 919.921 aw FT variation /*tag= aw	variation	variation	variation	FT variation 836838 FT /*tag= as //octo- "roolsoo/836 838
GGNGGNGGNGCNAARGCNAAYCARGAYAGRGUNAARAGRCCNAUGAAYGCNUUYAUGGUN 180 TGGTCCCGCGGCAGGCCGCAAGATGGCCCCAGGAGAACCCCAAGATGCACAACTCGGAG 300 : :	AACCTCTCGGGCCCGGCGGGGGGGGGGGGGGGGGGGGGG	ATGTACAGCATGATGATGAGACCGACCTGCACTCGCCCGGCGGGCG	; Score 292.2; DB 20; Length 1161; b; Pred. No. 2e-37; 103; Mismatches 100; Indels 0; Gaps	301032, "cun")" 841086, "agy")"	211023, "agy")"		.1008,	5 987. "Cgp")"	. 963,	.957,	5948, "agy")"	.939, "cun"	3930, "cun")"	921, "	.912, "agy"	. 909,		-	030

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RESULT 6
AADIII110
ID AADI
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XX Humma
XX Humma
XX Humma
XX Heim
XX Heim
XX Heim
XX Homc

The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can bused in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head
                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                                                                                                                                                                                                                                                                         Claim 57; Page 87; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES. (SLOK) SLOAN KETTERING INST CANCER (CORR) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-0489101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; SOX2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JAN-2001; 2001WO-US02015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD11110 standard; DNA; 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human SOX2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01d LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gure AO,
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RESULT 7
AAK52388
ID AAK5
XX AAK5
AC AAK5
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX O9-2
PF 05-F
XX O9-2
PF 19-3
PR 19-3
PR 19-5
PR 1
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99988
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Best Local
                                         Tang YT,
Zhao QA,
                                                                                                                                                    20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                      01-SEP-2000;
                                                                                                                                                                                                                                          20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                    03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                      05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                        (HYSE-)
                                                                                                                                                                                               15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1085 BP; 253 A; 348 C; 348 G; 136 T; 0 other;
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les 298; Conserv
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                                                                                                           HYSEQ
                  Liu C,
Wang D,
Yang Y,
                                                                                                                                                  2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-062325.
2000US-063325.
2000US-0693325.
2000US-0728422.
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                                                                                                           INC
                  Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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Pred. No. 4.1e-33
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                                         Chen
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Xue AJ,

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RESULT 8
AAK532A
ID AAK53
AC AAK52
XX AAK54
DT 06-N
DT 06-N
DE Huma
XX Hum
KW Hum
KW Vacc
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Best Local S
Matches 298
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                                                                                                  Human; cytokine;
vaccine; peptide
                                                                                                                                                 Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                          AAK53268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation
                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
               WO200157190-A2
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                                                                                                                                                                                                                                                                                                                                                                           AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCG
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                                                                       system
                                                                                                                                                                                                                                         standard; cDNA; 1116
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                                                                                                                                                                               (first entry)
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                                                                         factor; im
n disorder;
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                                                                   immunomodulatory; cancer, rimunomodulatory; cancer, rimunomodulatory; cancer, rimunomodulator;
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Pred. No. 4.1e-33;
0; Mismatches 56
                                                                                                                                                                                                                                          ΒP
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15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Zhao QA, Wang D,
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                       Sequence 1116 BP; 256 A; 362 C; 362 G; 136
                                                                                                                                                                                                                                                                                                                                                               Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listin were missing at the time of publication.
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les 298; Conserv
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                                                                                                                                              AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCCG
                                                                                                                                                                                             CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA
AGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA 262
                                                                                                                                                                                                                                              CGGGGGGGCGGCGGCAACTCCACCGCGGCGGCGGCGGCGGCAACCAGAAAAAACAGCC
                                               AGTGGAAGGTCATGTCCGAGGCCGAGAAGCGGCCGTTCATCGACGAGGCCAAGCGGCTGC
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2000US-0598075.
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2000US-0663561.
2000US-0693325.
2000US-0728422.
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D, Wang J, Zha
Wejhrman T,
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, Zhang J, Ren
n T, Goodrich R;
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Pred. No. 4.1e
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15-SEP-2000;
20-OCT-2000;
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Xue AJ,
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Zhao
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P-PSDB; AAM79151.
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27-APR-2000;
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                                                                                                                                                                                                           inflammation
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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CGGGGGGGGGGGGAACTCCACCGCGGGGGGGGGGGGGGAACCAGAAAAAACAGCC
                                                             cids encoding polypeptides with cytokine-like activities in diagnosis and gene therapy -
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
Wang D,
Yang Y,
                                                                                            Conservative
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2000US-0693325.
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2000US-0620325.
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                                                                                                                                          BP; 262 A; 361 C; 364 G; 139
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Wang J, Zhang J, Ren F, (
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA;
                                                                                                      52.9%;
                                                                                                                                                                                                                 leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
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Pred. No. 4.1e-33;
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                                                                                          Mismatches
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM830302) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may induc production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines o peptide therapy. The polypeptides have various cytokine-like activities e.g. stem cell growth factor activity, haematoppiesis regulating
    activity,
                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                     Nucleic
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DB; AAM80239.
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Wang D,
Yang Y,
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    tissue
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Wang J, Zhang J, Re
Wejhrman T, Goodrich
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                      genes
                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2002
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                                                                                                                                                                                                                  Ishikawa K,
                                                                                                                                                                                                                                                                   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
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DB; ABB57082.
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                                                                                                                                                                                                                  Asai S,
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                                                                                                                                                                                                                     Takahashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 264.4;
Pred. No. 4e-3
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                                                                                                                                                                                                                             Human; small cell lung cancer; therapy; hCAAP; nucleic acid; melanoma; cancer; colon; breast; head; neck; transitional car leimyosarcoma; synovial sarcoma; cytostatic; SOX3; ds.
                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                 Location/Qualifiers 441..1773
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82.9%;
                                                                                                                                                                                                                                                                                                                                                   cancer associated gene,
                              "Human SOX3 protein"
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No. 6.7e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a ChAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCIC-9, encoding human SOX3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded isolated nucleic acid comprising an NA Group 3 or 4 molecule -
1133
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                                                                                                                                      1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2509 BP; 456 A; 818 C; 757 G; 478 T; 0 other;
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Local Similarity 80.9%;
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                                CGGCCGGCGCGG 499
                                                                                                                                                    AGGCCAAGCGGCTGCGCGCGCGCATGAAGGAGCACCCGGATTACAAGTACCGGCCGC
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                                                                                                                                                                                                                                                                                                                                                                            GCGCCAAGGCCAACCAGGACCGGGTCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCC
CTCCCGGTGCCG
                                                                                                  GCCGCAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGCGGGCTCCTGG 487
                                                                                                                                      AGCGCTTGGGCGCCGACTGGAAACTGCTGACCGACGCCGAGAAGCGACCATTCATCGACG
                                                                                                                                                                                                                                                                         GCGGGCAGCGCCAAAATGGCCCTGGAGAACCCCCAAGATGCACAATTCTGAGATCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                            CC The invention relates to isolated polynucleotide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPCR) primers (II) is useful from the production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II), (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC afood supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations of the produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at figure in the printed constitution in the printed constitution.
                                                                                                                                            Query Match
Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 23542; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #23542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS87738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS87738 standard; cDNA; 2378
                                                                                                         93
CAGCAGCGGTGGTGCGAGCGGAGGTGGCGGGGGTACAG----
                                  CGGGGGCGGAGGCGGGGGGCGGCGGCGGCGGGGGCCCAAGGCCAACCAGGACCGGGT 212
                                                                      CCCGGGAGGCGCAGGCAAGAGTAGTGCGAACGCAGCCGGCGGCGGCGCAACTCGGGCGGCGG
                                                                                                      2001-639362/73
DB; ABG23551.
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upplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RT,
                                                                                                                                                                                                                  2378 BP; 590 A; 708 C; 664 G; 416 T; 0 other;
                                                                                                                                             Conservative
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                                                                                                                                                           49.0%;
78.7%;
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                                                                                                                                            0;
                                                                                                                                            Score 245.2; DB 23
Pred. No. 3.6e-30;
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                              DB 23;
                                                                                                                                             Indels
ACCCAGGACCGTGT
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RESULT 14
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The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a
                                                                                                                                                                                                                                        (LUDW-)
(SLOK )
(CORR )
                                                                                                           Claim
                                                                                                                             Isolated polypeptide, used to treat or characterized by expression of a hCAAP isolated nucleic acid comprising an NA
                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; small cell lung cancer; therapy; hCAAP; nucleic acid; melanoma; cancer; colon; breast; head; neck; transitional car leimyosarcoma; synovial sarcoma; cytostatic; SOX21; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human small cell lung cancer associated
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                                                                                                                                                                                                                                      LUDWIG INST CANCER RES.
SLOAN KETTERING INST CANCER RES.
CORNELL RES FOUND INC.
                                                                                                                                                                                 AAE05814.
                                                                                                         Page 100-105; 152pp; English.
                                                                                                                                                                                                                Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1167..1997
                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human SOX21 protein"
                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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                                                                                                                             e.g. cancer, is encoded Group 3 or 4 molecule -
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RESULT 15
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Best Local
11-APR-2000;
21-JUN-2000;
01-SEP-2000;
05-SEP-2000;
14-SEP-2000;
19-DEC-2000;
08-JAN-2001;
                                                                                                                                                                            Lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, medanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-10, encoding human SOX21 protein.
                                                                          11-APR-2001;
                                                                                           18-OCT-2001
                                                                                                             WO200177168-A2
                                                                                                                                                  tumour;
                                                                                                                                                         Human; cytostatic; antitumour;
                                                                                                                                                                                                29-JAN-2002
                                                                                                                                                                                                                  AAS61625;
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                                                                                                                                                                                                                                                                                1430 GAAGGACAAGTTCGCCTTCCCGGTGCCCTACGGCCTGGGCGGCGTGG
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ω
                                                                                                                                                                           small cell carcinoma antigen,
                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                              CATGAAGGAGCACCCGGATTACAAGTACCGGCGGCGCGCAAGACCCAAGACGCTGCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                lung cancer;
2000US-196780P.
2000US-213361P.
2000US-229763P.
2000US-230629P.
2000US-232565P.
2000US-257037P.
2001US-260796P.
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                                                                         2001WO-US11859
                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                    CDNA;
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Pred. No. 1.2e-27;
                                                                                                                                                                                                                                    ВP
                                                                                                                                                          lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 149;
                                                                                                                                                                            CDNA #166.
                                                                                                                                                          small cell
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                                                                                                                                                          cancer
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                                                                                                                                                         antigen;
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Search completed: October 10, Job time: 91 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel isolated lung small cell cancer antigen CC polynucleotides (I) and polypeptides (II) used in a method of detecting CC cancer in a patient. The method is optionally performed by CC utilising oligonucleotides (III), where the biological sample CC irom the patient is contacted with (III), detecting the amount of polynucleotide to (III) in the sample and comparing the CC amount of polynucleotide to a predetermined cut-off value and thereby CC determining cancer in a patient. (I), (II) or antigen-presenting cells CC expressing (II) is useful for stimulating and/or expanding T cells CC expressing (II) is useful for stimulating and/or expanding T cells CC specific for a tumour protein. The method comprises contacting T cells CC and/or expansion of the components under conditions to permit the stimulation CC and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of cancer in a patient. An CC isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. Ansolated A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.1
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung tumour polynucleotide and polypeptides useful in the
rapy diagnosis of cancer especially lung cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 180; 295pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer antigen coding sequences of the invention.
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                                                                                                                      255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 GATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCGA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGACCACGTCAAGCGGCCCATGAACGCCTTCATGGTGGTGGTCGCGGGCTCAGCGGCGCAA 74
                                                                                                                                                                                                                                    CGCCATGCACATGAAGGAGCACCCCGACTACAAGTACCGGCCGCGGCGCCAAGCCCCAAGAC
                                                                                                                                                                                                                                                                                                                                                        GTGGAAACTGCTCACAGAGTCGGAGAAGCGGCCGTTCATCGACGAGGGCCAAGCGTCTACG
                                                                                                                Wang T, Mohamath R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%;
84.1%;
                              2002, 14:28:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 220.8; DB 24; Length 412;
Pred. No. 2.7e-26;
0; Mismatches 47; Indels 0;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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   pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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   Issued_Patents_NA:*
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-08-860-635A-18
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US-08-468-579B-6
US-08-468-579B-2
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US-08-468-579B-2
US-08-468-577B-2
US-08-468-577B-5
US-08-468-577B-1
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US-08-33-35A-2
US-09-03-687A-1
US-09-03-687A-2
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US-09-03-687A-2
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8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.6	8.6	8.6	8.6	8.6	æ. 6	8.6	8.6	8.6	8.6	8.6
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Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 14, Appl	Sequence 1, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 8, Appli	Sequence 8, Appli

ALIGNMENTS

US-08-860-635A-20 Sequence 20, Application US/08860635A Patent No. 6143878 GENERAL INFORMATION: FILING DATE: 29 NOV-1995 ATTORNEY/AGENT INFORMATION: NAME: Didiglio, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 1098 TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343 TELEFAX: 516-742-4366 APPLICANT: Koopman, Peter APPLICANT: Goodfellow, Peter TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND TITLE OF INVENTION: USE IN THE REGENERATION OF NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: Scully, Scott, Murphy & Presser ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette FILING DATE: 29-MAY-1 CLASSIFICATION: 514 PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: APPLICATION NUMBER: US STATE: NY APPLICATION NUMBER: AU PM9714 FILING DATE: 29-NOV-1994 APPLICATION NUMBER: AU PM9835 FILING DATE: 05-DEC-1994 APPLICATION NUMBER: PCT/AU95/00799 FILING DATE: 29-NOV-1995 COUNTRY: COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: FastSEQ Version 1.5 U.S.A. IBM Compatible 29-MAY-1997 US/08/860,635A BONE OR CARTILAGE

INFORMATION FOR SEQ ID NO:

10981

SEQUENCE CHARACTERISTICS: LENGTH: 3923 base pair

MOLECULE TYPE:

TOPOLOGY: linear

nucleic acid 3923 base pairs

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US-09-281-476-20
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Best Local
                                                                                     APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/00799
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10981
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                        INFORMATION FOR SEQ ID NO:
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APPLICANT: Goodfellow, Peter
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF
NUMBER OF SEQUENCES: 21
CORRESSEONDENCE ADDRESS:
                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                            TELEX:
                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 400 Garden City Plaza CITY: Garden City
     LENGTH:
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3923 base pairs
                                                                              516-742-4366
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63.2%;
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-281-476-20
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US-08-196-016A-1
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Best Local Similarity
Matches 215; Conserv
           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1661 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SILVERSIDES, David W. APPLICANT: DANEAU, Isabelle M.F. APPLICANT: HOUDE, Alain TITLE OF INVENTION: SRY GENOMIC TITLE OF INVENTION: SEXING
                                                                                                   TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                      TELEFAX: 201
TELEFAX: 133521
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                                                                                                                                       NAME: JACKSON, David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                            APPLICATION NUMBER: US/08/196,016A FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                    201-343-1684
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                                                                                                                                                                                                                                                                                      PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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63.2%;
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Pred. No. 1.6e-22;
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                                                                                                                                                                                                                                                                     Version
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TOPOLOGY: linear

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                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1667 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                               1052 GGAGAGCAGCCAGGACCACGTCAAGCGACCCATGAACGCCTTCATTGTGTGTCTCGTGA 1111
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CHROMOSOME/SEGMENT: Y-chromosome,
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                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                     NAME: JACKSON, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                  FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON, David A.
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                             TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
                                                                                                                                                                                                                APPLICATION NUMBER:
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STRANDEDNESS
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             nucleic acid
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Pred. No. 2.1
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US-08-860-635A-18
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APPLICANT: Koopman, Peter
APPLICANT: Goodfellow, Peter
APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1098
TELECOMMUNICATION INFORMATION:
TELEOPHONE: 516-742-4343
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                                                                                                                                                                                                     APPLICATION NUMBER: US/08/860,635A FILING DATE: 29-MAY-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA: AU PM9714 APPLICATION NUMBER: AU PM9714
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                     APPLICATION NUMBER: AU PFILING DATE: 29-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 11530
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                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                     AU PM9835
                                                                                                                                PCT/AU95/00799
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Pred. No. 2.4e-20;
0; Mismatches 72
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RESULT 6
US-09-281-476-18
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APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/00799
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: D1G1g110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Koopman
APPLICANT: Goodfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koopman, Peter
APPLICANT: Goodfellow, Peter
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2249 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 CCGATTACAAGTACCAGCCCCGGCGGA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 CGGATTATAAATACCGGCCCCGGCGGA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Disaccine Medium Type: Disaccine
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Scully, Scott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 CCGCGGCGGCGGCCGGCAACCAGAAAAACAGCCCGGACCGCGTCAAGCGGCCCATGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2249 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 25.9%;
Local Similarity 67.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGCGCTGCACATGAAGGAGCACC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCACAACGCGGAGCTCAGCAAGACTCTGGGGCAAGCTCTGGAGGCTGCTGAACGAGAGCG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTGTCGGAGACGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGCCTTCATGGTGTGGGCGCAGGCTGCGCGCAGGAAGCTGGCAGACCAGTACCCGCATC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCCTTCATGGTGTGCTCCCGCGGGCAGCGCGCAAGATGGCCCAAGAAGACCCCCAAGA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAGAGACCCTTCGTGGAGGAGGCGGAGCGGCTGCGCGTGCAGCACAAGAAAAGACCACC 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18, Application US/09281476
o. 6316597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 Garden City Plaza
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                                                                                                                                                                                                                                                                                                                                          08/860,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/281,476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-239-276-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: US-09-281-476-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08239276 Patent No. 5840836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Rabin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                           APPLICATION NUMBER: 1
FILING DATE: 14-JUN-
PRIOR APPLICATION DATA:
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: OS-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                 SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          810 CCGATTACAAGTACCAGCCCCGGCGGA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                069
                                 FILING DATE:
                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 05-MAY-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGCGCTGCACATGAAGGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 CCATGCCCGTGCGCGTCAACGGCTCCAGCAAGAACAAGCCACACGTCAAGCGACCCATGA 629
                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                     ZIP: 10591-5144
                                                                                                                                                                                                                                                                                                                                                                     CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 CCGCGGCGGCGGCGGCAGCAGCAGAAAAAACAGCCGGGACCGGTCAAGCGGCCCATGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2249 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGATTATAAATACCGGCCCCGGCGGA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTTGTCGGAGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCCTTCATGGTGTGGGCGCAGGCTGCGCGCAGGAAGCTGGCAGACCAGTACCCGCATC 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabin, Daniel
                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                    Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                               UMBER: US 07/441,703
04-DEC-1989
                                                                                  14-JUN-1991
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67.8%;
                                                                                                                                                                                                                                                                    System 7.5
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                                                                                                US 07/715,181
US 07/312,543
                                                                                                                                                                                                                   US/08/239,276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 129.4; DB 4
Pred. No. 3.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                    1.4 Mb storage
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FILING DATE: 17-FEB-1989 ATTORNEY/AGENT INFORMATION: NAME: Kurt G. Briscoe

REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI

251.4-KGB

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TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
US-08-239-276-6
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Best Local Similarity 62.8%;
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5981700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (914) 332-1844 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                              STREET: 000
CITY: Tarrytown
CTATE: New York
TATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1255 CGTGGAG 1261
                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
APPLICATION NUMBER: US 07/872,646
                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTG 248
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
SOFTWARE: WordPerfect
                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                 10591-5144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08468579B
                                                                                                                                                                                                                                                                                                                                                                    E: Sprung Kramer Schaefer & Briscoe 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabin, Daniel
                                                                                                                                            06-JUN-1995
                 08-JUN-1992
                                                                                                                                                                                                                       System 7.5
                                                                                                                                                                   US/08/468,579B
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                                                                                                                                                                                                                                                            3.50 inch, 1.4 Mb storage
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Pred. No. le
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le-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (914) 332-1844 INFORMATION FOR SEQ ID NO: 6:
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FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1075 CCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCTTTGGATCTCGCTG 1134
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1255 CGTGGAG 1261
                                                  SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
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STRANDEDNESS: sing
TOPOLOGY: linear
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APPLICATION NUMBER: US/08/468,577B FILING DATE: O6-JUN-1995 CLASSIFICATION: 514
                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect
                                                                                                                                                                                  STREET: 660 Whit
CITY: Tarrytown
STATE: New York
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                                                                                                                                                                                                                   E: Sprung Kramer Schaefer & Briscoe 660 White Plains Road
                                                                                                                                                                                                                                                                                                                     Rabin,
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                                                                                                                                                                                                                                                                                      PANCREATIC ISLET CELL ANTIGENS OBTAINED BY MOLECULAR CLONING
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Pred. No. 1e-13;
0; Mismatches 92;
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                                                                                                                       1.4 Mb
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FILING DATE: 05-MAY-PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:

US 07/872,646

APPLICATION NUMBER: US 0 FILING DATE: 05-MAY-1994

US 08/239,276

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RESULT 10
US-08-239-276-2
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Patent No. 5840836
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 155;
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TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3243 nucleotides
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                  TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 10
                                                                                                                                    CORRESPONDENCE ADDRESS:
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REGISTION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
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                                                     COUNTRY:
                                                                                                       STREET:
                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                       RY: USA
10591-5144
                                                                     Tarrytown : New York
                                                                                                    E: Sprung Kramer
660 White Plains
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04-DEC-1989
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3.50 inch,
                                                                                                                    Schaefer & Briscoe
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1.4 Mb storage
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                                                                                               Sequence 2, Application US/08468579B
Patent No. 5981700
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.9%;
Best Local Similarity 60.2%;
Matches 147; Conservative
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STREET: 600
CITY: Tarrytown
CMARE: New York
                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                2040 CNCA 2043
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LENGTH: 5051 nucleotic
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILLING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                358 ACCA 361
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kurt G. Briscoe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: System 'SOFTHARE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          CGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGAAAATCCTTCAGGCCTTCCCCGACATGCATAACTCCAACATTAGCAAAATCTTA 1919
                                                                                                                                                                                                                                                                                                                                                                                     GGATCTCGCTGGAAATCAATGTCCAACCAGGAGAAGCAACCTTATTATGAAGAGCAGGCC
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                                          E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5051 nucleotides
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Pred. No. 2
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COMPUTER READABLE FORM:

10591-5144

COUNTRY:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

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                                                                                        US-08-468-577B-2
                                                                                                          RESULT 12
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                                                Sequence 2, Application US/08468577B
Patent No. 6001804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5051 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
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                                                                                                                                                                                                                                                                                                          1920
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APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
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APPLICATION NUMBER: US 0.
FILING DATE: 08-JUN-1992
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APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
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                                                                                                                                                                2040 CNCA 2043
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                                                                                                                                                                                                                                                                        298
                                                                                                                                                                                                                                                                                                                                           238 GGCGCCGAGTGGAAACTTTTGTCGGAGACGGAGAGGCGGCCGTTCATCGACGAGGCTAAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                 178 CGGCGCAAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/468,579B FILING DATE: O6-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
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REFERENCE/DOCKET NUMBER: MDI
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Local Similarity 60.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                ACCA 361
                                                                                                                                                                                                                                   CGGCTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAA 357
                                                                                                                                                                                                                                                                                                         GGATCTCGCTGGAAATCAATGTCCAACCAGGAGAAGCAACCTTATTATGAAGAGCAGGCC 1979
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   PANCREATIC ISLET CELL ANTIGENS
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Best Local S
Matches 147
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                1920
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-TEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: KUTT G. Briscoe
REGISTRATION NUMBER: 33,141
REGISTRATION NUMBER: 33,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-19
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                                                                                                                                                                                                                                                                                                  1800 AGCAGCGAGCCACACTTAAGCGACCAATGAATGCATTCATGGTTTGGGCAAAGGATGAG 1859
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PRIOR APPLICATION DATA:
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2040 CNCA 2043
                                                                                                                                                                                                                        1860 AGGAGAAAATCCTTCAGGCCTTCCCCGACATGCATAACTCCAACATTAGCAAAATCTTA 1919
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                                                                                                                                                                                                                                            178 CGGCGCAAGATGGCCCAAGGAGAACCCCCAAGATGCACTCGGAGGATCAGCAAGCGCCTG 237
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                                    358 ACCA 361
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 08-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 05-MAY-1994
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OPERATING SYSTEM: System
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/441,703 FILING DATE: 04-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 60.2 es 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5051 nucleotides
                                                                        CGGCTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAA 357
                                                                                                                                                GGATCTCGCTGGAAATCAATGTCCAACCAGGAGAAGCAACCTTATTATGAAGAGCAGGCC 1979
                                                                                                                                                                                    GGCGCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAG 297
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660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IUMBER: US 07/872,646
08-JUN-1992
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Pred. No. 2e-11;
0; Mismatches 97; Indels
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RESULT 13 US-08-239-276-5

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Patent No. 5840836
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1570 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KUIT G. BILSCOE
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (914) 332-1700
                    309 GCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGC 352
                                                                                                                                                                                                                             129 CCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCCGCGGGCAGCGGCGAGCGCCAAGAT 188
342 TCATCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGC 385
                                                                    283 GAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAGGAACAGGCTCTGCTGATCG-
                                                                                                      249 GAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGC 308
                                                                                                                                        223 CCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCTTGGATCTCGCTG
                                                                                                                                                                          189 GGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTG 248
                                                                                                                                                                                                              163 CCACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGAT 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: System
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                      141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (914)
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                   Score 80.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                               8; DB 2;
1.3e-09;
                                                                                                                                                                                                                                                                                  82;
                                                                                                                                                                                                                                                                                                                  Length 1570;
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Patent No. 5981700
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 14-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 08-JUN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rabin, Daniel TITLE OF INVENTION: PANCE TITLE OF INVENTION: OBTA
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                     309 GCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGC 352
                                                                                                                                                                                                                        129 CCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGAT 188
                                                       283 GAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAGGAACAGGCTCTGCTGATCG-
                                                                                                                                                                189 GGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 05-MAY-1994
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OPERATING SYSTEM: System
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                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                              CCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCTTGGATCTCGCTG
                                                                                                                                                                                                    CCACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGAT 222
                                                                                           GAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGC 308
                                                                                                                                                                                                                                                                         141;
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Kurt G. Briscoe
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14-JUN-1991
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06-JUN-1995
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NO: 5:
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                                                                                                                                                                                                                                                                                           16.2%;
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Pred. No. 1.3e-09;
0; Mismatches 82;
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342 TCATCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGC 385

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
PILING DATE: 17-FEB-1989
ATTORNEY, ACENT INFORMATION:
NAME: KURT G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE, DOCKET NUMBER: MDI 251.8-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPHONE: (914) 332-1844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1570 nucleotides
TURE: 1570 nucleotides
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US-08-468-577B-5
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Best Local Similarity 62.5.
7. 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/239,276
ETILING DATE: 05-MAY-1994
PRIOR APPLICATION UNMBER: US 07/872,646
ETILING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/715,181
ETILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/7441,703
PRIOR APPLICATION UNMBER: US 07/441,703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
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                         249 GAAACTTTTGTCGGAGACGGGGGGGGCGGTCATCGACGAGGCTAAGCGGCTGCGAGC 308
                                                                                            223 CCTGCAAGCCTTCCCAGACATGCACAACTCCAGCATCAGCAAGATCCCTTGGATCTCGCTG 282
                                                                                                                                           189 GGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCCGCCGAGTG 248
                                                                                                                                                                                       163 CCACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCCAAGGATGAGCGGAGGAAGAT 222
                                                                                                                                                                                                                                  129 CCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGCTCCCGCGGGCAGCGGCGCCAAGAT 188
283 GAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAGGAACAGGCTCTGCTGATCG- 341
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CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                              16.2%; Score 80.8; DB 3; Length 1570; 62.9%; Pred. No. 1.3e-09; ative 0; Mismatches 82; Indels 1
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Search completed: October 10, 2002, 17:33:01 Job time: 31.7333 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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BE672418

AI571299

AI480221

AI356682

AW055151
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AI566261
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AI971
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BI917204
               BE792833
BG827056
   BF305566
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AN094794 gal7f03 x
AW071909 ws56c10.x
AW131791 xt34f05.x
AW131791 xt06a10.x
AW131791 xt04600.x
BE206866 ba04909 y
BE677418 7a60e05.x
AI571299 tn44e04.x
AI480221 tm72905.x
AI356682 qy22a10.x
AW028031 ws63a01.x
AW028031 ws63a01.x
AW028031 ws63a01.x
AW028031 ws63a01.x
AI566261 tq70d10.x
BE792833 601584834
BG827056 602149106
BF305566 601489087
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BI917204 603181352
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408	408.2	415.4	417.4	417.4	421	430.6	430.8	435	435.4	435.4	439.8	440.2	441	441	441	443.6	444	445	451	452	453	454.2	459	459.4	462.4	463	463
			83.5		•		•					•		•	•	•	•			•	•	•	•		•	92.6	•
606	518	784	506	427	465	517	472	448	463	462	567	473	739	450	443	452	600	483	490	480	478	460	460	465	465	861	834
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BM083874	AW044044	BF305813	AW533022	AW615144	AW297711	AI112078	AI097136	AW131705	AI199308	BF512088	AI145897	AI990431	BF305922	AI052267	AI373018	AI631443	AI102567	AI421743	AI418146	AI146406	BF513177	AI292258	AW005368	AI146367	AI096977	BE795592	BE797259
BM083874 imageqc_6	٤	BF305813 601889179	JI-R-BUO-	AW615144 hg73e05.x		AI112078 UI-R-Y0-m	AI097136 qb60h04.x			8 UI-H-BW		AI990431 wt74c08.x		AI052267 oy58e06.x	AI373018 qz02g05.x	AI631443 wa89a09.x	AI102567 EST211856	3 tf39b01	AI418146 tf68e09.x	AI146406 ga06b04.x	7	AI292258 qm76c01.x	AW005368 wz85h12.x		AI096977 qb42c12.x	2 601589	BE797259 601587618

ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1 BF939816 SOURCE ORGANISM JOURNAL COMMENT REFERENCE FEATURES DEFINITION TITLE AUTHORS source nac81b12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3440614 3' similar to SW:SOX2_SHEEP P54231 TRANSCRIPTION FACTOR SOX-2. [1] ;contains TAR1.t1 TAR1 repetitive element ;, mRNA sequence.
BF939816 BF939816.1 GI:12357136 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 580)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (Dipublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov High quality sequence stop: 505. Location/Qualifiers Homo sapiens Immigra EST /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGB:3440614"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glibblastoma (pooled)"
/lab_host="DH10B"

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RESULT 2
B1917204
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ORIGIN
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 694)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                603181352F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245477 5',
                                                                                                                                                                                                                                                                                                                                                                           BI917204
                                                                                                                                                                                                                    Homo sapiens
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cDNA Library Preparation: Life Technologies, Inc.
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the Not I and Eco RI sites of the modified pT/T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
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COMMENT

DEFINITION rocas

A1094/94 509 bp mRNA linear EST 01-0CT-1998 qa17f03.x1 NCI_CGAP_Brn23 Homo sapitens coDA clone IMAGB:1687037 3' similar to 9b:X71136 SOX-10 PROTEIN (HUMAN);contains MER22.tl TAR1

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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11619 row: g column: 14
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/db_xref="taxon:9606"
/clone="IMAGE:5245477"
/clone_lib="NIR_MGC_121"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note this is a NIH_MGC Library."

1 others
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Pred. No. 7.7e-81;
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1 (Dases I to 509)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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Sonaldo, Ph.D.
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h quality sequence stop: 447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1687037"
/clone_1ib="NCI_CGAP_Brn23"
/tissue_type="911oblastoma (pooled)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 537)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 459.
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                                                                                                                   adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed
                                                                                                                                                                                                Ph.D.
                                                                                Soares and M.Fatima Bonaldo." 161 c 191 g 60 t
                                                                                                                                                                                                                                                                              /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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s (Pharmacia), digested with Not I and cloned into
  Score 499; DB 9;
Pred. No. 1.1e-80;
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                   Length 537;
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                                                                                                               Possible reversed clone: polyT not found Seq primer: -40UP from Gibco High quality sequence stop: 472.
                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
                                                                                                                                                                                                                                                                                                                                                                             Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
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  /clone_lib="NCI_CGAP_Brn50"
/tissue_type="medulloblastoma"
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                        /clone="IMAGE: 2619969"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michae.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 537)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAAACC
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                                                 wr06a10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480730 3's similar to gb:X71136 SOX-10 PROTEIN (HUMAN); mRNA sequence.
AI971611.1 GI:5768437
                                                                                                               AI971611
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/note="Organ: brain; vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from medulloblastoma tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is normalized. Library constructed by Bento Soares and M. Fatima Bonaldo. "a 165 c 196 g 62 t 2 others
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Pred. No. 1.1e-80;
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Ph.D., Michael

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FEATURES
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ATGGACAGTTACGCGCACAT 500
                                                   AATAGCATGGCGAGCGGNGTCGGGGTGGGCGCGGCCTGNGCGCGGGGGGGGAACCAGCGC
                                                                                                      AATAGCATGGCGAGCGGGGTCGGGGTTGGGCCCCGGGCCTGGGCGCGTGAACCAGCGC
                                                                                                                                                                                                         AAGACGCTCATGAAGAAAGGATAAGTACACGCTGCCCGGCGGCCTGCTGGCCCCCGGCCGC
                                                                                                                                                                                                                                                               CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACC
                                                                                                                                                                                                                                                                                         CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGCGGAAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo,
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primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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Pred. No. 1.7e-80;
Pred. matches 2; Indels
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                                                                                                                  GCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGG
                                      CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACC
                                                                                                                                                                                             CGCAAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGC
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CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACC
                                                                            GCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGG
                                                                                                                                                           CGCAAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Seq primer: -40RP from Gibco
High quality sequence stop: 518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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//lab_host="DH108" (phage-resistant)"
//note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECCRI; cDNA made by oligo-dT priming. Directionally
cloned into EccRLYXhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 205 c 231 g 69 t
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/clone=lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 728)
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BE672418.1 GI:10032959
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                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ?. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                              162
                                                                  Conservative
                                                                                                                                       /note-"vector: p1773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1250631, 1469064-1470983, and 147592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "a Subtraction by Bento Soares and M. Fatima Bonaldo."
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/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3223136"
                                                                              99.4%;
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Insert Length: 1184 Std Error: 0.00
Seq primer: -400P from Gibco
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1 (bases 1 to 507)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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                                                                                                                                                                                                                                                                                  CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:2170494"
/clone_lib="NCI_CGAP_Brn25"
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                                                                                                                                                                                                                            tm72g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163704 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN); contains TAR1 repetitive element; mRNA sequence.
A1480221
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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(CGAP/BTGAP), Tumor Gene Index
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the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
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/lab_host="DH10B"
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Pred. No. 3.3e-80;
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                                                                        AATAGCATGGCGAGCGGGGTCGGGGTGGGCGCGGCCTGGGCGCGGGCGTGAACCAGCGC 480
                                                                                                          AAGACGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGGCTGCTGGCCCCCGGCGGC
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Insert Length: 740 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Hento Soares and M.Fatina Bonaldo."

3 162 c 188 g 60 t 3 others
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/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 5.1e-80;
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                                                AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGTGGTCCCGCGGGCAGCGG
                                                                                AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGTCCCCGCGGGCAGCGG 180
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 965)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (Dipublished (1998)
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965 bp mRNA linear EST 15-FEB-1999
gy22a10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2012730 3'
similar to gb:X71136 SOX-10 PROTEIN (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Insert Length: 1190 Std Error: 0.00
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/clone=lib="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 1.2e-78;
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Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/lmage.html
Insert Length: 1352 Std Error: 0.00
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High quality sequence stop: 501.
Location/Qualifiers
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                   adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

192 c 214 g 64 t 4 others
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/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
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1 (bases 1 to 485)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (DGAP/BTGAP), Tumor Gene 
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Insert Length: 1189 Std Error: 0.00
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Best Local
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                                                                                                                                                                                                                                                                                                                                              GGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGCGCTGCACATGAA
                                                                                                                                                                                              CGGGGTGGGCGCCGGCCTNGGCGCGGGCGTGAACCAGCGCATGGACAGTTACGCGCACAT
                                                                                                                                                                                                                                                                                               GGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACCAAGACGCTCATGAAGAAGGA
                                                                                tq70d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2214163 3' similar to gb:X71136 SOX-10 PROTEIN (HUMAN);contains MER22.t1 TAR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco High quality sequence stop: '
Mammalia; Eutheria;
1 (bases 1 to 514)
                                   Homo sapiens
                                                             EST
             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                       AI566261.1 GI:4524713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 479; DB 9;
Pred. No. 4.5e-77;
             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominldae; Homo.
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Best Local :
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       387
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                                     CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAAACC
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   GCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGG
                                                                                                                                                                                                                                                                                                                   AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCCGCGGGCAGCGG
                                                                                                                                                                                                                                                                                                                                               ACTTCGGGGGCGGCGGCGAACTCCACCGCGGCGGCGGCGGCGGCAACCAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                   CACAGCGCCCGCATGTACAACATGATGGAGACGGAGCTGAAGCCGCCGGGCCCGCAGCAA
                                                                      CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGGCGGAAAACC
                                                                                                                                                                                                                                                                                AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGTGCCCGCGGGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1142 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
//lab_host="hH10B (phage-resistant)"
//lab_host="hH10B (phage-resistant)"
//note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastatic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1e-76;
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467; Conserv
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High quality sequence stop: 740.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BE792833.1 GI:10214031
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    158 a
                                                                                                                                                                                                                                          ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3939033"
/clone_lib="NIH_MGC_7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                93.4%;
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421 AATAGCATGGCGAGCGGGGTCGGGGTGGGCGCCGGCCTGGGCGCGGGCGTGAACCAGCGC
                               214 AACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTGTCGGAGACGGAGAAG 273
                                                                                                     121 TTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCAC
                                                                                                                                                                                                                                                                                                94 GCGGCGGCCGGCAACCAGAAAAACAGCCCGGACCGCGTCAAGCGGCCCATGAATGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                              34 GAGCTGAAGCCGCCGGGCCCGCAGCAAACTTCGGGGGGGCGGCGGCGGCAACTCCACCGCG
                                                                                                                                                                                                                                                                                                                                                               TTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCAC 213
GCGGCGGCCGGCAACCAGAAAAACAGCCCGGACCGCGTCAAGCGGCCCATGAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM787 row: d column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: lung; Vector: pOTB); Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAC(G). Size-selected >500bp for average insert size 1.8kb Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: xho1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 467; DB IV,
Pred. No. 6.8e-75;
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Searc Job t	DЬ	Qy	Db	Qy	В	Qy	ф	Qy	DЪ
Search completed: October 10, 2002, 20:27:13 Job time: 702.733 secs	421 GGCCTGGGCGCGGGCGTC	454 GGCCTGGGCGCGGCGTC	361 CCCGGCGGGCTGCTGGCC	394 CCCGGCGGGCTGCTGGCC	301 TATAAATACCGGCCCCGG	334 TATAAATACCGGCCCCGC	241 CGGCCGTTCATCGACGAC	274 CGGCCGTTCATCGACGAC	181 AACTCGGAGATCAGCAAG
0, 2002, 20:27:13	421 GGCCTGGGCGCGGGCGTGAACCAGCGCATGGACAGTTACGCGCACAT 467	GGCCTGGGCGCGGGGTGAACCAGCGCATGGACAGTTACGCGCACAT 500	CCCGGCGGCTGCTGCCCCCGGCGGCAATAGCATGGCGAGCGGGGTCGGGGTGGGCCC	- ()	TATAAATACCGGCCCGGGGAAAACCAAGACGCTCATGAAGAAGGATAAGTACACGCTG 360	TATAAATACCGGCCCCGGCGGAAAACCAAGACGCTCATGAAGAAGGATAAGTACACGCTG	ы.	CGGCCGTTCATCGACGAGGCTAAGCGGCTGCGACGCTGCACATGAAGGAGCACCCCGAT	181 AACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTGTCGGAGACGGAGAAG
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Listing first 45 summaries
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(LUDW-) LUDWIG INST CANCER RES (SLOK ) SLOAN KETTERING INST CANCELL RES FOUND INC.
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                                                                                                                          2000US-0489101.
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ALIGNMENTS

Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; SOX2; ds. AAD11110 standard; DNA; 1085 BP 19-JAN-2001; 2001WO-US02015. WO200153349-A2 Human small cell lung cancer associated gene, SOX2 (first entry) Location/Qualifiers 13..966 /*tag= a /product= "Human SOX2 protein"

CANCER RES

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           AAK52388 standard; cDNA; 1087 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 57; Page 87; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by isolated nucleic acid comprising an NA Group 3 or 4 molecule -
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27-APR-2000;
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           121 AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGTGCCCGCGGGCAGCGG
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                                   500;
                                                                                                                                              Similarity
                                                                                                                                  Conservative
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                       Sequence 1087 BP; 250 A; 346 C; 357 G; 134 T; 0 other;
                                                                                                                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3064-3066; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                  reatment of cancer, leukaemia, nervous system disorders, arthritis and
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Yang Y, Wejhrman T,
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2000US-0598075.
2000US-0620325.
2000US-0654936.
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2000US-06633561.
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2000US-0728422.
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Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy
Score 500; DB 22;
Pred. No. 7.6e-95;
'· wismatches 0;
                                                                                                                                                                                                              2111
from
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the sequence 1
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
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15-SEP-2000;
20-OCT-2000;
                                                                                                                                             Tang YT,
Zhao QA,
Xue AJ,
                 Claim 1;
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                                              Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                                                                                                                                 (HYSE-)
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DB; AAM80135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                 HYSEQ INC.
                                                                                                                                           Liu C,
Wang D,
Yang Y,
               Page 4995; 6221pp; English
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2000US-0560875.
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2000US-0620325.
2000US-0654936.
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              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                 AAK52284 standard;
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                                                                                             polynucleotide SEQ ID NO 829.
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(first entry)

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Query Match
Best Local
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ATGGACAGTTACGCGCACAT 526
                                              ATGGACAGTTACGCGCACAT 500
                                                                                                  AATAGCATGGCGAGCGGGTCGGGGTGGGCGCGCGCGGGCGTGAACCAGCGC
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Pred. No. 7.7e-95;
, Mismatches 0;
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27-APR-2000;
20-JUN-2000;
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15-SEP-2000;
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     CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAAATACCGGCCCCGGCGGAAAACC
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DB; AAM79151.
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in diagnosis and gene therapy -
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
Wang D,
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2000US-0560875.

2000US-0598075.

2000US-0620325.

2000US-0654936.

2000US-0654936.

2000US-0693325.

2000US-0728422.
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F, (
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from
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R, Wang
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AAK537 66-N
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XX O6-N
AXX Huma
DE Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; pert'
                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell polyliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activinty, tissue growth factor activity, haematopoissis resultiving and activity and may be useful in the diagnostis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
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tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 2901.
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 5070; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAM80239
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27-APR-2000;
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   inflammation
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, Wang D,
Yang Y,
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2000US-0654936.
2000US-0663561.
2000US-0693325.
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2000US-0560875.
2000US-0598075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation; cell differentiation; gene therapy;
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R, Wang
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                                                                                                                                                                                                                                                                                                                                                                                              Mouse ischaemic condition related cDNA sequence SEQ ID NO:179
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABI99318 standard; cDNA; 2283
                                                                                                                                                                                                                                    WO200188188-A2
                                                                                                                                                                                                                                                                                                                          vasospastic
                                                                                                                                                                                                                                                                                                                                                    Mouse; ischaemia;
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                                                                                                                                          18-MAY-2001;
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                                                (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
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                                                                                                                                                                                                                                                                                                                                 ischaemia; ischaemic
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    Asai
                                                                                                                                             2001WO-JP04192
s,
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         Takahashi Y,
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         Nagata
            Η,
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            Υ;
                                                                                                                                                                                                                                                                                                                                 disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive is chaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB573700 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The capression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 chapter are used in the exemplification of the present invention.
                                                   Ъ
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Best Local :
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2283 BP; 597 A; 583 C; 614 G; 488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                          410
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830
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-034733/04.
                                                                                                                                                                                                                     CTGGGCGCCGAGTGGAAACTTTTGTCGGAGAGCGGAGAAGCGGCCGTTCATCGACGAGGCT
                                                                                                                                                                                                                                                                           CAGCGGCGTAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGC
                                                                                                                                                                                                                                                                                          CAGCGGCGCAAGATGGCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGC
                                                                                                                                                                                                                                                                                                                                               AAAAACAGCCCGGACCGCGTCAAGCGGCCCCATGAATGCCTTCATGGTGTGGTCCCGCGGG 174
                                                                                                                                                                                                                                                                                                                                                                                        468;
                                                                                                                                                              AAGAACAGCCCGGACCGCGTCAAGAGGCCCCATGAACGCCTTCATGGTATGGTCCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTCGGGGGGGGGGGCGGC------GGCAACTCCACCGCGGCGGCGGCGGCGGCAACCAG
                                                                  GCCGCCAATAGCATGGCGAGCGGGGGTCGGGGTGGGCGCCCTGGGCGCGCGGGCGTGAAC
                                                                                                        CAGCGCATGGACAGTTACGCGCACAT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page
CAGCGCATGGACAGCTACGCGCACAT
                                                    GCCGCGAACAGCATGGCGAGCGGGGTTGGGGTGGGCGCCCGGCCTGGGTGGCGGGCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB57082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518-521; 2690pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.6%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 432.8; DB 2
Pred. No. 6.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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RESULT 7
AAS61666
ID AAS6

AAS61666 standard;

cDNA;

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Best Local S
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01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                              determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AsSG1460-AsSG1874 represent novel human lung small cell cancer antigen coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide by the polynucleotide to (III) in the sample and comparing the part of polynucleotide to a predetermined cut-off value and thereby amount of polynucleotide to a predetermined cut-off value and thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung tumour polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer \,
                                                                                                                                                                                                                                                                     Sequence 395 BP; 83 A; 128 C; 144 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 192; 295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-010896/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200177168-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; antitumour; lung small cell cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS61666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2001; 2001WO-US11859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung small cell carcinoma antigen, cDNA #207.
                                  121
                                                                  106
                                                                                                                                  46
                                                                                                    61
                                                                                                                                                                  1 CACAGCGCCCGCATGTACAACATGATGGAGACGGAGCTGAAGCCGCCGGGCCCGCAGCAA 60
                AGCCCGGACCGCCTCAAGCGGCCCATGAATGCCTTCATGGTGTGGGTCCCGCGGGCAGCGG 180
                                                                                                                                ACTTCGGGGGGCGGCGGCGGCAACTCCACCGCGGCGGCGGCGGCGGCGGCAACCAGAAAAAAC 120
AGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGG
                                                                  l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang T,
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-196780P.
2000US-213361P.
2000US-229763P.
2000US-230629P.
2000US-232565P.
2000US-257037P.
2001US-260796P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mohamath R,
                                                                                                                                                                                                                 70.0%;
                                                                                                                                                                                                    0;
                                                                                                                                                                                                                   Score 350;
Pred. No.
                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                 8.1e-64;
                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                   Length 395;
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RESULT 8
AAX16.151
ID AAX1
AAX16.151
XX AAX1
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                                                population. The method comprises: (a) detecting Sox1 gene expression in the cells; and (b) isolating those cells expressing Sox1. Also described is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Sox1 expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence encodes human Sox1. Detection of Sox1 expressing cells is important in diagnosing and treating cancers of the neurological disorders, especially for repair of accidentally induced trauma in the CNS or for correction of congenital or pathological diseases of the CNS. A patient with a neurological disorder can act as a self-donor. Cells may be isolated from the patient and either sorted to extract neuronblasts or treated in order to differentiate neuronblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolating neuroblastic cells from a population - by detecting the expression of the Sox1 gene in the cells and sorting the cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Sox1; neuronal stem cell gene; neuroblastic cell; cancer; nervous system; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Sox1 encoding cDNA
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extract neuroblasts, or treated in order to differentiate neuroblasts, from specific or general precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A method has been developed for isolating neuroblastic cells from a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lovell-Badge R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9900516-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolate those cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW94461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATACCGGCCCCG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGAGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGACGAGGCTAAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 45-47; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note = "specifically claimed Sox1 control sequence" 60..1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pevny LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/product= "Sox1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressing Sox1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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SS X

Sequence 1542 BP;

238 A; 565 C; 560 G; 179 T; 0 other;

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RESULT 9
AADILI11
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AADILIX
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Best Local Simi
Matches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; small cell lung cancer; therapy; hCAAP; nucleic acid; melanoma; cancer; colon; breast; head; neck; transitional can leimyosarcoma; synovial sarcoma; cytostatic; SOXI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human small cell lung cancer associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD11111 standard; DNA;
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WPI; 2001-457597/49
P-PSDB; AAE05811.
                                                                                                                                                                                                         21-JAN-2000; 2000US-0489101.
                                                                                                                                                                                                                                                       19-JAN-2001; 2001WO-US02015.
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                                                                      Stockert E,
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                                                                                                               LUDWIG INST CANCER RES.
SLOAN KETTERING INST CANCER
CORNELL RES FOUND INC.
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                                                                      Scanlan
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 61..1224
                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Human SOX1 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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Pred. No. 4.5e-49;
0; Mismatches 80;
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RESULT 10
AAX16152
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Best Local S
Matches 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onest of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-2, encoding human SOX1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded isolated nucleic acid comprising an NA Group 3 or 4 molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4091 BP; 924 A; 1109 C; 1110 G; 943 T; 5 other;
                                                                                                                                                                                                                                Chicken Sox1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                             AAX16152 standard; cDNA to mRNA;
                                                                                                                                             nervous
                                                                                                                                                                                                                                                                                              22-APR-1999 (first
                                                                                   Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 CGGGGGGCGCCGCCAACTCCACCGCGGCGGCGGCCGGCGGCAACCAGAAAAAAACAGCC 124
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                                                                                                                                             system;
                                                                                                                                             Sox1; neuronal stem cell gene; neuroblastic cell; cancer;
system; neurological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                   2312
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Best Local S
Matches 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Soxl expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence represents chicken Soxl cDNA. Detection of Soxl expressing cells is important in diagnosing and treating cancers of the nervous system. Neural stem cells are useful for the treatment of neurological disorders, especially for repair of accidentally induced trauma in the CNS or for correction of congenital or pathological diseases of the CNS. A patient with a neurological disorder can act as self-donor. Cells may be isolated from the patient and either sorted to extract neuroblasts, or treated in order to differentiate neuroblasts, from specific or general precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolating neuroblastic cells from a population - by detecting the expression of the Sox1 gene in the cells and sorting the cells to isolate those cells expressing Sox1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           population.
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                                                                                                                                                                                                                                                                                                          222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 GCCGCCGGGCCAGCAAACTTCGGGGGGGGGGGGGGGGGAACTCCACCGCGGCGGCGGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ethod has been developed for isolating neuroblastic cells from a cell ulation. The method comprises: (a) detecting Sox1 gene expression in cells; and (b) isolating those cells expressing Sox1. Also described
CGTCGGCGTGATCCCCGGC
                                                                                                                                                     | CGGCCCCGGCGGAAAACCAAGACGCTCATGAAGAAGGATAAGTACACGCTGCCCGGCGG
                                                                                                                                                                                                                     CATCGACGAGGCTAAGCGGCTGCGAGCGCTGCACATGAAGGAGCACCCGGATTATAAATA 341
                                                                                                                                                                                                                                                                                          GATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTGTCGGAGAAGACGGAGAAGCGGCCGTT 281
                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCGGCAACCAGAAAAACAGCCCGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGT 161
                                 CGCGGGCGTGAACCAGCGC
                                                              GCTGCTGG----GCGCCGGGCCGGCCGGCGGGCGGCCTCCCGCCGTCGGCGTGGGCATGGG
                                                                                              GCTGCTGGCCCCCGGCGGCAATAGCATGGCGAGCGGGGTCGGGGTGGGCGCCGGCCTGGG
                                                                                                                                 CCGGCCCCGGCGGAAGACCAAGACGCTGCTCAAGAAGGACAAGTACTCGCTGGCCGGAGG
                                                                                                                                                                                                   CATCGACGAGGCGAAGCGGCTGCGGGCGCTGCACATGAAGGAGCACCCGGATTATAAATA
                                                                                                                                                                                                                                                                     GATCAGCAAGCGGCTGGGCGCCGAGTGGAAGGTGATGTCGGAGGCCGAGAAGCGGCCTTT
                                                                                                                                                                                                                                                                                                                                       GTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCCAGGAGAACCCCCAAGATGCACAACTCGGA 221
                                                                                                                                                                                                                                                                                                                                                                                                         CGGCGGCGGGGCAAAGCGGGGCAGGACCGCGTGAAGCGCCCCATGAACGCCTTCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2312 BP; 421 A; 739 C; 714 G; 438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 41-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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77.0%;
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694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 266.2; DB Pred. No. 2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       population. The method comprises: (a) detecting Sox1 gene expression in the cells; and (b) isolating those cells expressing Sox1. Also described is a method for producing a cell committed to the neuronal lineage, comprising; (a) transfecting a pluripotent stem cell with a genetic construct encoding Sox1 expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells
                                                                                                                                                                                                                                                                                                                                             produced. The present sequence represents mouse Soxl cDNA. Detection of Soxl expressing cells is important in diagnosing and treating cancers of the nervous system. Neural stem cells are useful for the treatment of neurological disorders, especially for repair of accidentally induced trauma in the CNS or for correction of congenital or pathological diseases of the CNS. A patient with a neurological disorder can act as self-donor. Cells may be isolated from the patient and either sorted to extract neuroblasts, or treated in order to differentiate neuroblasts,
                                                                                                                                                                                                                                                                                                  Sequence 2376 BP; 439 A; 772 C; 745 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolating neuroblastic cells from a population - by detecting the expression of the Sox1 gene in the cells and sorting the cells to isolate those cells expressing Sox1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method has been developed for isolating neuroblastic cells from a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 43-44; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; Sox1; neuronal stem cell gene; neuroblastic nervous system; neurological disorder; ss.
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AGTGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGC
                                            CGGACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCA 184
                                                                             AGATGGCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCG
                                                                                                                                                                        CGGGGGGCGGCGGCAACTCCACCGCGGCGGCGGCGGCGGCAACCAGAAAAAACAGCC
                                                                                                                                                                                                                                                                                                                                 specific or general precursors.
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Pred. No. 2e-45;
0; Mismatches 91;
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             The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a hCAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is a small cell lung cancer associated gene designated as NY-SCLC-9, encoding human SOX3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer leimyosarcoma; synovial sarcoma; cytostatic; SOX3; ds.
                                                                                                                                                                                                                                                                            Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encode isolated nucleic acid comprising an NA Group 3 or 4 molecule
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                                                                                                                                                                                                                                                Claim
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                2001-457597/49
                                                                                                                                                                                                                                               57; Page 98-99; 152pp; English.
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RESULT 13
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                                                                                                                                                                                                                                             Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer leimyosarcoma; synovial sarcoma; cytostatic; SOX21; ds.
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                                                                                                                                                                                                                                                                                           Human small cell lung cancer associated gene, SOX21.
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                    (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER (CORR ) CORNELL RES FOUND INC.
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 Stockert E,
                                                                   21-JAN-2000; 2000US-0489101.
                                                                                          19-JAN-2001; 2001WO-US02015
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es 318; Conserv
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 Scanlan MJ,
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73.3%;
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Jager D,
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Pred. No. 6.5e-40;
0; Mismatches 107;
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of a CAAP, and determine regression, progression or onset of a condition characterised by expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders are small and non-small cell lung cancer melanoma, colon, breast, head The present sequence is a small cell lung cancer associated gene
          DNA encoding novel human diagnostic protein #23542
                                               13-FEB-2002
                                                                                                          AAS87738 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encode isolated nucleic acid comprising an NA Group 3 or 4 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                      307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated as NY-SCLC-10, encoding human SOX21 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GGGGGCGGCGGCAACTCCACCGCGGCGGCGGCGGCAACCAGAAAAAACAGCCCG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCGCGTCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAG
                                                                                                                                                                                                                              GACAGTTACGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAAACTTTTGTCGGAGACGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGA 306
                                                                                                                                                                                             GTGCCTGAGTCGC
                                                                                                                                                                                                                                                       GCCGAGCACCCTGCGCTCAAGGCGGGGGGGCGGCGGCGGCGGCGGCGGCGGCCTG
                                                                                                                                                                                                                                                                                  AGCATGGCGAGCGGGGTCGGGGTGGGCGCGCGCGGGCGTGAACCAGCGCATG 483
                                                                                                                                                                                                                                                                                                                                               CTCATGAAGAAGGATAAGTACACGCTGCCCG---GCGGGCTGCTGGCCCCCGGCGGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTGCACATGAAGGAGCACCCGGGATTATAAATACCGGCCCCGGCGGGAAAACCAAGACG
                                                                                                                                                                                                                                                                                                                    CTCCTCAAGAAGGACAAGTTCGCCTTCCCGGTGCCCTACGGCCTGGGCGGCGTGGCGGAC
                                                                                                                                                                                                                                                                                                                                                                                 GCCATGCACATGAAGGAGCACCCCGACTACAAGTACCGGCCGCGGCGCAAGCCCAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCTTGGGCGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCCCCAGGAGAACCCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGGCCCGGGCGGCGGCTGCAGCCGGCGGCAGGGCGAGAGCATGTCCAAGCCGGTG 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAAACTGCTCACAGAGTCGGAGAAGCGGCCGTTCATCGACGAGGCCCAAGCGTCTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 100-105; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates
                                                                                                                                                                                                                            496
                                                                                                                                                                                             1554
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71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to nucleic acids and encoded
                                                                                                            2378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 225;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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7.5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (II) is useful as hybridisation probes, CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC control of (II) is useful activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical considers involving aberrant protein expression or biological activity. CC The polypeptide and polypucleotide sequences have applications in CC diagnostics forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at figure at the invention.
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 23542; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                733
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266 CGGAGAAGCGGCCGTTCATCGACGAGGCTAAGCGGCTGCGAGCGCTGCACATGAAGGAGC
                                                                                                                                                                                                                      87 CACCGCGGCGGCCGGCGGCAACCAGAAAAACAGCCCGGACCGCGTCAAGCGGCCC-A 145
                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 334; Conserv
                                                         AGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAACTTTTGTCGGAGA
                                                                                                                                      TGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCCAAGAAACCCCCA
                                                                                                                                                                                               AGCGGTGGTGCGAGCGGAGGTGGCGGGGGTACAGACCCCAGGACCGTGTGAAACGGCCCAA
                                                                                                                                                                                                                                                                            GGAGGCGCAGGCAAGAGTAGTGCGAACGCAGCCGGCGCGCGAACTCGGGCGGCGGCAGC
                                                                                                                                                                                                                                                                                                                 AGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCCGCCGACTGGAAACTGCTGACCGACG
                                                                                                                   TGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGCGCCAAAATGGCCCCCGGAGAACCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2378 BP; 590 A; 708 C; 664 G; 416 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                           44.0%;
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                                                                                                                                                                                                                                                                                                                                                      Score 220; DB 23;
Pred. No. 7.5e-37;
0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                           Length 2378;
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325
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RESULT 15
AAS61625
ID AAS61
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              The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for the cells.
                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000US-196780P.
21-JUN-2000; 2000US-213361P.
01-SEP-2000; 2000US-229763P.
05-SEP-2000; 2000US-230629P.
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19-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; antitumour; lung small cell cancer antigen;
tumour; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung small cell carcinoma antigen, cDNA #166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang T,
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2000US-229763P.
2000US-230629P.
2000US-232565P.
2000US-257037P.
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immune response in a patient and for
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lung cancer -
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                       (I) is useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells fi biological sample and for inhibiting the development of cancer in patient. AAS61460-AAS61874 represent novel human lung small cell cancer antigen coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 412 BP; 83 A; 133 C; 144 G; 51 T; 1 other;
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